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(71) Applicant *(for all designated States except US)*: **THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR DISEASES CONTROL AND PREVENTION** [US/US]; Technology Transfer Office, 4770 Buford Highway (K79), Atlanta, GA 30341 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **CHANG, Gwong-Jen, J.** [US/US]; 4237 Beaver Creek Drive, Ft. Collins, CO 80526 (US). **CRILL, Wayne, D.** [US/US]; 1121 Akin Avenue, Fort Collins, CO 80521 (US).

(74) Agent: **CASH, David**; Klarquist Sparkman, LLP, Suite 1600, One World Trade Center, 121 Southwest Salmon Street, Portland, OR 97204 (US).

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(54) **Title:** LOCALIZATION AND CHARACTERIZATION OF FLAVIVIRUS ENVELOPE GLYCOPROTEIN CROSS-REACTIVE EPITOPES AND METHODS FOR THEIR USE

(57) **Abstract:** Disclosed herein is a method for identifying flavivirus cross-reactive epitopes. Also provided are flavivirus E-glycoprotein cross-reactive epitopes and flavivirus E-glycoprotein crossreactive epitopes having reduced or ablated cross-reactivity (and polypeptides comprising such epitopes), as well as methods of using these molecules to elicit an immune response against a flavivirus and to detect a flaviviral infection.

LOCALIZATION AND CHARACTERIZATION OF FLAVIVIRUS ENVELOPE GLYCOPROTEIN CROSS-REACTIVE EPITOPES AND METHODS FOR THEIR USE

PRIORITY CLAIM

This application claims the benefit of U.S. Provisional Patent Application No. 60/591,898 filed July 27, 2004, which is incorporated herein by reference in its entirety.

STATEMENT OF GOVERNMENT SUPPORT

This invention was made by the Centers for Disease Control and Prevention, an agency of the United States Government. Therefore, the U.S. Government has certain rights in this invention.

FIELD

This disclosure relates to a structure-based rational mutagenesis method for identifying flavivirus envelope (E)-glycoprotein cross-reactive epitopes. The disclosure further relates to flavivirus E-glycoprotein cross-reactive epitopes and mutants thereof having reduced or ablated cross-reactivity. Flavivirus cross-reactive E-glycoprotein epitopes with reduced or ablated cross-reactivity are useful in the diagnosis, inhibition and treatment of diseases caused by flaviviruses.

BACKGROUND

The *Flaviviridae* are a diverse family of enveloped viruses infecting both arthropods and vertebrates. Flaviviruses have a positive-sense single-stranded RNA genome 10.7 kb in length, transcribed into a single polyprotein precursor encoding three structural proteins, capsid, premembrane (prM), envelope (E), and seven non-structural proteins (Lindenbach & Rice, *Flaviviridae: the viruses and their replication.* In *Fields Virology*, 4th ed., Knipe and Howley. Eds., Philadelphia, Lippincott Williams & Wilkins, pp. 991-1041, 2001; Rice *et al.*, *Science* 229:726-33, 1985). The flavivirus E-glycoprotein is the primary antigen, inducing protective immunity; it is essential for membrane fusion, and mediates binding to cellular receptors (Allison *et al.*, *J. Virol.* 75:4268-75, 2001; Crill & Roehrig, *J. Virol.* 75:7769-73, 2001; Rey *et al.*, *Nature* 375:291-98, 1995). Flavivirus E-glycoprotein therefore directly affects host range, tissue tropism, and the virulence of these viruses.

The flavivirus E-glycoprotein contains three structural and functional domains. Domain I (DI) is an 8-stranded β-barrel containing two large insertion loops that form the elongated finger-like domain II (DII) (Rey *et al.*, *Nature* 375:291-98, 1995). DII is involved in stabilizing the E-glycoprotein dimer and contains the internal fusion peptide (Allison *et al.*, *J. Virol.* 75:4268-75, 2001). Domain III (DIII) forms a ten-stranded β-barrel with an immunoglobulin-like fold and contains the cellular receptor-binding motifs (Crill & Roehrig, *J. Virol.* 75:7769-73, 2001; Modis *et al.*, *PNAS* 100:6986-91, 2003). DI and DIII contain predominately type-specific and subcomplex-reactive epitopes, whereas DII contains the major flavivirus group- and subgroup-cross-reactive epitopes, which are sensitive to reduction and denaturation and are formed from discontinuous amino acid sequences (Mandl *et al.*, *J. Virol.* 63:564-71, 1989; Rey *et al.*, *Nature* 375:291-98, 1995; Roehrig *et al.*, *Virology* 246:317-28, 1998).

Members of the *Flaviviridae* family that infect humans frequently cause severe morbidity and mortality, and epidemics of flaviviruses continue to be a major public health concern worldwide. More than two billion people are at risk of being infected with members of the genus *Flavivirus* which includes at least 70 distinct virus species (Burke & Monath, *Flaviviruses.* In *Fields Virology*, 4th ed., Knipe and Howley. Eds., Philadelphia, Lippincott Williams & Wilkins, pp. 1043-1125, 2001; Kuno *et al.*, *J. Virol.* 72:73-83, 1998; Solomon & Mallewa, *J. Infect.* 42:104-15, 2001). The medically important flaviviruses include yellow fever (YF) virus in Africa, Latin and South America; Japanese encephalitis (JE) virus in Asia and Australia; West Nile (WN) virus in Africa, Central Europe, and most recently in North America; tick-borne encephalitis (TBE) complex viruses in the temperate regions of Europe, North America and Asia; and the four serotypes of dengue viruses (DEN-1, -2, -3, and -4) in tropical and subtropical regions of the world (Lindenbach & Rice, *Flaviviridae: the viruses and their replication.* In *Fields Virology*, 4th ed., Knipe and Howley. Eds., Philadelphia, Lippincott Williams & Wilkins, pp. 991-1041, 2001).

Human infection by flaviviruses results in a humoral immune response involving virus species-specific as well as flavivirus cross-reactive antibodies (Calisher *et al.*, *J. Gen. Virol.* 70:37-43, 1989; Tesh *et al.*, *Emerg. Inf. Dis.* 8:245-51, 2002). The presence of flavivirus cross-reactive antibodies in human sera produces two public health concerns upon secondary infection with a heterologous flavivirus. Serodiagnosis of secondary flavivirus infections, especially in areas with multiple co-circulating flaviviruses, can be particularly difficult due to the inability to differentiate primary from secondary cross-reactive serum antibodies using currently available viral antigens. Therefore, definitive epidemiological information either cannot be obtained or is delayed to the point that effective control and prevention strategies may be delayed. Additionally, the presence of sub-neutralizing levels of flavivirus cross-reactive serum antibodies may result in increasing the severity of secondary flavivirus infections due to antibody-dependant enhancement (ADE), in particular, following secondary dengue virus infection (Ferguson *et al.*, *PNAS* 96:790-94, 1999; Halstead, *Rev. Infect. Dis.* 11:830-39, 1989; Takada & Kawaoka, *Rev. Med. Virol.* 13:387-98, 2003; Wallace *et al.*, *J. Gen Virol.* 84:1723-28, 2003). Thus, there exists a need for a method for identifying and characterizing flavivirus cross-reactive epitopes for improved flavivirus serodiagnosis and development of flavivirus vaccines.

SUMMARY OF THE DISCLOSURE

Multiple flavivirus E-glycoprotein cross-reactive epitopes and mutant E-glycoprotein polypeptides thereof exhibiting reduced or ablated cross-reactivity have been identified. In various embodiments, these E-glycoprotein polypeptides with reduced or ablated cross-reactivity are capable of eliciting effective type-specific immune responses against flaviviruses. In one example, the identified cross-reactive epitopes incorporate the highly conserved Gly_{104}, Gly_{106}, and Leu_{107} residues. In another example, the identified cross-reactive epitope centers on the strictly conserved Trp_{231} residue and its structurally related neighbors Glu_{126} and Thr_{226}.

Also described herein are recombinant flavivirus E-glycoprotein constructs that can be used directly or indirectly to stimulate flavivirus type-specific antibodies. These constructs are designed to elicit T-cell, B-cell, or both T-cell and B-cell responses against flavivirus type-specific epitopes. The constructs, when integrated into a vector, can be used as immunogens, can be used as DNA vaccines, and can be used as sources of recombinant protein for stimulation of immune responses in subjects, as well as for protein boosts to subjects who have received a nucleic acid construct previously. Also provided are methods of identifying and characterizing flavivirus E-glycoprotein amino acid residues incorporated into cross-reactive epitopes, using structure-based rational mutagenesis.

The foregoing and other features and advantages will become more apparent from the following detailed description of several embodiments, which proceeds with reference to the accompanying figures.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a diagrammatical representation of the quaternary structure of the DEN-2 virus E-glycoprotein homodimer, top view, looking down towards the viral surface, showing the locations of flavivirus cross-reactive epitope residues (space-filling representation). The structural and functional domains I, II, and III are also shown.

Figure 2 is a series of diagrammatical representations of the structural locations of cross-reactive epitope residues for flavivirus cross-reactive monoclonal antibodies (mAbs) in the atomic structure of the DEN-2 virus E-glycoprotein dimer, as well as a bar graph indicating fold reductions in mAb reactivities assayed by indirect immuno-fluorescence assay (IFA) and/or antigen-capture ELISA (Ag-ELISA) for mutations at these E-glycoprotein positions.

FIG. 2A is a diagrammatical representation of a portion of the atomic structure of the DEN-2 virus E-glycoprotein homodimer, showing the flavivirus group-reactive mAb 4G2 and 6B6C-1 epitope residues from the fusion peptide region of DII. The flavivirus fusion peptide comprises the highly conserved E-glycoprotein residues 98-113, which form a surface exposed loop of hydrophobic residues rich in glycine at the tip of DII (Rey *et al.*, *Nature* 375:291-98, 1995; Allison *et al.*, *J. Virol.* 75:4268-75, 2001). The view is looking downward toward the viral membrane surface at an angle of approximately 45°, while looking in towards the fusion peptide region about 45° off of parallel to the dimer's longitudinal axis. The molecular surfaces of DI and DIII from the alternate sub-unit are depicted as space-filling Van der Waals surfaces to highlight the close fitting of the fusion peptide into this region. Fusion peptide residues 100-108 are depicted as stick representations with the participating amino acids labeled. Glycan moieties attached to Asn_{153} and Asn_{67} are labeled CHO153 and CHO67, respectively.

FIG. 2B is a diagrammatical representation of a portion of the atomic structure of the DEN-2 virus E-glycoprotein homodimer, showing the flavivirus subgroup-reactive mAb 1B7-5 epitope residues. The view and labeling are the same as in FIG. 2A. Identified residues are depicted as sticks and labeled.

FIG. 2C is a bar graph showing fold decreases in mAb reactivities in Ag-ELISA for DEN-2 VLPs with substitutions at the listed residues. mAbs 4G2 and 6B6C-1 are flavivirus group-reactive and 1B7-5 is flavivirus subgroup-reactive. Substitutions at G_{104} and W_{231} produced plasmids that were unable to secrete measurable VLP antigen into tissue culture media. Therefore, fold decreases in mAb reactivities for these two constructs are from IFA. Wild-type plasmid did not produce an endpoint nearly as far out in IFA as in Ag-ELISA (see Table 3), therefore the fold reductions for substitutions at G_{104} and W_{231} were not as great as for other constructs measured by Ag-ELISA, even though substitutions at these two positions appeared to completely ablate mAb reactivity.

Figure 3 is a bar graph showing the percent of cross-reactive epitope residue substitutions altering reactivities of mAbs of different cross-reactivities. The total number of SLEV and WNV mAbs of each type is shown in the legend on the y-axis, and the number of substitutions altering these mAbs is shown in the columns.

BRIEF DESCRIPTION OF THE APPENDICES

Appendix I contains Tables 1-13.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids, as defined in 37 C.F.R. 1.822. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. In the accompanying sequence listing:

SEQ ID NOs: 1-12 show the nucleic acid sequences of mutagenic primers used to generate the $K_{64}N$ mutation, $T_{76}M$ mutation, $Q_{77}R$ mutation, $G_{104}H$ mutation, $G_{106}Q$ mutation, $L_{107}K$ mutation, $E_{126}A$ mutation, $T_{226}N$ mutation, $W_{231}F$ mutation, $W_{231}L$ mutation, $H_{244}R$ mutation, and $K_{247}R$ mutation, respectively, in the pCB8D2-2J-2-9-1 DEN-2 prM/E expression plasmid.

SEQ ID NOs: 13 and 14 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen.

SEQ ID NOs: 15 and 16 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $G_{104}H$ substitution.

SEQ ID NOs: 17 and 18 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $G_{106}Q$ substitution.

SEQ ID NOs: 19 and 20 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $L_{107}K$ substitution.

SEQ ID NOs: 21 and 22 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $E_{126}A$ substitution.

SEQ ID NOs: 23 and 24 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $T_{226}N$ substitution.

SEQ ID NOs: 25 and 26 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $W_{231}F$ substitution.

SEQ ID NOs: 27 and 28 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the $W_{231}L$ substitution.

SEQ ID NOs: 29 and 30 show the nucleic and amino acid sequences of a recombinant DEN-2 virus E-glycoprotein antigen incorporating the double $E_{126}A$/ $T_{226}N$ substitution.

SEQ ID NOs: 31-79 show the nucleic acid sequences of mutagenic primers used to generate site-specific mutations into the SLEV and WNV E genes.

SEQ ID NOs: 80 and 81 show the nucleic and amino acid sequences of a recombinant SLEV virus E-glycoprotein antigen.

SEQ ID NOs: 82 and 83 show the nucleic and amino acid sequences of a recombinant SLEV virus E-glycoprotein antigen incorporating the $G_{106}Q$ substitution.

SEQ ID NOs: 84 and 85 show the nucleic and amino acid sequences of a recombinant WNV virus E-glycoprotein antigen.

SEQ ID NOs: 86 and 87 show the nucleic and amino acid sequences of a recombinant WNV virus E-glycoprotein antigen incorporating the $G_{106}V$ substitution.

DETAILED DESCRIPTION

I. Abbreviations

ADE	antibody-dependant enhancement
Ag-ELISA	antigen-capture ELISA
D	domain
DEN	dengue
DENV	dengue virus
E	envelope
ELISA	enzyme-linked immunoabsorbent assay
IFA	indirect immuno-fluorescence assay
JE	Japanese encephalitis
JEV	Japanese encephalitis virus
mAb	monoclonal antibody
MHIAF	murine hyper-immune ascetic fluid
MVEV	Murray Valley encephalitis virus
PCR	polymerase chain reaction
prM	premembrane
SLE	St. Louis encephalitis

SLEV	St. Louis encephalitis virus
TBE	tick-borne encephalitis
VLP	virus-like particle
WN	West Nile
WNV	West Nile virus
YF	yellow fever

II. Terms

Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in Benjamin Lewin, *Genes VII*, published by Oxford University Press, 2000 (ISBN 019879276X); Kendrew *et al.* (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Publishers, 1994 (ISBN 0632021829); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by Wiley, John & Sons, Inc., 1995 (ISBN 0471186341); and other similar references.

As used herein, the singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. Also, as used herein, the term "comprises" means "includes." Hence "comprising A or B" means including A, B, or A and B. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including explanations of terms, will control. The materials, methods, and examples are illustrative only and not intended to be limiting.

In order to facilitate review of the various embodiments of this disclosure, the following explanations of specific terms are provided:

Animal: Living multi-cellular vertebrate organisms, a category that includes, for example, mammals and birds. The term mammal includes both human and non-human mammals. Similarly, the term "subject" includes both human and veterinary subjects, for example, humans, non-human primates, dogs, cats, horses, and cows.

Antibody: A protein (or protein complex) that includes one or more polypeptides substantially encoded by immunoglobulin genes or fragments of immunoglobulin genes. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

The basic immunoglobulin (antibody) structural unit is generally a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" (about 50-70 kDa) chain. The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms "variable light chain" (V_L) and "variable heavy chain" (V_H) refer, respectively, to these light and heavy chains.

As used herein, the term "antibody" includes intact immunoglobulins as well as a number of well-characterized fragments. For instance, Fabs, Fvs, and single-chain Fvs (SCFvs) that bind to target protein (or epitope within a protein or fusion protein) would also be specific binding agents for that protein (or epitope). These antibody fragments are as follows: (1) Fab, the fragment which contains a monovalent antigen-binding fragment of an antibody molecule produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an antibody molecule obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) $(Fab')_2$, the fragment of the antibody obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; (4) $F(ab')_2$, a dimer of two Fab' fragments held together by two disulfide bonds; (5) Fv, a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (6) single chain antibody, a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Methods of making these fragments are routine (see, for example, Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999).

Antibodies for use in the methods and compositions of this disclosure can be monoclonal or polyclonal. Merely by way of example, monoclonal antibodies can be prepared from murine hybridomas according to the classical method of Kohler and Milstein (*Nature* 256:495-97, 1975) or derivative methods thereof. Detailed procedures for monoclonal antibody production are described in Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

Antibody binding affinity: The strength of binding between a single antibody binding site and a ligand (*e.g.*, an antigen or epitope). The affinity of an antibody binding site X for a ligand Y is represented by the dissociation constant (K_d), which is the concentration of Y that is required to occupy half of the binding sites of X present in a solution. A smaller (K_d) indicates a stronger or higher-affinity interaction between X and Y and a lower concentration of ligand is needed to occupy the sites. In general, antibody binding affinity can be affected by the alteration, modification and/or substitution of one or more amino acids in the epitope recognized by the antibody paratope.

In one example, antibody binding affinity is measured by end-point titration in an Ag-ELISA assay. Antibody binding affinity is substantially lowered (or measurably reduced) by the modification and/or substitution of one or more amino acids in the epitope recognized by the antibody paratope if the end-point titer of a specific antibody for the modified/substituted epitope differs by at least 4-fold, such as at least 10-fold, at least 100-fold or greater, as compared to the unaltered epitope.

Antigen: A compound, composition, or substance that can stimulate the production of antibodies or a T-cell response in an animal, including compositions that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous immunogens. In one embodiment, an antigen is a flavivirus antigen.

cDNA (complementary DNA): A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences that determine transcription. cDNA is synthesized in the laboratory by reverse transcription from messenger RNA extracted from cells.

Epitope: An antigenic determinant. These are particular chemical groups, such as contiguous or non-contiguous peptide sequences, on a molecule that are antigenic, that is, that elicit a specific immune response. An antibody binds a particular antigenic epitope based on the three dimensional structure of the antibody and the matching (or cognate) three dimensional structure of the epitope.

A "cross-reactive epitope" is an epitope found in two or more antigens expressed by different genes, and responsible for inducing cross-reactive antibodies. For example, a "flavivirus cross-reactive epitope" is a flavivirus epitope found in a peptide from two or more flaviviruses, and responsible for inducing flavivirus cross-reactive antibodies.

A "substituted epitope" comprises at least one structural substitution in the epitope, such as a substitution of one amino acid for another. In certain provided embodiments, amino acid substitutions at probable or identified cross-reactive epitope residues are designed to reduce or ablate cross-reactive antibody recognition without substantially altering E-glycoprotein structural conformation or affecting type-specific antibody binding sites, disrupting dimer interactions, or impairing particle formation, maturation, or secretion.

Flavivirus cross-reactive antibody: An antibody that recognizes (that is, specifically binds to) an epitope found on a peptide from more than one species of flavivirus. Flavivirus cross-reactive antibodies are classified as either complex cross-reactive or group cross-reactive antibodies. Complex cross-reactive antibodies recognize epitopes shared by all viruses within a complex, such as the JE virus complex or the DEN virus complex. Group cross-reactive antibodies recognize epitopes shared by all members of the genus *Flavivirus*.

Antibody cross-reactivity is further refined within the sub-complex and sub-group cross-reactive categories. Sub-complex cross-reactive antibodies recognize epitopes shared by most, but not all, members of a particular flavivirus complex (*e.g.*, DENV-1, -2, and -3, but not DENV-4), while sub-group cross-reactive antibodies recognize epitopes shared by flaviviruses from several complexes, but not all members of the flavivirus group (*e.g.*, all members of the DEN virus and JE virus complexes, but not all members of the tick-borne virus complex). Specific, non-limiting examples of flavivirus cross-reactive antibodies include the group cross-reactive mAbs 4G2 and

6B6C-1, the sub-group cross-reactive mAb 1B7-5, and the sub-complex cross-reactive mAb 10A1D-2.

Flavivirus E-glycoprotein: A structural envelope protein that mediates binding of flavivirus virions to cellular receptors on host cells. The flavivirus E-glycoprotein is required for membrane fusion, and is the primary antigen inducing protective immunity to flavivirus infection. Flavivirus E-glycoprotein affects host range, tissue tropism and viral virulence. The flavivirus E-glycoprotein contains three structural and functional domains, DI-DIII. In mature virus particles the E-glycoprotein forms head to tail homodimers lying flat and forming a dense lattice on the viral surface.

Flavivirus E-glycoprotein domain: A domain of a protein is a part of a protein that shares common structural, physiochemical and/or functional features; for example hydrophobic, polar, globular, helical domains or properties, for example a DNA binding domain, an ATP binding domain, and the like. The flavivirus E-glycoprotein contains three recognized structural and functional domains, DI-DIII. DI is an 8-stranded β-barrel containing two large insertion loops that form the elongated finger-like DII. DII is involved in stabilizing the E-glycoprotein dimer and contains the internal fusion peptide that mediates flaviviral entry into host cells via membrane fusion. DIII forms a ten-stranded β-barrel with an immunoglobulin-like fold and contains the cellular receptor-binding motifs. DI and DIII contain predominately type- and subtype-specific epitopes, whereas DII contains the major flavivirus group and subgroup cross-reactive epitopes, which are sensitive to reduction and denaturation and are therefore believed to be formed from discontinuous amino acid sequences.

Flavivirus type-specific antibody: An antibody that recognizes (that is, specifically binds to) an epitope found on a peptide from only one specific member of the flaviviruses. Specific, non-limiting examples of flavivirus type-specific antibodies include: DI mAb 9A4D-1, DII mAb 1A5D-1, and DIII mAbs 3H5, 9A3D-8 and 9D12, which only recognize epitopes found in the DENV-2 E-glycoprotein.

Hybridization: Oligonucleotides and their analogs hybridize by hydrogen bonding, which includes Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary bases. Generally, nucleic acid consists of nitrogenous bases that are either pyrimidines (cytosine (C), uracil (U), and thymine (T)) or purines (adenine (A) and guanine (G)). These nitrogenous bases form hydrogen bonds between a pyrimidine and a purine, and the bonding of the pyrimidine to the purine is referred to as "base pairing." More specifically, A will hydrogen bond to T or U, and G will bond to C. "Complementary" refers to the base pairing that occurs between to distinct nucleic acid sequences or two distinct regions of the same nucleic acid sequence.

"Specifically hybridizable" and "specifically complementary" are terms that indicate a sufficient degree of complementarity such that stable and specific binding occurs between the oligonucleotide (or its analog) and the DNA or RNA target. The oligonucleotide or oligonucleotide analog need not be 100% complementary to its target sequence to be specifically hybridizable. An oligonucleotide or analog is specifically hybridizable when binding of the oligonucleotide or analog to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA, and there is a sufficient degree of complementarity to avoid non-specific binding of the oligonucleotide or analog to non-target sequences under conditions where specific binding is desired, for example under physiological conditions in the case of *in vivo* assays or systems. Such binding is referred to as specific hybridization.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method of choice and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (especially the Na^+ and/or Mg^{++} concentration) of the hybridization buffer will determine the stringency of hybridization, though wash times also influence stringency. Calculations regarding hybridization conditions required for attaining particular degrees of stringency are discussed by Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, chapters 9 and 11; and Ausubel *et al. Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999.

For purposes of the present disclosure, "stringent conditions" encompass conditions under which hybridization will only occur if there is less than 25% mismatch between the hybridization molecule and the target sequence. "Stringent conditions" may be broken down into particular levels of stringency for more precise definition. Thus, as used herein, "moderate stringency" conditions are those under which molecules with more than 25% sequence mismatch will not hybridize; conditions of "medium stringency" are those under which molecules with more than 15% mismatch will not hybridize, and conditions of "high stringency" are those under which sequences with more than 10% mismatch will not hybridize. Conditions of "very high stringency" are those under which sequences with more than 6% mismatch will not hybridize.

"Specific hybridization" refers to the binding, duplexing, or hybridizing of a molecule only or substantially only to a particular nucleotide sequence when that sequence is present in a complex mixture (for example, total cellular DNA or RNA). Specific hybridization may also occur under conditions of varying stringency.

Immune stimulatory composition: A term used herein to mean a composition useful for stimulating or eliciting a specific immune response (or immunogenic response) in a vertebrate. The immune stimulatory composition can be a protein antigen or a plasmid vector used to express a protein antigen. In some embodiments, the immunogenic response is protective or provides protective immunity, in that it enables the vertebrate animal to better resist infection with or disease progression from the organism against which the immune stimulatory composition is directed.

Without wishing to be bound by a specific theory, it is believed that an immunogenic response induced by an immune stimulatory composition may arise from the generation of an antibody specific to one or more of the epitopes provided in the immune stimulatory composition. Alternatively, the response may comprise a T-helper or cytotoxic cell-based response to one or more of the epitopes provided in the immune stimulatory composition. All three of these responses may originate from naïve or memory cells. One specific example of a type of immune stimulatory composition is a vaccine.

In some embodiments, an "effective amount" or "immune-stimulatory amount" of an immune stimulatory composition is an amount which, when administered to a subject, is sufficient to engender a detectable immune response. Such a response may comprise, for instance, generation of an antibody specific to one or more of the epitopes provided in the immune stimulatory composition. Alternatively, the response may comprise a T-helper or CTL-based response to one or more of the epitopes provided in the immune stimulatory composition. All three of these responses may originate from naïve or memory cells. In other embodiments, a "protective effective amount" of an immune stimulatory composition is an amount which, when administered to a subject, is sufficient to confer protective immunity upon the subject.

Inhibiting or treating a disease: Inhibiting the full development of a disease or condition, for example, in a subject who is at risk for a disease. Specific examples of diseases include dengue fever, dengue hemorrhagic fever, yellow fever, Japanese encephalitis, tick-borne encephalitis, and West Nile disease. "Treatment" refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition after it has begun to develop. As used herein, the term "ameliorating," with reference to a disease, pathological condition or symptom, refers to any observable beneficial effect of the treatment. The beneficial effect can be evidenced, for example, by a delayed onset of clinical symptoms of the disease in a susceptible subject, a reduction in severity of some or all clinical symptoms of the disease, a slower progression of the disease, a reduction in the number of relapses of the disease, an improvement in the overall health or well-being of the subject, or by other parameters well known in the art that are specific to the particular disease.

Isolated: An "isolated" or "purified" biological component (such as a nucleic acid, peptide, protein, protein complex, or particle) has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, that is, other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids, peptides and proteins that have been "isolated" or "purified" thus include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids, peptides and proteins prepared by recombinant expression in a host cell, as well as chemically synthesized nucleic acids or proteins. The term "isolated" or "purified" does not require absolute purity; rather, it is intended as a relative term. Thus, for example, an isolated biological component is one in which the biological component is more enriched than the biological component is in its natural environment within a cell, or other production vessel. Preferably, a preparation is purified such that the biological component represents at least 50%, such as at least 70%, at least 90%, at least 95%, or greater, of the total biological component content of the preparation.

Nucleic acid molecule: A polymeric form of nucleotides, which may include both sense and anti-sense strands of RNA, cDNA, genomic DNA, and synthetic forms and mixed polymers of the above. A nucleotide refers to a ribonucleotide, deoxynucleotide or a modified form of either type of nucleotide. The term "nucleic acid molecule" as used herein is synonymous with "nucleic acid" and "polynucleotide." A nucleic acid molecule is usually at least 10 bases in length, unless otherwise specified. The term includes single- and double-stranded forms of DNA. A polynucleotide may include either or both naturally occurring and modified nucleotides linked together by naturally occurring and/or non-naturally occurring nucleotide linkages.

Oligonucleotide : A nucleic acid molecule generally comprising a length of 300 bases or fewer. The term often refers to single-stranded deoxyribonucleotides, but it can refer as well to single- or double-stranded ribonucleotides, RNA:DNA hybrids and double-stranded DNAs, among others. The term "oligonucleotide" also includes oligonucleosides (that is, an oligonucleotide minus the phosphate) and any other organic base polymer.

In some examples, oligonucleotides are about 10 to about 90 bases in length, for example, 12, 13, 14, 15, 16, 17, 18, 19 or 20 bases in length. Other oligonucleotides are about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60 bases, about 65 bases, about 70 bases, about 75 bases or about 80 bases in length. Oligonucleotides may be single-stranded, for example, for use as probes or primers, or may be double-stranded, for example, for use in the construction of a mutant gene. Oligonucleotides can be either sense or anti-sense oligonucleotides. An oligonucleotide can be modified as discussed above in reference to nucleic acid molecules. Oligonucleotides can be obtained from existing nucleic acid sources (for example, genomic or cDNA), but can also be synthetic (for example, produced by laboratory or *in vitro* oligonucleotide synthesis).

Operably linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence is the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame. If introns are present, the operably linked DNA sequences may not be contiguous.

Paratope: That portion of an antibody that is responsible for its binding to an antigenic determinant (epitope) on an antigen.

Polypeptide: A polymer in which the monomers are amino acid residues joined together through amide bonds. When the amino acids are alpha-amino acids, either the L-optical isomer or the D-optical isomer can be used, the L-isomers being preferred for many biological uses. The terms "polypeptide" or "protein" as used herein are intended to encompass any amino acid molecule and include modified amino acid molecules such as glycoproteins. The term "polypeptide" is specifically intended to cover naturally occurring proteins, as well as those which are recombinantly or synthetically produced.

Probes and primers: A probe comprises an isolated nucleic acid molecule attached to a detectable label or other reporter molecule. Typical labels include radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed, for example, in Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989 and Ausubel *et al. Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999.

Primers are short nucleic acid molecules, for instance DNA oligonucleotides 6 nucleotides or more in length, for example that hybridize to contiguous complementary nucleotides or a sequence to be amplified. Longer DNA oligonucleotides may be about 10, 12, 15, 20, 25, 30, or 50 nucleotides or more in length. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then the primer extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, for example, by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods known in the art. Other examples of amplification include strand displacement amplification, as disclosed in U.S. Patent No. 5,744,311; transcription-free isothermal amplification, as disclosed in U.S. Patent No. 6,033,881; repair chain reaction amplification, as disclosed in WO 90/01069; ligase chain reaction amplification, as disclosed in EP-A-320 308; gap filling ligase chain reaction amplification, as disclosed in 5,427,930; and NASBA™ RNA transcription-free amplification, as disclosed in U.S. Patent No. 6,025,134.

Methods for preparing and using nucleic acid probes and primers are described, for example, in Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; Ausubel *et al. Short Protocols in Molecular Biology*, 4th ed., John Wiley & Sons, Inc., 1999; and Innis *et al. PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc., San Diego, CA, 1990. Amplification primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, © 1991, Whitehead Institute for Biomedical Research, Cambridge, MA). One of ordinary skill in the art will appreciate that the specificity of a particular probe or primer increases with its length. Thus, in order to obtain greater specificity, probes and primers can be selected that comprise at least 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides of a target nucleotide sequences.

Recombinant nucleic acid: A nucleic acid molecule that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination is accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, *e.g.*, by genetic engineering techniques such as those described in Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of a natural nucleic acid molecule.

Regulatory sequences or elements: These terms refer generally to a class of DNA sequences that influence or control expression of genes. Included in the term are promoters, enhancers, locus control regions (LCRs), insulators/boundary elements, silencers, matrix attachment regions (MARs, also referred to as scaffold attachment regions), repressor, transcriptional terminators, origins of replication, centromeres, and meiotic recombination hotspots. Promoters are sequences of DNA near the 5'-end of a gene that act as a binding site for DNA-dependent RNA polymerase, and from which transcription is initiated. Enhancers are control elements that elevate the level of transcription from a promoter, usually independently of the enhancer's orientation or distance from the promoter. LCRs confer tissue-specific and temporally regulated expression to genes to which they are linked. LCRs function independently of their position in relation to the gene, but are copy-number dependent. It is believed that they function to open the nucleosome structure, so other factors can bind to the DNA. LCRs may also affect replication timing and origin usage. Insulators (also know as boundary elements) are DNA sequences that prevent the activation (or inactivation) of transcription of a gene, by blocking effects of surrounding chromatin. Silencers and repressors are control elements that suppress gene expression; they act on a gene independently of their orientation or distance from the gene. MARs are sequences within DNA that bind to the nuclear scaffold; they can affect transcription, possibly by separating chromosomes into regulatory domains. It is believed that MARs mediate higher-order, looped structures within chromosomes. Transcriptional terminators are regions within the gene vicinity where RNA Polymerase is released from the template. Origins of replication are regions of the genome, during DNA synthesis or replication phases of cell division, that begin the replication process of DNA. Meiotic recombination hotspots are regions of the genome that recombine more frequently than average during meiosis.

Sequence identity: The similarity between two nucleic acid sequences, or two amino acid sequences, is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman (*Adv. Appl. Math.*, 2:482, 1981); Needleman and Wunsch (*J. Mol. Biol.*, 48:443, 1970); Pearson and Lipman (*Proc. Natl. Acad. Sci.*, 85:2444, 1988); Higgins and Sharp (*Gene*, 73:237-44, 1988); Higgins and Sharp (*CABIOS*, 5:151-53, 1989); Corpet *et al.* (*Nuc. Acids Res.*, 16:10881-90, 1988); Huang *et al.* (*Comp. Appls. Biosci.*, 8:155-65, 1992); and Pearson *et al.* (*Meth. Mol. Biol.*, 24:307-31, 1994). Altschul *et al.* (*Nature Genet.*, 6:119-29, 1994) presents a detailed consideration of sequence alignment methods and homology calculations.

The alignment tools ALIGN (Myers and Miller, *CABIOS* 4:11-17, 1989) or LFASTA (Pearson and Lipman, 1988) may be used to perform sequence comparisons (Internet Program © 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFASTA compares regions of local similarity. These alignment tools and their respective tutorials are available on the Internet at the NCSA website. Alternatively, for comparisons of amino acid sequences of greater than about 30 amino acids, the "Blast 2 sequences" function can be employed using the default

BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the "Blast 2 sequences" function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). The BLAST sequence comparison system is available, for instance, from the NCBI web site; see also Altschul *et al.*, *J. Mol. Biol.*, 215:403-10, 1990; Gish. and States, *Nature Genet.*, 3:266-72, 1993; Madden *et al.*, *Meth. Enzymol.*, 266:131-41, 1996; Altschul *et al.*, *Nucleic Acids Res.*, 25:3389-402, 1997; and Zhang and Madden, *Genome Res.*, 7:649-56, 1997.

Orthologs (equivalent to proteins of other species) of proteins are in some instances characterized by possession of greater than 75% sequence identity counted over the full-length alignment with the amino acid sequence of specific protein using ALIGN set to default parameters. Proteins with even greater similarity to a reference sequence will show increasing percentage identities when assessed by this method, such as at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, or at least 98% sequence identity. In addition, sequence identity can be compared over the full length of one or both binding domains of the disclosed fusion proteins.

When significantly less than the entire sequence is being compared for sequence identity, homologous sequences will typically possess at least 80% sequence identity over short windows of 10-20, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 99% depending on their similarity to the reference sequence. Sequence identity over such short windows can be determined using LFASTA; methods are described at the NCSA website. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided. Similar homology concepts apply for nucleic acids as are described for protein. An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that each encode substantially the same protein.

Specific binding agent: An agent that binds substantially only to a defined target. Thus a protein-specific binding agent binds substantially only the defined protein, or to a specific region within the protein. As used herein, protein-specific binding agents include antibodies and other agents that bind substantially to a specified polypeptide. The antibodies may be monoclonal or polyclonal antibodies that are specific for the polypeptide, as well as immunologically effective portions ("fragments") thereof.

The determination that a particular agent binds substantially only to a specific polypeptide may readily be made by using or adapting routine procedures. Examples of suitable *in vitro* assays which make use of the Western blotting procedure include IFA and Ag-ELISA, and are described in many standard texts, including Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

Transformed: A "transformed" cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. The term encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector may include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker genes and other genetic elements known in the art.

III. Overview of Several Embodiments

Isolated mutant flavivirus polypeptides exhibiting measurably reduced antibody cross-reactivity (compared to corresponding wild-type polypeptides) are disclosed herein. In one embodiment, the isolated flavivirus polypeptides are flavivirus E-glycoproteins that include an amino acid sequence as shown in SEQ ID NO: 14, wherein at least one of the amino acids at position 104, 106, 107, 126, 226, or 231 is substituted (compared to corresponding wild-type E-glycoproteins). Specific, non-limiting examples of the amino acid substitutions at positions 104, 106, 107, 126, 226, and 231 include: $G_{104}H$ (SEQ ID NO: 16), $G_{106}Q$ (SEQ ID NO: 18), $L_{107}K$ (SEQ ID NO: 20), $E_{126}A$ (SEQ ID NO: 22), $T_{226}N$ (SEQ ID NO: 24), $W_{231}F$ (SEQ ID NO: 26), and $W_{231}L$ (SEQ ID NO: 28). Also disclosed are isolated nucleic acid molecules encoding the flavivirus polypeptides with at least one amino acid substitution at position 104, 106, 107, 126, 226, or 231 of SEQ ID NO: 14. Representative nucleic acid molecules are shown in SEQ ID NOs: 15, 17, 19, 21, 23, 25, and 27.

In another embodiment, the isolated flavivirus polypeptides are flavivirus E-glycoproteins that include an amino acid sequence as shown in SEQ ID NO: 81, wherein at least one of the amino acids at position 106 is substituted (compared to corresponding wild-type E-glycoproteins). Specific, non-limiting examples of the amino acid substitutions at position 106 include: $G_{106}Q$ (SEQ ID NO: 83). Also disclosed are isolated nucleic acid molecules encoding the flavivirus polypeptides with at least one amino acid substitution at position106 of SEQ ID NO: 81. A representative nucleic acid molecule is shown in SEQ ID NO: 82.

In yet another embodiment, the isolated flavivirus polypeptides are flavivirus E-glycoproteins that include an amino acid sequence as shown in SEQ ID NO: 85, wherein at least one of the amino acids at position 106 is substituted (compared to corresponding wild-type E-glycoproteins). Specific, non-limiting examples of the amino acid substitutions at position 106 include: $G_{106}V$ (SEQ ID NO: 87). Also disclosed are isolated nucleic acid molecules encoding the flavivirus polypeptides with at least one amino acid substitution at position106 of SEQ ID NO: 85. A representative nucleic acid molecule is shown in SEQ ID NO: 86.

Pharmaceutical and immune stimulatory compositions are also disclosed that include one or more flavivirus E-glycoprotein polypeptides exhibiting measurably reduced antibody cross-reactivity, with at least one amino acid substitution at position 104, 106, 107, 126, 226, or 231 of SEQ ID NO: 14. Also disclosed are pharmaceutical and immune stimulatory compositions that include one or more nucleic acid molecules encoding the flavivirus polypeptides with at least one amino acid substitution at position 104, 106, 107, 126, 226, or 231 of SEQ ID NO: 14. Representative nucleic acid molecules are shown in SEQ ID NOs: 15, 17, 19, 21, 23, 25, and 27.

Also disclosed are pharmaceutical and immune stimulatory compositions that include one or more flavivirus E-glycoprotein polypeptides exhibiting measurably reduced antibody cross-reactivity, with at least one amino acid substitution at position 106 of SEQ ID NO: 81 or SEQ ID NO: 85. Also disclosed are pharmaceutical and immune stimulatory compositions that include one or more nucleic acid molecules encoding the flavivirus polypeptides with at least one amino acid substitution at position 106 of SEQ ID NO: 81 or SEQ ID NO: 85. Representative nucleic acid molecules are shown in SEQ ID NOs: 82 and 86.

In another embodiment, a method is provided for identifying and modifying a flavivirus cross-reactive epitope. This method includes selecting a candidate cross-reactive epitope using a structure-based design approach, and designing a substituted epitope including at least one amino acid residue substitution compared to the candidate epitope. The candidate epitope is then contacted with a specific binding agent under conditions whereby a candidate epitope/specific binding agent complex can form. Likewise, the substituted epitope is contacted with the same specific binding agent under the same conditions used for candidate epitope/specific binding agent complex formation. A candidate epitope is identified as a flavivirus cross-reactive epitope when the substituted epitope has a substantially lower binding affinity for the specific binding agent compared to the candidate epitope, and wherein the flavivirus cross-reactive epitope binds to a specific binding agent that binds to at least two flaviviruses. In specific, non-limiting examples, the at least two flaviviruses are selected from dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus. In yet another specific example of the provided method, the specific binding agent is a flavivirus cross-reactive antibody.

In a further specific example of the provided method, the structure-based design approach includes identifying at least one conserved flavivirus amino acid between two or more flavivirus groups or subgroups, and mapping the conserved flavivirus amino acid onto a structure of a flavivirus E-glycoprotein. In another specific example, the conserved flavivirus amino acid exhibits two or more of the following structural characteristics: it is located in DII of the E-glycoprotein, it is conserved across the flaviviruses, it is on the outer or lateral surface of the E-glycoprotein dimer, it has at least 35% surface accessibility potential, its side chain projection is accessible for antibody paratopes, or it has a high β-factor.

In yet a further specific example of the provided method, the structure-based design approach includes identifying at least one conserved flavivirus amino acid between two or more flavivirus complexes or subcomplexes, and mapping the conserved flavivirus amino acid onto a structure of a flavivirus E-glycoprotein. In still another specific example, the conserved flavivirus amino acid exhibits two or more of the following structural characteristics: it has at least 35% surface accessibility potential, it is on the outer or lateral surface of the E-glycoprotein dimer, it is conserved across the flaviviruses, its side chain projection is accessible for antibody paratopes, or it has a high β-factor.

In another embodiment, a method is provided for detecting a flavivirus antibody in a sample. This method includes contacting the sample with the disclosed mutant flavivirus polypeptides under conditions whereby a polypeptide/antibody complex can form, and detecting polypeptide/antibody complex formation, thereby detecting a flavivirus antibody in a sample. Also disclosed are methods of diagnosing a flavivirus infection in a subject. In one embodiment, the method includes contacting a sample from the subject with the disclosed mutant flavivirus polypeptides under conditions whereby a polypeptide/antibody complex can form, and detecting polypeptide/antibody complex formation, thereby diagnosing a flavivirus infection in a subject.

Also disclosed is a flavivirus E-glycoprotein engineered to comprise at least one amino acid residue substitution according to the methods described herein.

IV. Identifying Flavivirus Cross-Reactive Epitopes

The current disclosure provides methods for identifying flavivirus cross-reactive epitopes, as well as distinguishing such epitopes from species-specific (or type-specific) epitopes.

In one embodiment, the method comprises a structure-based design approach, which optionally includes one or more of the following requirements in order to identify cross-reactive epitopes: 1) the epitope is located in DII of the E-glycoprotein, for example, amino acids 52-135 and 195-285 in the TBE virus E-glycoprotein, 52-132 and 193-280 in the DEN-2 virus E-glycoprotein, and conserved across the flaviviruses or multiple flaviviral species; 2) the epitope is on the outer or lateral surface of the E-glycoprotein dimer; 3) the epitope has at least 35% surface accessibility potential; 4) one or more side chain projections of amino acids within the epitope are accessible to antibody paratopes; and 5) residues with high temperature (β) factors are favored.

In one embodiment, a structure-based design approach comprises a procedural algorithm developed to localize epitopes responsible for inducing flavivirus cross-reactive antibodies. Strictly-conserved flavivirus residues are initially identified. These residues are mapped, for example, onto a 2.0 Å resolution E-glycoprotein structure for TBE virus (Rey *et al.*, *Nature* 375:291-98, 1995), a high resolution DEN-2 virus E-glycoprotein structure (Modis *et al.*, *PNAS* 100:6986-91, 2003), or other similar structure. Optionally, strictly-conserved flavivirus residues are also mapped onto a computer predicted homology model structure for the DEN-2 virus E-glycoprotein using, for example, the Swiss-Pdb Viewer 3.7 structure analysis software (Guex *et al.*, *Electrophoresis* 18:2714-23, 1997).

The following criteria (individually or in combination of two or more) are then employed in certain embodiments to select probable flavivirus group or subgroup cross-reactive epitope residues: 1) an amino acid located in DII (for example, amino acids 52-135 and 195-285 in the TBE virus E-glycoprotein (Rey *et al.*, *Nature* 375:291-98, 1995); 52-132 and 193-280 in the DEN-2 virus E-glycoprotein (Modis *et al.*, *PNAS* 100:6986-91, 2003)), and conserved among more than one flavivirus; 2) amino acids on the outer or lateral surface of the E-glycoprotein dimer; 3) amino acids with at least 35% surface accessibility potential; 4) side chain projections accessible to antibody paratopes; and 5) residues with high temperature (β) factors should be favored, as these residues tend to be flexible and are able to conform to the antibody paratope, increasing the antibody-antigen (Ab-Ag) affinity.

Similar criteria (individually or in combination of two or more) are employed in certain embodiments to select probable flavivirus complex or subcomplex cross-reactive epitope residues. The procedural algorithm for the identification of flavivirus complex and sub-complex cross-reactive epitopes utilizes the following optimality criteria: 1) The identification and selection of amino acid residues with ≥35% of their surface solvent accessible. These residues are identified from the published atomic structure coordinates of the DENV-2 soluble ectodomain of the envelope glycoprotein and homology models of SLEV and WNV derived from the DENV-2 structure (Modis *et al., Proc. Natl. Acad. Sci. USA* 100:6986-91, 2003). In addition to examination of amino acid residues in structural domain II, residues in domains I and III were examined, since published results indicate that some complex and sub-complex cross-reactive epitopes are mapped onto domains I and III in addition to domain II (Roehrig *et al.*, *Virology* 246:317-28, 1998). 2) Amino acids on the outer or lateral surface of the E-glycoprotein dimer, and accessible to antibody. 3) Amino acid conservation across the flavivirus complex (based upon a structural alignment of the protein sequences). Residues conserved across all member viruses of the same complex are favored. If conserved within but not across the entire complex, then residues with shared identities between WNV and SLEV are favored in the JEV complex, and residues with shared identities between DENV-2 and two or more other viruses in the DENV complex are favored over those shared with DENV-2 and only one other DENV complex virus. 4) Side chain projections exposed towards the outer surface and accessible to antibody paratopes. 5) Residues with high temperature (β-) factors should be favored, as these residues tend to be flexible and are able to conform to the antibody paratope, increasing the antibody-antigen affinity. Amino acid residues with high temperature factors are more commonly found in antigen epitopes than lower temperature factor residues. 6) Following identification of potential individual flavivirus complex and sub-complex cross-reactive epitope residues, all residues are mapped and highlighted on the same E-glycoprotein dimer structure together. With this technique, groups of potential cross-reactive epitope residues forming clusters (and hence probable epitopes) are readily identified. 7) Residues fitting all of these criteria and occurring in structural clusters approximately 20 x 30 Å^2 (which is the average "footprint" of an antibody Fab that interacts with an antigen epitope) are favored over residues that are more isolated in the protein structure. 8) Within an identified structural cluster of potential epitope residues, residues that more completely satisfy greater numbers of the optimality criteria are selected for the first round of mutagenesis analysis.

A. Outer and/or Lateral Surface Amino Acids

In one embodiment, the outer and/or lateral surface of the E-glycoprotein dimer comprises those residues which are exposed on the surface of the E-glycoprotein dimer in a way that they are physically capable of interacting with a host-derived immunoglobulin antibody molecule. The flavivirus virion contains a host cell-derived lipid bilayer, with E-glycoprotein dimers imbedded within this lipid bilayer via their trans-membrane domains. The ectodomains of the E-glycoprotein dimers lie on top of this bilayer, forming a dense lattice and essentially coating the virion in a protein shell. Because of this structural organization, there are regions of the E-glycoprotein that, under general assembled virion conditions, cannot physically interact with an immunoglobulin molecule, and therefore are highly unlikely to form part of an antibody epitope. Such inaccessible regions include the trans-membrane domains (because they are imbedded within the lipid bilayer and are covered by the ectodomain) and more than two-thirds of the residues of the ectodomain itself, which are either on the bottom surface of the dimer (and therefore packed between the lipid layer and the ectodomain), or are packed into the interior of this globular protein rather than on its surface. Because of these structural constraints, under normal conditions immunoglobulin molecules can only interact with residues on the outer exposed surface of the E-glycoprotein dimer, and with a subset of residues on the outer lateral surface. Because of the close packing of E-glycoprotein dimers into a network across the surface of the virion, and the difficulty of a large immunoglobulin molecule accessing these narrow spaces, it is believed that only some of the lateral surface residues are available for immunoglobulin interaction. For these reasons, only residues located on the outer or lateral surface of the E-glycoprotein are considered as participating in possible flavivirus cross-reactive epitopes. An inspection of the location of a residue (*e.g.*, a residue conserved among more than one flavivirus, such as Gly_{104}, Gly_{106}, Leu_{107}, or Trp_{231}) in the E-glycoprotein dimer atomic structure allows for a determination as to whether or not a residue is located on the outer or lateral surface of the dimer.

B. Surface Accessibility Potential

In one embodiment, surface accessibility potential comprises that portion of the predicted electron density surrounding any amino acid residue's side chain that is exposed on the surface of the protein, and theoretically available to interact with another molecule. For any given "surface" residue, its surface accessibility is affected by the local (and surrounding) secondary structure of the alpha-carbon main chain, and the positions and types of immediately surrounding side-chain projections. Thus, by definition, maximum accessibility would be for a residue X in the peptide GGXGG in an extended conformation, as the glycine residues have no side chains and therefore amino acid X's surface accessibility is not constrained by either the alpha-carbon backbone shape or the surrounding residues' side chain projections (see, *e.g.*, Li *et al.*, *Nature Struct. Bio.* 10:482-88, 2003; and Faelber *et al.*, *J. Mol. Biol.* 313:83-97, 2001).

C. Accessible Side Chain Projections

In one embodiment, the side chain projection(s) accessible for antibody paratopes comprises a qualitative assessment of how exposed and/or available a given amino acid's reactive side chain is to interact with a hypothetical immunoglobulin molecule. The angle of projection of a side chain is determined primarily by its position in the primary amino acid chain. However, upon folding of this polypeptide chain, the side chain projections are additionally altered or affected by electrostatic and other forces from surrounding residues. The accessibility of an amino acid's side chain projections to be bound by antibody is a specific criterion that is inherent in an amino acid's "surface accessibility." Hence, theoretical amino acid X could have 50% surface accessibility and yet its side-chain may still be directed towards the interior of the protein and therefore be unlikely to interact energetically with an immunoglobulin molecule (see, *e.g.*, Li *et al.*, *Nature Struct. Bio.* 10:482-88, 2003; Faelber *et al.*, *J. Mol. Biol.* 313:83-97, 2001; and Eyal *et al.*, *J. Comp. Chem.* 25: 712-24, 2003).

D. High Temperature Factors

In one embodiment, a temperature or β-factor comprises a criterion which represents a particular amino acid's potential flexibility within the protein. Any given atom within a protein structure is defined by four parameters, the three x, y and z coordinates, defining its position in space, and its β- or temperature factor. For well defined, high-resolution crystal structures, β-values are typically ≤ 20 Å^2. High β-values, for example, ≥ 40 Å^2 can be a signal that there is little confidence in the assignment of these atoms within the protein (for example, if the protein is disordered and does not consistently fold into the same structure). However, in well-defined atomic-level resolution protein structures, high β-factors associated with particular atoms for individual amino acids are typically interpreted as indicators of that residue or atom's potential flexibility. This criterion is relevant to epitope determination, as shape complementarity of the molecular surfaces of both the antibody paratope and the antigen epitope is know to be an important factor effecting antibody avidity. Flexible residues, identified by their higher β-factors, are better able to make slight positional adjustments, thereby improving shape complementarity and the energetics of the Ag-Ab interaction. It has been demonstrated that epitope amino acids involved in antibody interactions are more likely to have high β-factors than are amino acids from the same protein that do not interact with antibodies (see, *e.g.*, Mylvaganam *et al.*, *J. Mol. Biol.* 281:301-22, 1998).

Amino acid substitutions at probable cross-reactive epitope residues are modeled, selecting substitutions that should reduce or ablate antibody recognition without altering E-glycoprotein structural conformation, disrupting dimer interactions, or impairing particle formation, maturation, or secretion. For this reason, cysteine residues otherwise satisfying the cross-reactive epitope criteria are not recommended for mutagenesis because their involvement in disulphide bridging is believed to be necessary for proper E-glycoprotein structure and function (Modis *et al.*, *PNAS* 100:6986-91, 2003; Rey *et al.*, *Nature* 375:291-98, 1995). Stability calculations are performed for all possible amino acid substitutions of candidate residues using, for example, the FOLD-X server (Guerois *et al.*, *J. Mol. Biol.* 320:369-87, 2002; available on the internet) and the TBE virus E-glycoprotein pdb file coordinates (Rey *et al.*, *Nature* 375:291-98, 1995). By way of example, amino acid substitutions modeled in the TBE virus E-glycoprotein with free energies of folding equal to or less than that of the non-mutated wild-type E-glycoprotein are re-examined with the Swiss-PdbViewer software, to identify those substitutions that minimized local structural disturbances while maintaining structurally relevant biochemical interactions such as hydrogen bonding and/or charge interactions with neighboring amino acids.

Optionally, upon the successful identification of cross-reactive epitope residues, the E-glycoprotein structure can be further analyzed to identify additional residues forming cross-reactive epitopes. By way of example, a "nearest neighbor" search is conducted of the surface of the E-glycoprotein structure, looking for additional residues located within 10-15 Å of the identified residue. This distance is within the binding footprint of a single antibody paratope (Faebler *et al.*, *J. Mol. Biol.* 313:83-97, 2001). In this second iteration of cross-reactive epitope residue identification, the same five optimality criterion as above are used, with one change. The criterion of strict conservation across the flaviviruses is relaxed to now include variable residues. In this way, residues either conserved in their physiochemical nature and/or conserved only within a particular flavivirus complex (such as the four DEN serotypes) or subgroup can be identified.

Also provided are methods for designing a substituted epitope comprising at least one amino acid residue substitution compared to a wild-type candidate epitope; obtaining a first sample comprising the candidate epitope; obtaining a second sample comprising the substituted epitope; contacting the first sample with a specific binding agent; and contacting the second sample with the specific binding agent, wherein the cross-reactive epitope is identified when the substituted epitope has a substantially lower binding affinity for the specific binding agent compared to the candidate epitope. Antibody binding affinities can be determined by many methods well known in the art, such as end-point titration in an Ag-ELISA assay, competition binding in an ELISA assay, a solid-phase radioimmunoassay, and the Biacore® surface plasmon resonance technique (Malmqvist, *Biochem. Soc. Trans.* 27:335-40, 1999; and Drake *et al.*, *Anal. Biochem.* 328:35-43, 2004).

In some embodiments the specific binding agent is an antibody, for example, a polyclonal antibody or a mAb. A specific, non-limiting example of a polyclonal antibody is polyclonal anti-DEN-2 MHIAF. Specific, non-limiting examples of mAbs include 4G2 (ATCC No. HB-112), 6B6C-1, 1B7-5, 10A1D-2, 1A5D-1, and 1B4C-2 (Roehrig *et al.*, *Virology* 246:317-28, 1998).

V. Flavivirus Cross-Reactive Epitopes and Variants Thereof

The disclosure also provides an isolated polypeptide comprising at least one flavivirus cross-reactive epitope residue, wherein the antibody cross-reactivity of the at least one flavivirus cross-reactive epitope has been reduced or ablated. In one embodiment, one or more amino acid substitutions of one or more flavivirus cross-reactive epitope residues causes the reduction or ablation of antibody cross-reactivity. In another embodiment, the at least one flavivirus cross-reactive epitope residue with reduced or ablated cross-reactivity has measurably lower binding affinity with one or more flavivirus group-reactive mAbs, due to substitution of the flavivirus cross-reactive epitope residue(s), but its binding with one or more DEN-2 virus type-specific mAbs is not affected.

Specific, non-limiting examples of an isolated polypeptide comprising at least one flavivirus cross-reactive epitope residue with reduced or ablated cross-reactivity include, the amino acid sequences shown in SEQ ID NO: 16 ($G_{104}H$), SEQ ID NO: 18 ($G_{106}Q$), SEQ ID NO: 20 ($L_{107}K$), SEQ ID NO: 22 ($E_{126}A$), SEQ ID NO: 24 ($T_{226}N$), SEQ ID NO: 26 ($W_{231}F$), SEQ ID NO: 28 ($W_{231}L$), SEQ ID NO: 30 ($E_{126}A$/ $T_{226}N$), SEQ ID NO: 83, and SEQ ID NO: 87.

Manipulation of the nucleotide sequence of a flavivirus cross-reactive epitope using standard procedures, including for instance site-directed mutagenesis or PCR and M13 primer mutagenesis, can be used to produce variants with reduced or ablated cross-reactivity. Details of these techniques are provided in Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. The simplest modifications involve the substitution of one or more amino acids for amino acids having similar physiochemical and/or structural properties. These so-called conservative substitutions are likely to have minimal impact on the activity and/or structure of the resultant protein. Examples of conservative substitutions are shown below.

Original Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Substitutions that should reduce or ablate antibody recognition without altering E-glycoprotein structural conformation, disrupting dimer interactions, or impairing particle formation, maturation, or secretion include: Gly to His, Gly to Gln, Leu to Lys, Glu to Ala, Thr to Asn, Trp to Phe, and Trp to Leu.

The substitutions which in general are expected to produce the greatest changes in protein properties will be non-conservative, for instance changes in which (a) a hydrophilic residue, for example, seryl or threonyl, is substituted for (or by) a hydrophobic residue, for example, leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, for example, lysyl, arginyl, or histadyl, is substituted for (or by) an electronegative residue, for example, glutamyl or aspartyl; or (d) a residue having a bulky side chain, for example, phenylalanine, is substituted for (or by) one not having a side chain, for example, glycine.

The disclosure also provides isolated nucleic acids that encode the described polypeptides. Nucleic acids of the invention thus include nucleic acids that encode: 1) polypeptides comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity; and 2) polypeptides that that are at least 95% identical to the polypeptides comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity.

Recombinant nucleic acids may, for instance, contain all or part of a disclosed nucleic acid operably linked to a regulatory sequence or element, such as a promoter, for instance, as part of a clone designed to express a protein. Cloning and expression systems are commercially available for such purposes and are well known in the art. The disclosure also provides cells or organisms transformed with recombinant nucleic acid constructs that encode all or part of the described polypeptides. Also disclosed are virus-like particles (VLPs) that include one or more of the described flavivirus E-glycoprotein polypeptides.

VI. Specific Binding Agents

This disclosure provides specific binding agents that bind to polypeptides disclosed herein, *e.g.*, flavivirus E-glycoprotein polypeptides with reduced or ablated cross-reactivity. The binding agent may be useful for identifying flavivirus cross-reactive epitopes, and for detecting and purifying polypeptides comprising flavivirus cross-reactive epitopes. Examples of the binding agents are a polyclonal or monoclonal antibody, and fragments thereof, that bind to polypeptides disclosed herein. A specific, non-limiting example of a polyclonal antibody is polyclonal anti-DEN-2 MHIAF. Specific, non-limiting examples of mAbs include 4G2, 6B6C-1, 1B7-5, 10A1D-2, 1A5D-1, and 1B4C-2.

Monoclonal or polyclonal antibodies can be raised to recognize the polypeptides described herein, or variants thereof. Optimally, antibodies raised against these polypeptides will specifically detect the polypeptide with which the antibodies are generated. That is, antibodies raised against the polypeptide will recognize and bind the polypeptide, and will not substantially recognize or bind to other polypeptides or antigens. The determination that an antibody specifically binds to a target polypeptide is made by any one of a number of standard immunoassay methods; for instance, the Western blotting technique (Sambrook *et al.* (ed.), *Molecular Cloning: A Laboratory Manual*, 2^{nd} ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), Ag-ELISA and IFA.

Substantially pure flavivirus recombinant polypeptide antigens suitable for use as immunogens can be isolated from the transformed cells described herein, using methods well known in the art. Monoclonal or polyclonal antibodies to the antigens can then be prepared.

Monoclonal antibodies to the polypeptides can be prepared from murine hybridomas according to the classic method of Kohler & Milstein (*Nature* 256:495-97, 1975), or a derivative method thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein immunogen (for example, a polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, a portion of a polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, or a synthetic peptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity) over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall (*Meth. Enzymol.*, 70:419-39, 1980), or a derivative method thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

Polyclonal antiserum containing antibodies can be prepared by immunizing suitable animals with a polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, a portion of a polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, or a synthetic peptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, which can be unmodified or modified, to enhance immunogenicity.

Effective antibody production (whether monoclonal or polyclonal) is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with either inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appear to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis *et al.* (*J. Clin. Endocrinol. Metab.*, 33:988-91, 1971).

Booster injections can be given at regular intervals, and antiserum harvested when the antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony *et al.*, *Handbook of Experimental Immunology*, Wier, D. (ed.), Chapter 19, Blackwell, 1973. A plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM).

Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher (*Manual of Clinical Immunology*, Ch. 42, 1980).

Antibody fragments may be used in place of whole antibodies and may be readily expressed in prokaryotic host cells. Methods of making and using immunologically effective portions of monoclonal antibodies, also referred to as "antibody fragments," are well known and include those described in Better & Horowitz, *Methods Enzymol.* 178:476-96, 1989; Glockshuber *et al.*, *Biochemistry* 29:1362-67, 1990; and U.S. Patent Nos. 5,648,237 (Expression of Functional Antibody Fragments); 4,946,778 (Single Polypeptide Chain Binding Molecules); and 5,455,030 (Immunotherapy Using Single Chain Polypeptide Binding Molecules), and references cited therein. Conditions whereby a polypeptide/binding agent complex can form, as well as assays for the detection of the formation of a polypeptide/binding agent complex and quantitation of binding affinities of the binding agent and polypeptide, are standard in the art. Such assays can include, but are not limited to, Western blotting, immunoprecipitation, immunofluorescence, immunocytochemistry, immunohistochemistry, fluorescence activated cell sorting (FACS), fluorescence *in situ* hybridization (FISH), immunomagnetic assays, ELISA, ELISPOT (Coligan *et al.*, *Current Protocols in Immunology,* Wiley, NY, 1995), agglutination assays, flocculation assays, cell panning, *etc.*, as are well known to one of skill in the art.

Binding agents of this disclosure can be bound to a substrate (for example, beads, tubes, slides, plates, nitrocellulose sheets, *etc.*) or conjugated with a detectable moiety, or both bound and conjugated. The detectable moieties contemplated for the present disclosure can include, but are not limited to, an immunofluorescent moiety (for example, fluorescein, rhodamine), a radioactive moiety (for example, ^{32}P, ^{125}I, ^{35}S), an enzyme moiety (for example, horseradish peroxidase, alkaline phosphatase), a colloidal gold moiety, and a biotin moiety. Such conjugation techniques are standard in the art (for example, see Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999; Yang et al., *Nature,* 382:319-24, 1996).

VII. Detection of Flavivirus Antibodies

The present disclosure further provides a method of detecting a flavivirus-reactive antibody in a sample, comprising contacting the sample with a polypeptide or peptide of this disclosure under condition whereby an antibody/polypeptide complex can form; and detecting formation of the complex, thereby detecting flavivirus antibody in a sample.

The method of detecting flavivirus-reactive antibody in a sample can be performed, for example, by contacting a fluid or tissue sample from a subject with a polypeptide of this disclosure and detecting the binding of the polypeptide to the antibody. A fluid sample of this method can comprise any biological fluid which could contain the antibody, such as cerebrospinal fluid, blood, bile plasma, serum, saliva and urine. Other possible examples of body fluids include sputum, mucus and the like.

Enzyme immunoassays such as IFA, ELISA and immunoblotting can be readily adapted to accomplish the detection of flavivirus antibodies according to the methods of this disclosure. An ELISA method effective for the detection of the antibodies can, for example, be as follows: 1) bind the polypeptide to a substrate; 2) contact the bound polypeptide with a fluid or tissue sample containing the antibody; 3) contact the above with a secondary antibody bound to a detectable moiety which is reactive with the bound antibody (for example, horseradish peroxidase enzyme or alkaline phosphatase enzyme); 4) contact the above with the substrate for the enzyme; 5) contact the above with a color reagent; and 6) observe/measure color change or development.

Another immunologic technique that can be useful in the detection of flavivirus antibodies uses mAbs for detection of antibodies specifically reactive with flavivirus polypeptides in a competitive inhibition assay. Briefly, a sample is contacted with a polypeptide of this invention which is bound to a substrate (for example, a 96-well plate). Excess sample is thoroughly washed away. A labeled (for example, enzyme-linked, fluorescent, radioactive, *etc.*) mAb is then contacted with any previously formed polypeptide-antibody complexes and the amount of mAb binding is measured. The amount of inhibition of mAb binding is measured relative to a control (no antibody), allowing for detection and measurement of antibody in the sample. The degree of mAb binding inhibition can be a very specific assay for detecting a particular flavivirus variety or strain, when based on mAb binding specificity for a particular variety or strain of flavivirus. mAbs can also be used for direct detection of flavivirus in cells by, for example, IFA according to standard methods.

As a further example, a micro-agglutination test can be used to detect the presence of flavivirus antibodies in a sample. Briefly, latex beads, red blood cells or other agglutinable particles are coated with a polypeptide of this disclosure and mixed with a sample, such that antibodies in the sample that are specifically reactive with the antigen crosslink with the antigen, causing agglutination. The agglutinated polypeptide-antibody complexes form a precipitate, visible with the naked eye or measurable by spectrophotometer.

In yet another example, a microsphere-based immunoassay can be used to detect the presence of flavivirus antibodies in a sample. Briefly, microsphere beads are coated with a polypeptide of this disclosure and mixed with a sample, such that antibodies in the sample that are specifically reactive with the antigen bind the antigen. The bead-bound polypeptide-antibody complexes are allowed to react with fluorescent-dye labeled anti-species antibody (such as FITC-labeled goat anti-human IgM), and are measured using a microsphere reader (such as a Luminex instrument).

The present disclosure further provides a method of diagnosing a flavivirus infection in a subject, comprising contacting a sample from the subject with the polypeptide of this disclosure under conditions whereby an antibody/polypeptide complex can form; and detecting antibody/polypeptide complex formation, thereby diagnosing a flavivirus infection in a subject.

In examples of the diagnostic methods, the polypeptide of this disclosure can be bound to a substrate and contacted with a fluid sample such as blood, serum, urine or saliva. This sample can be taken directly from the patient or in a partially purified form. In this manner, antibodies specific for the polypeptide (the primary antibody) will specifically react with the bound polypeptide. Thereafter, a secondary antibody bound to, or labeled with, a detectable moiety can be added to enhance the detection of the primary antibody. Generally, the secondary antibody will be selected for its ability to react with multiple sites on the primary antibody. Thus, for example, several molecules of the secondary antibodies can react with each primary antibody, making the primary antibody more detectable.

The detectable moiety allows for visual detection of a precipitate or a color change, visual detection by microscopy, or automated detection by spectrometry, radiometric measurement or the like. Examples of detectable moieties include fluorescein, rhodamine, Cy5, and Cy3 (for fluorescence microscopy and/or the microsphere-based immunoassay), horseradish peroxidase (for either light or electron microscopy and biochemical detection), biotin-streptavidin (for light or electron microscopy) and alkaline phosphatase (for biochemical detection by color change).

VIII. Pharmaceutical and Immune Stimulatory Compositions and Uses Thereof

Pharmaceutical compositions including flavivirus nucleic acid sequences or flavivirus polypeptides comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity are also encompassed by the present disclosure. These pharmaceutical compositions include a therapeutically effective amount of one or more active compounds, such as flavivirus polypeptides comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity, or one or more nucleic acid molecules encoding these polypeptides, in conjunction with a pharmaceutically acceptable carrier. It is contemplated that in certain embodiments, flavivirus nucleic acid sequences or flavivirus polypeptides comprising multiple flavivirus cross-reactive epitopes with reduced or ablated cross-reactivity will be useful in preparing the pharmaceutical compositions of the disclosure.

Disclosed herein are substances suitable for use as immune stimulatory compositions for the inhibition or treatment of a flavivirus infection, for example, a dengue virus infection. In one embodiment, an immune stimulatory composition contains a flavivirus polypeptide including at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity. In a further embodiment, the immune stimulatory composition contains a nucleic acid vector that includes flavivirus nucleic acid molecules described herein, or that includes a nucleic acid sequence encoding at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity. In a specific, non-limiting example, a nucleic acid sequence encoding at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity is expressed in a transcriptional unit, such as those described in published PCT Application Nos. PCT/US99/12298 and PCT/US02/10764 (both of which are incorporated herein in their entirety).

The provided immune stimulatory flavivirus polypeptides, constructs or vectors encoding such polypeptides, are combined with a pharmaceutically acceptable carrier or vehicle for administration as an immune stimulatory composition to human or animal subjects. In a particular embodiment, the immune stimulatory composition administered to a subject directs the synthesis of a mutant flavivirus E-glycoprotein as described herein, and a cell within the body of the subject, after incorporating the nucleic acid within it, secretes VLPs comprising the mutant E-glycoprotein with reduced or ablated cross-reactivity. It is believed that such VLPs then serve as an *in vivo* immune stimulatory composition, stimulating the immune system of the subject to generate protective immunological responses. In some embodiments, more than one immune stimulatory flavivirus polypeptide, construct or vector may be combined to form a single preparation.

The immunogenic formulations may be conveniently presented in unit dosage form and prepared using conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of a sterile liquid carrier, for example, water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets commonly used by one of ordinary skill in the art.

In certain embodiments, unit dosage formulations are those containing a dose or unit, or an appropriate fraction thereof, of the administered ingredient. It should be understood that in addition to the ingredients particularly mentioned above, formulations encompassed herein may include other agents commonly used by one of ordinary skill in the art.

The compositions provided herein, including those for use as immune stimulatory compositions, may be administered through different routes, such as oral, including buccal and sublingual, rectal, parenteral, aerosol, nasal, intramuscular, subcutaneous, intradermal, and topical. They may be administered in different forms, including but not limited to solutions, emulsions and suspensions, microspheres, particles, microparticles, nanoparticles, and liposomes.

The volume of administration will vary depending on the route of administration. By way of example, intramuscular injections may range from about 0.1 ml to about 1.0 ml. Those of ordinary skill in the art will know appropriate volumes for different routes of administration.

A relatively recent development in the field of immune stimulatory compounds (for example, vaccines) is the direct injection of nucleic acid molecules encoding peptide antigens (broadly described in Janeway & Travers, *Immunobiology: The Immune System In Health and Disease,* page 13.25, Garland Publishing, Inc., New York, 1997; and McDonnell & Askari, *N. Engl. J. Med.* 334:42-45, 1996). Vectors that include nucleic acid molecules described herein, or that include a nucleic acid sequence encoding a flavivirus polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity may be utilized in such DNA vaccination methods.

Thus, the term "immune stimulatory composition" as used herein also includes nucleic acid vaccines in which a nucleic acid molecule encoding a flavivirus polypeptide comprising at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity is administered to a subject in a pharmaceutical composition. For genetic immunization, suitable delivery methods known to those skilled in the art include direct injection of plasmid DNA into muscles (Wolff *et al., Hum. Mol. Genet.* 1:363, 1992), delivery of DNA complexed with specific protein carriers (Wu *et al., J. Biol. Chem.* 264:16985, 1989), co-precipitation of DNA with calcium phosphate (Benvenisty and Reshef, *Proc. Natl. Acad. Sci.* 83:9551, 1986), encapsulation of DNA in liposomes (Kaneda *et al., Science* 243:375, 1989), particle bombardment (Tang *et al., Nature* 356:152, 1992; Eisenbraun *et al., DNA Cell Biol.* 12:791, 1993), and *in vivo* infection using cloned retroviral vectors (Seeger *et al., Proc. Natl. Acad. Sci.* 81:5849, 1984). Similarly, nucleic acid vaccine preparations can be administered via viral carrier.

The amount of immunostimulatory compound in each dose of an immune stimulatory composition is selected as an amount that induces an immunostimulatory or immunoprotective response without significant, adverse side effects. Such amount will vary depending upon which specific immunogen is employed and how it is presented. Initial injections may range from about 1 μg to about 1 mg, with some embodiments having a range of about 10 μg to about 800 μg,and still other embodiments a range of from about 25 μg to about 500 μg. Following an initial administration of the immune stimulatory composition, subjects may receive one or several booster administrations, adequately spaced. Booster administrations may range from about 1 μg to about 1 mg, with other embodiments having a range of about 10 μg to about 750 μg, and still others a range of about 50 μg to about 500 μg. Periodic boosters at intervals of 1-5 years, for instance three years, may be desirable to maintain the desired levels of protective immunity.

It is also contemplated that the provided immunostimulatory molecules and compositions can be administered to a subject indirectly, by first stimulating a cell *in vitro*, which stimulated cell is thereafter administered to the subject to elicit an immune response. Additionally, the pharmaceutical or immune stimulatory compositions or methods of treatment may be administered in combination with other therapeutic treatments.

IX. Kits

Also provided herein are kits useful in the detection and/or diagnosis of flaviviruses. An example of an assay kit provided herein is a recombinant flavivirus polypeptide (or fragment thereof) as an antigen and an enzyme-conjugated anti-human antibody as a second antibody. Examples of such kits also can include one or more enzymatic substrates. Such kits can be used to test if a sample from a subject contains antibodies against a flavivirus-specific protein. In such a kit, an appropriate amount of a flavivirus polypeptide (or fragment thereof) is provided in one or more containers, or held on a substrate. A flavivirus polypeptide can be provided in an aqueous solution or as a freeze-dried or lyophilized powder, for instance. The container(s) in which the flavivirus polypeptide(s) are supplied can be any conventional container that is capable of holding the supplied form, for instance, microfuge tubes, ampoules, or bottles.

The amount of each polypeptide supplied in the kit can be any appropriate amount, and can depend on the market to which the product is directed. For instance, if the kit is adapted for research or clinical use, the amount of each polypeptide provided would likely be an amount sufficient for several assays. General guidelines for determining appropriate amounts can be found, for example, in Ausubel *et al.* (eds.), *Short Protocols in Molecular Biology*, John Wiley and Sons, New York, NY, 1999 and Harlow and Lane, *Using Antibodies: A Laboratory Manual*, CSHL, New York, 1999.

The subject matter of the present disclosure is further illustrated by the following non-limiting Examples.

Example 1

Identification of DII cross-reactive epitope residues

This example demonstrates the identification of flavivirus cross-reactive epitopes using a structure-based rational mutagenesis method.

Cell culture, virus strain and recombinant plasmid

COS-1 cells (ATCC CRL 1650; Manassas, VA) were grown at 37°C with 5% CO_2 on Dulbecco's modified Eagle's minimal essential medium (DMEM, GIBCO, Grand Island, NY) supplemented with 10% heat-inactivated fetal bovine serum (FBS, Hyclone Laboratories, Inc., Logan, UT), 110 mg/l sodium pyruvate, 0.1 mM nonessential amino acids, 2 mM L-glutamine, 20 ml/l 7.5% $NaHCO_3$, 100U/ml penicillin, and 100 µg/ml streptomycin. CHO cells (ATCC CCL 61; Manassas, VA) were grown under the same conditions as COS-1 cells with DMEM/F12 nutrient mixture (GIBCO, Grand Island, NY).

Flavivirus plasmids capable of expressing extracellular VLPs composed of prM/M and E-glycoproteins for JE, WN, SLE, and the four DEN virus serotypes have been constructed (Chang *et al.*, *J. Virol.* 74:4244-52, 2000; Chang *et al.*, *Virology* 306:170-80, 2003; Davis *et al.*, *J. Virol.* 75:4040-47, 2001). These VLPs, produced by recombinant plasmid-transformed eukaryotic cells, contain the flavivirus prM/M and E-glycoproteins in their native viral conformations, and although non-infectious, they maintain many of the same properties as mature virus particles including, hemagglutination activity, membrane fusion, and the induction of protective immune responses in animals (Chang *et al.*, *J. Virol.* 74:4244-52, 2000; Chang *et al.*, *Virology* 306:170-80, 2003; Davis *et al.*, *J. Virol.* 75:4040-47, 2001; Hunt, *et al.*, *J. Virol. Methods* 97:133-49, 2001).

The recombinant expression plasmid pCB8D2-2J-2-9-1 (the DEN-2 prM/E expression plasmid, Chang *et al.*, *Virology* 306:170-80, 2003) was used as the template DNA for both site-directed mutagenesis and for transient expression of DEN-2 recombinant antigen (see below). This plasmid includes the human cytomegalovirus early gene promoter, Kozak sequence, JE virus signal sequence, DEN-2 virus prM/M gene, DEN-2 virus chimeric E gene (with amino-terminal 80% from DEN-2 virus and carboxy-terminal 20% from JE virus), and bovine growth hormone poly(A) signal. The replacement of the terminal 20% of DEN-2 virus E gene sequences with JE virus E gene sequences dramatically increases the secretion of extracellular VLPs into the culture medium without altering the native DEN-2 virus E-glycoprotein conformation (Chang *et al.*, *Virology* 306:170-80, 2003).

Procedural algorithm

To localize the epitopes responsible for inducing flavivirus cross-reactive antibodies, the following procedural algorithm was developed: Strictly-conserved flavivirus residues were initially identified. These residues were mapped onto the 2.0 Å resolution E-glycoprotein structure for TBE virus (Rey *et al.*, *Nature* 375:291-98, 1995) and onto a computer predicted homology model structure for the DEN-2 virus E-glycoprotein using the Swiss-Pdb Viewer 3.7 structure analysis software (Guex *et al.*, *Electrophoresis* 18:2714-23, 1997; available on the ExPASy Molecular Biology Server). A brief review of high resolution structures for antigen-antibody complexes revealed that 10-20 residues typically are involved in making direct contacts between the antigen epitope and antibody paratope. These contacts result in 20-30 residues that are "buried" by the typical antibody footprint, measuring approximately 20 x 30 Å. On average however, only 25% of the buried side chains, or 4-6 residues, account for most of the mAb binding energy (Arevalo *et al.*, *Nature* 356:859-63, 1993; Bhat *et al.*, *PNAS* 91:1089-93, 1994; Davies & Cohen, *PNAS* 93:7-12, 1996; Faebler *et al.*, *J. Mol. Biol.* 313:83-97, 2001; Fleury *et al.*, *Nature St. Biol.* 6:530-34, 1999; Li *et al.*, *Biochemistry* 39:6296-6309, 2000; Lo *et al.*, *J. Mol. Biol.* 285:2177-98, 1999; and Mylvaganam *et al.*, *J. Mol. Biol.* 281:301-22, 1998).

The following criteria were developed to select probable flavivirus group cross-reactive epitope residues: 1) an amino acid located in DII (for example, amino acids 52-135 and 195-285 in the TBE virus E-glycoprotein (Rey *et al.*, *Nature* 375:291-98, 1995); 52-132 and 193-280 in the DEN-2 virus E-glycoprotein (Modis *et al.*, *PNAS* 100:6986-91, 2003)) and conserved among more than one flavivirus; 2) amino acids on the outer or lateral surface of the E-glycoprotein dimer; 3) amino acids with at least 35% surface accessibility potential; 4) side chain projections accessible to antibody paratopes; and 5) residues with high temperature (β-) factors should be favored, as these residues tend to be flexible and are able to conform to the antibody paratope, increasing the antibody-antigen affinity.

Using this structure-based design approach, candidate flavivirus cross-reactive epitope residues were narrowed down from a total of 53 conserved amino acids in DII (38 invariant and 15 almost completely conserved), to less than ten probable DII cross-reactive epitope residues. Amino acid substitutions at these probable cross-reactive epitope residues were computer modeled, selecting substitutions that should reduce or ablate antibody recognition without altering E-glycoprotein structural conformation, disrupting dimer interactions, or impairing particle formation, maturation, or secretion. For this reason, cysteine residues otherwise satisfying the cross-reactive epitope criteria were not considered for mutagenesis because of their involvement in disulphide bridging necessary for proper E-glycoprotein structure and function (Modis *et al.*, *PNAS* 100:6986-91, 2003; Rey *et al.*, *Nature* 375:291-98, 1995).

Stability calculations were performed for all possible amino acid substitutions of candidate residues using the FOLD-X server (Guerois *et al.*, *J. Mol. Biol.* 320:369-87, 2002; available on the internet) and the TBE virus E-glycoprotein pdb file coordinates (Rey *et al.*, *Nature* 375:291-98, 1995). Amino acid substitutions modeled in the TBE virus E-glycoprotein with free energies of folding equal to or less than that of the non-mutated wild-type E-glycoprotein were re-examined with the Swiss-PdbViewer software to identify those substitutions that minimized local structural disturbances while maintaining structurally relevant biochemical interactions such as hydrogen bonding and/or charge interactions with neighboring amino acids. Because the outer surface of mature flavivirus particles are covered in a dense network of E and prM/M proteins, any conformational changes in the E-glycoprotein are likely to induce concerted reorganization across the surface of the virion (Kuhn *et al.*, *Cell* 108:717-25, 2002; Modis *et al.*, *PNAS* 100:6986-91, 2003). A comparison of the *a priori* stability calculations based on the TBE virus E-glycoprotein structure with *a posteriori* stability calculations from the DEN-2 virus atomic structure are shown in Table 2.

Site-directed mutagenesis

Site-specific mutations were introduced into the DEN-2 virus E gene using the Stratagene Quick Change® multi site-directed mutagenesis kit (Stratagene, La Jolla, CA) and pCB8D2-2J-2-9-1 as DNA template following the manufacturer's recommended protocols. The sequences of the mutagenic primers used for all constructs are listed in Table 1. Four or five colonies from each mutagenic PCR transformation were selected and grown in 5 ml LB broth cultures, mini-prepped and sequenced. Structural gene regions and regulatory elements of all purified plasmids were sequenced entirely upon identification of the correct mutation. Automated DNA sequencing was performed using a Beckman Coulter CEQ™ 8000 genetic analysis system (Beckman Coulter, Fullerton, CA) and analyzed using Beckman Coulter CEQ™ 8000 (Beckman Coulter, Fullerton, CA) and Lasergene® software (DNASTAR, Madison, WI).

Transient expression of DEN-2 virus recombinant antigens in COS-1 or CHO cells

COS-1 and CHO cells were electroporated with pCB8D2-2J-2-9-1 using the protocol described by Chang *et al.* (*J. Virol.* 74:4244-52, 2000). Electroporated cells were recovered in 50 ml DMEM, seeded into 150 cm^2 culture flasks for VLP expression and into 96 well tissue culture plates (Costar® #3603; Corning, Inc., Corning, NY) for IFA, and incubated at 37°C with 5% CO_2. Six to eight hours following electroporation, the growth medium in the 150 cm^2 culture flasks was replaced with DMEM containing 2% FBS. Cells in 96 well plates for IFA were fixed 14-18 hours post electroporation. Tissue-culture medium and cells were harvested 48 and 96 hours post electroporation for antigen characterization.

Characterization of mutant pCB8D2-J2-2-9-1 infected cells and secreted antigen

Fourteen to eighteen hours following electroporation, 96 well tissue culture plates containing cells transformed with the mutated pCB8D2-2J-2-9-1 clones were washed twice with phosphate buffered saline (PBS), fixed with 3:1 acetone:PBS for 10 minutes and air dried. E-glycoprotein-specific mAbs specific for each of the three E-glycoprotein domains were used to determine affinity reductions in DII cross-reactive epitopes by indirect IFA as described by Chang *et al.* (*J. Virol.* 74:4244-52, 2000).

Tissue culture medium was harvested 48 hours and 96 hours following electroporation. Cell debris was removed from tissue culture media by centrifugation for 30 minutes at 10,000 rpm. Ag-ELISA was used to detect secreted antigen from the mutagenized pCB8D2-2J-2-9-1 transformed COS-1 cells. Secreted antigen was captured with polyclonal rabbit anti-DEN-2 sera (Roehrig *et al.*, *Virology* 246:317-28, 1998) at a 1:10,000 dilution. Murine hyper-immune ascetic fluid (MHIAF) specific for DEN-2 virus was used at a 1:3000 dilution to detect captured antigen, and this MHIAF was detected using horseradish peroxidase conjugated goat anti-mouse HIAF at a 1:5000 dilution. Secreted antigen from tissue culture medium was concentrated by centrifugation overnight at 19,000 rpm, and resuspended in TNE buffer (50mM Tris, 100mM NaCl, 10mM EDTA, pH 7.5) to 1/200th the original volume. Concentrated antigen was analyzed with a panel of anti-DEN-2 mAbs in Ag-ELISA to determine mAb end point reactivities of the mutated antigens following the protocol of Roehrig *et al.* (*Virology* 246:317-28, 1998).

Affinity reductions in DII cross-reactive epitopes

Three anti-DEN-2 mAbs, 4G2, 6B6C-1 and 1B7-5, were used to determine affinity reductions in DII cross-reactive epitopes. These three mAbs share several characteristics: they recognize surface accessible epitopes in DII, they are flavivirus group- or subgroup-reactive, they are reduction-denaturation sensitive, they block virus-mediated cell-membrane fusion, they neutralize virus infectivity, and tryptic fragment mapping indicates that the binding domains of these three mAbs are formed by two discontinuous DEN-2 virus E-glycoprotein peptide fragments, aa1-120 and 158-400 (Aaskov *et al.*, *Arch Virol.* 105:209-21, 1989; Henchal *et al.*, *Am. J. Trop. Med. Hyg.* 34:162-69, 1985; Megret *et al.*, *Virology* 187:480-91, 1992; Roehrig *et al.*, *Virology* 246:317-28, 1998). Prospective cross-reactive epitope residues were assessed by looking for decreases in the reactivity of these three DII flavivirus cross-reactive mAbs for the mutant plasmid transfected cells by IFA, and mutant VLPs in Ag-ELISA. Proper E-glycoprotein folding and structural conformation was assessed with a panel of E-glycoprotein DEN virus complex-, subcomplex-, and type-specific mAbs.

Four potential flavivirus cross-reactive epitope residues were initially focused on. Single amino acid substitutions were introduced into the DEN-2 prM/E expression plasmid at the following positions (of SEQ ID NO: 14): Gly_{106} to Glu ($G_{106}Q$), Trp_{231} to Phe ($W_{231}F$), His_{244} to Arg ($H_{244}R$), and Lys_{247} to Arg ($K_{247}R$) (Table 1). Substitutions at Gly_{106} and Trp_{231} strongly interfered with the binding of flavivirus cross-reactive mAbs (Table 3). However, substitutions at His_{244} and Lys_{247} did not have a measurable effect on the binding of the cross reactive mAbs or of any other mAbs from the panel.

Gly_{106} is located within the fusion peptide at the very tip of DII in the E-glycoprotein monomer (Allison *et al.*, *J. Virol.* 73:5605-12, 1999; FIGS. 1 and 2). As with the other fusion peptide residues, Gly_{106} is strongly conserved across the flaviviruses, the one exception being Modoc virus with alanine at this position (Table 4). Gly_{106} is located at the distal end of each E-monomer along the upper and outer-lateral surface of the dimer. This residue has moderately high surface accessibility, and its relatively high temperature (β-) factor suggests its potential flexibility. The substitution of a large, bulky, polar glutamine for the glycine at this position was modeled. The glutamine substitution fit well into the surrounding region, did not appear to disrupt the local hydrogen bonding network, and produced acceptable stability calculations using the TBE virus E-glycoprotein structure coordinates (Table 2).

Trp_{231} is located in a long intervening loop sequence between DII β-strands h and i (Modis *et al.*, *PNAS* 100:6986-91, 2003; FIG. 1). Trp_{231} lays in a trough on the upper and outer surface of DII (FIG. 2). It is structurally close to the glycan on Asn_{67}, and lies laterally exterior to the disulfide bridge between Cys_{60} and Cys_{121}. The large hydrophobic side chain lays parallel to the dimer surface within this trough. This residue is only moderately surface accessible yet its high temperature (β-) factor and the lack of hydrogen bonding from surrounding residues to the side chain suggest its potential flexibility. Although all of the substitutions that were modeled at Trp_{231} were predicted to induce substantially high energetic costs from the stability analyses, the phenylalanine substitution was the least costly substitution at this position (Table 2). The phenylalanine fit well into the surrounding molecular region with limited disruption of the local hydrogen bonding network.

Binding of the $G_{106}Q$ mutant to either of the two flavivirus group-reactive mAbs, 4G2 and 6B6C-1, was not detected (Table 3). DEN-2 type-specific mAbs 1A5D-1 and 1B4C-2 (DII and DI, respectively) exhibited reduced affinities for $G_{106}Q$ transfected cells and for secreted VLPs. Dengue complex-specific mAb 10A1D-2 also exhibited moderately reduced reactivity for the $G_{106}Q$ VLP antigen (Table 3). However, the reactivity of the $G_{106}Q$ mutant was unchanged from the reactivity of the wild-type pCB8D2-2J-2-9-1 antigen for polyclonal anti-DEN-2 MHIAF, as well as for the remaining subcomplex- and type-specific mAbs: 9A4D-1 (DI), 4E5 (DII), and 3H5, 9A3D-8, 10A4D-2, 9D12, and 1A1D-2 (DIII) (Table 3).

The $W_{231}F$ substitution also abolished the binding of both flavivirus group-reactive mAbs, 4G2 and 6B6C-1, as well as that of flavivirus subgroup-reactive mAb 1B7-5 (Table 3). This substitution additionally interfered with the binding of type-specific DI mAb 1B4C-2, but the binding of the remaining subcomplex- and type-specific DI, DII and DIII mAbs and a polyclonal DEN-2 MHIAF were unchanged relative to the non-mutated wild-type plasmid (Table 3). In three separate experiments, secretion of $W_{231}F$ VLP antigen into the tissue culture medium from transiently transfected COS-1 cells was not detected. Consequently, the effects of this substitution could only be analyzed by IFA of plasmid transfected cells.

The $H_{244}R$ and $K_{247}R$ substitutions did not have an effect on the binding of any mAbs in either IFA of transfected cells, or in Ag-ELISA of secreted VLP antigen.

Example 2

Identification of additional cross-reactive epitopes through nearest neighbor search

This example demonstrates the identification of additional cross-reactive epitopes using a "nearest neighbor" search.

Following the identification of cross-reactive epitope residues G_{106} and W_{231} (DEN-2 numbering), the E-glycoprotein atomic structure was reexamined to search for additional flavivirus cross-reactive epitope residues. A "nearest neighbor" search was conducted of the surface of the E-glycoprotein structure, looking for additional residues located within 10-15 Å of the identified residue. This distance is within the binding footprint of a single antibody paratope (Faebler *et al.*, *J. Mol. Biol.* 313:83-97, 2001). In this second iteration of cross-reactive epitope residue identification the same five optimality criterion as above were used, with one change. The criterion of strict conservation across the flaviviruses was relaxed to now include variable residues. In this way, residues either conserved in their physiochemical nature and/or conserved only within a particular flavivirus complex (such as the four DEN virus serotypes) could be identified.

This nearest neighbor search yielded another seven potential cross-reactive epitope residues. Amino acid substitutions at these positions were modeled into the TBE virus E-glycoprotein structure as described above. Mutagenic PCR primers were then synthesized (Table 1) and used to introduce mutations into the wild-type DEN-2 prM/E expression plasmid. Plasmids were transiently transfected into CHO cells, and transfected cells and secreted VLP antigen were analyzed with the anti-DEN-2 mAb panel (Table 3). The substitutions introduced at these positions (of SEQ ID NO: 14) were: Lys_{64} to Asn ($K_{64}N$), Thr_{76} to Met ($T_{76}M$), Gln_{77} to Arg ($Q_{77}R$), Gly_{104} to His ($G_{104}H$), Leu_{107} to Lys ($L_{107}K$), Glu_{126} to Ala ($E_{126}A$), and Thr_{226} to Asn ($T_{226}N$) (Table 2). A single double mutant combining substitutions at positions 126 and 226 ($E_{126}A/T_{226}N$) was also examined. Since the initial $W_{231}F$ substitution interfered with antigen secretion, the effects of an alternative substitution at this position, Trp_{231} to Leu ($W_{231}L$), were also examined.

The $G_{104}H$, $L_{107}K$, and $W_{231}L$ substitutions had the greatest effect on decreasing the reactivities of DII cross-reactive mAbs. Gly_{104} is located on the upper surface of the dimer at the tip of the tight loop structure which the fusion peptide adopts in the E-glycoprotein dimer (Modis *et al.*, *PNAS* 100:6986-91, 2003; FIG. 2). The residue has moderately high surface accessibility and a relatively high temperature (β-) factor. The replacement of this small aliphatic glycine was modeled with a large polar histidine at this position. The histidine residue fits well into this pocket and was predicted not to alter the hydrogen-bond network in the region. Moreover, because the tick-borne flaviviruses have a histidine at this position (Table 4) it seemed probable that this substitution would not disrupt the structure in this localized region or elsewhere within DII. In fact, *a posteriori* stability calculations based upon the DEN-2 E atomic structure (Modis *et al.*, *PNAS* 100:6986-91, 2003) indicate that the $G_{104}H$ substitution is energetically favorable (Table 2).

The $G_{104}H$ substitution, like both substitutions examined at Trp_{231}, produced a plasmid that was unable to secrete measurable VLP antigen into the tissue culture medium upon transfection of either COS-1 or CHO cells. Consequently, the effects of $G_{104}H$ and $W_{231}L$ substitutions were analyzed solely by IFA of plasmid transfected cells, as described above for $W_{231}F$. The $G_{104}H$ substitution ablated the reactivity of all three of the flavivirus cross-reactive mAbs, 4G2, 6B6C-1, and 1B7-5. The type-specific DII mAb 1A5D-1 also showed strongly reduced reactivity for cells transiently transcribed with this plasmid Table 3). $W_{231}L$ showed a reduction in mAb reactivities very similar to $W_{231}F$, knocking out any discernable recognition of all three cross-reactive mAbs (Table 3). The reactivity of DI mAb 1B4C-2 was also reduced by this mutation, but there were no discernable changes in the reactivities of the remaining subcomplex- and type-specific mAbs or the anti-DEN-2 MHIAF for either the $G_{104}H$ or $W_{231}L$ plasmid constructs (Table 3).

The $L_{107}K$ substituted plasmid exhibited a pattern of reduced reactivities for flavivirus cross-reactive mAbs unlike any of the other substitutions. Leu_{107} sits directly below Gly_{106} on the outer lateral surface of the E-protein dimer. This residue has relatively high surface accessibility and temperature (β-) factor, and its hydrophobic side-chain is directed laterally away from the dimer. This residue is also strongly conserved across the flaviviruses; the exceptions being the tick-borne Powassan virus, JE virus strain SA-14-14-2, and DEN-2 virus strain PUO-280 (Table 4). All of these viruses have a phenylalanine instead of a leucine at this position. A large basic lysine was substituted for the leucine at this position. Modeling of this $L_{107}K$ substitution indicated that it too was unlikely to alter the localized hydrogen bonding network. This observation and the low thermodynamic free energy (ddG) stability calculation (Table 2) suggested that this substitution was unlikely to induce localized or domain associated conformational changes.

Flavivirus group-reactive mAb 4G2 showed no discernable reactivity for this construct in either IFA of plasmid transfected cells, or by Ag-ELISA of secreted VLP antigen. However, the reactivities of the other two cross-reactive mAbs, 6B6C-1 and 1B7-5, were unchanged for this construct relative to the non-mutated wild-type plasmid (Table 3). $L_{107}K$ plasmid-transfected cells and secreted VLP antigen also showed moderately reduced reactivity for mAbs 1A5D-1, 10A1D-2 and 1B4C-2, while all other mAbs and the polyclonal MHIAF reactivities were not significantly different than they were for the wild-type plasmid (Table 3).

Unlike Leu_{107}, Glu_{126} appears to be incorporated into epitopes recognized by flavivirus group-reactive mAb 6B6C-1 and subgroup-reactive mAb 1B7-5, but not in the epitope of flavivirus group-reactive mAb 4G2. Glu_{126} is located 10-12Å from Trp_{231} in the same trough on the upper and outer surface of DII. The bulky side chain projects from the α-carbon backbone up into this trough producing a moderately high surface accessibility and a high β-factor (Fig. 2). The replacement of this large, negatively charged acidic glutamine was modeled with a small hydrophobic alanine at this position. This substitution was predicted to induce a moderately high, but acceptable energetic cost in the free energy stability analysis based on the TBE virus E-glycoprotein structure coordinates (TBE virus equals Lys_{126}, Table 2).

The $E_{126}A$ substitution reduced the reactivity of flavivirus group-reactive mAb 6B6C-1, and moderately reduced the reactivity of subgroup-reactive mAb 1B7-5 (Table 3). However, mAb 6B6C-1 exhibited reduced reactivity only by IFA of mutant plasmid transfected cells, and 1B7-5 only showed reactivity reductions for this construct in Ag-ELISA (Table 3). Similarly, type-specific DII mAb 1A5D-1 exhibited moderately reduced reactivity by Ag-ELISA, but there was no detectable reduction in its reactivity by IFA (Table 3). The $T_{226}N$ substitution did not alter the reactivity of any of the flavivirus group-reactive mAbs relative to the non-mutated wild-type plasmid, and the $E_{126}A/T_{226}N$ double mutant generally showed a similar pattern of reduction of mAb reactivity as did $E_{126}A$ alone. The two exceptions to this correlation were in the reactivities of mAbs 1B7-5 and 10A1D-2. $E_{126}A/T_{226}N$ exhibited the same moderate 87% reduction in Ag-ELISA reactivity for flavivirus subgroup-reactive mAb 1B7-5 as did $E_{126}A$. However, the double mutant also exhibited a strong 97% reduction for this same mAb by IFA, which was not observed for either single mutant (Table 3). DEN virus complex-specific mAb 10A1D-2 also exhibited moderate reactivity decreases by IFA for this double mutant (Table 3).

$K_{64}N$, $T_{76}M$, and $Q_{77}R$ were all unchanged in their reactivities for the flavivirus cross-reactive mAbs. The $T_{76}M$ VLP antigen did however show reduced reactivity for DII type-specific mAb 1A5D-1 and for DI mAb 1B4C-2 in Ag-ELISA (Table 3).

Example 3

Spatial characterization and organization of flavivirus group-reactive epitope residues

This example describes the spatial characterization and organization of exemplary flavivirus cross-reactive epitope residues.

The six residues (G_{104}, G_{106}, L_{107}, E_{126}, T_{226}, and W_{231}) identified as participating in the flavivirus cross-reactive epitopes are spatially arranged on the DEN-2 virus E-glycoprotein surface in two clusters (FIG. 1). The most prominent grouping of these residues is the clustering of three residues from the highly conserved fusion peptide region of DII (Allison *et al.*, *J. Virol.* 75:4268-75, 2001). These residues, Gly_{104}, Gly_{106}, and Leu_{107}, are almost completely conserved across the flaviviruses (Table 4).

The cross-reactive mAbs most strongly affected by substitutions in this region were 4G2 and 6B6C-1. These two mAbs are considered to be quite similar; both are flavivirus group-reactive and have been grouped into the A1 epitope of the E-glycoprotein (Gentry *et al.*, *Am. J. Trop. Med. Hyg.* 31:548-55, 1982; Henchal *et al.*, *Am. J. Trop. Med. Hyg.* 34:162-69, 1985; Mandl *et al.*, *J. Virol.* 63:564-71, 1989; Roehrig *et al.*, *Virology* 246:317-28, 1998). The data disclosed herein demonstrate that although the epitopes of these two mAbs spatially overlap, they do not contain exactly the same residues. Substitutions at G_{104}, G_{106}, or L_{107} knock out the ability of mAb 4G2 to bind to the E-glycoprotein. However, only substitutions at G_{104} and G_{106} interfere with the binding ability of mAb 6B6C-1. L_{107} is therefore not a component of the flavivirus group-reactive epitope recognized by mAb 6B6C-1.

The G_{104}H substitution dramatically reduced the reactivities of all three of the flavivirus cross-reactive mAbs for this construct (Table 3). Without being bound by theory, it is unlikely that a glycine residue, with no side chain, would directly participate in the binding energetics of an antibody-antigen (Ab-Ag) interaction. However, if a glycine residue is included in the buried surface area of this antibody epitope, the introduction of a large bulky hydrophobic side chain is likely to disrupt the Ab-Ag shape complementarity and hence increase the dissociation rate-constant (K_d) of the Ab-Ag interaction (Li *et al.*, *Nature Struct. Biol.* 10:482-88, 2003). G_{104}H also reduced the recognition of type-specific DII mAb 1A5D-1 (Table 3). The 1A5D-1 epitope is non-neutralizing, reduction sensitive and moderately surface accessible (Roehrig *et al.*, *Virology* 246:317-28, 1998). All of the fusion peptide substitutions introduced into this region reduced the reactivity of 1A5D-1, consistent with the interpretation that the buried surface area footprint of this mAb not only includes DEN-2 virus serotype-specific residues, but also includes these strongly conserved residues as well. A comparison of the DEN-2 atomic structure with flavivirus E-glycoprotein alignments identifies at least two unique DEN-2, DII, surface accessible residues (Glu_{71} and Asn_{83}), and a third residue variable within DEN-2 but distinct from the other DEN virus serotypes (Thr_{81}). All of these residues are within 10-22 Å of Gly_{104}, a distance well within the buried surface area of a typical Ab-Ag interface (Lo *et al.*, *J. Mol. Biol.* 285:2177-98, 1999). Alternatively, less surface accessible type-specific residues nearby could participate in mAb 1A5D-1 binding since this epitope itself is only moderately surface accessible (Roehrig *et al.*, *Virology* 246:317-28, 1998). Since this mAb is DEN-2 virus specific, these type-specific residues would be expected to provide the majority of the binding energy for 1A5D-1.

The G_{106}Q substitution also knocked out the reactivities of both of the flavivirus group-reactive mAbs, 4G2 and 6B6C-1, though it did not alter the binding of subgroup-reactive mAb 1B7-5 (Table 3, FIG. 2). Type-specific DII mAb 1A5D-1 again lost all measurable reactivity to the G_{106}Q construct, as did 1B4C-2. The 1A5D-1 epitope footprint appears to include conserved fusion peptide residues in addition to DEN-2 serotype-specific residues as discussed herein. The reduced reactivity of DI mAb 1B4C-2 for the G_{106}Q construct is difficult to explain. Because of the lack of biological activity of DI, epitope assignments to this domain can be problematic (Roehrig *et al.*, *Virology* 246:317-28, 1998). Without being bound by theory, the involvement of Gly_{106} as well as that of Leu_{107} are consistent with the possibility that either the previous DI assignment is incorrect, or that the 1B4C-2 mAb footprint includes residues from both DI and DII. However, if 1B4C-2 recognizes such an inter-domain epitope, this high affinity mAb would be expected to interfere with the E-glycoprotein dimer to trimer reorganization associated with virus-mediated membrane fusion, which it does not.

Leu_{107} is the third residue identified in the fusion peptide region of DII that is incorporated into flavivirus cross-reactive epitopes. Unlike the substitutions at E-glycoprotein positions 104 and 106, the $L_{107}K$ substitution knocked out the reactivity of flavivirus group-reactive mAb 4G2, but it did not alter the reactivity of the other flavivirus group-reactive mAb, 6B6C-1 (Table 3, FIG. 2). Beyond this discrepancy, the reactivity patterns of the rest of the mAbs for this construct were similar to that observed for the other fusion peptide substitutions. mAbs 1A5D-1, 10A1D-2, and 1B4C-2 all showed little to no reactivity for the $L_{107}K$ construct (Table 3).

Previous studies have examined the effects of mutagenesis in this fusion peptide region. Pletnev *et al.* (*J. Virol.* 67:4956-63, 1993) performed mutagenesis to fusion peptide residues 104 and 107 in a chimeric infectious clone containing the TBE virus structural genes and DEN-4 virus non-structural genes. TBE virus has a histidine at position 104 as do all of the tick-borne flaviviruses. Pletnev *et al.* constructed the opposite substitution that was constructed herein, $H_{104}G$, replacing the tick-associated histidine with the mosquito-associated glycine, but they were unable to recover live virus from this construct. They also constructed a double mutant $H_{104}G$/ $L_{107}F$ from which they were able to recover virus; however, they were unable to detect any effect of these mutations on mouse neurovirulence. Allison *et al.* (*J. Virol.* 75:4268-75, 2001) also performed mutagenesis at Leu_{107} examining the role of this residue in virus-mediated membrane fusion using TBE virus VLPs. They replaced Leu_{107} with phenylalanine, threonine, or aspartic acid. They found that all of these mutations reduced the rate of fusion. Moreover, consistent with the results presented herein, they found that the $L_{107}D$ substitution appeared to completely abolish the binding of their DII flavivirus group-reactive mAb A1.

The fourth residue identified as having a major effect on the flavivirus cross-reactive mAbs was Trp_{231}, an invariant residue across the flaviviruses (Table 4). Both substitutions introduced at Trp_{231} dramatically reduced the reactivity of all three of the flavivirus cross-reactive mAbs, 4G2, 6B6C-1, and 1B7-5. This residue is structurally distant from the fusion peptide region (FIGS. 1 and 2). It is somewhat surprising that substitutions at this residue affect the binding of mAbs also shown to recognize the distant fusion peptide residues. With out being bound by theory, the strict conservation of tryptophan (Table 4) and the predicted high energetic costs of substitutions at this position (Table 2) suggest that this residue could be important for proper DI/DII conformational structure and function. If this were the case, the loss of reactivity of mAbs recognizing fusion peptide residues could occur from the induction of localized structural disturbances across DII occurring at a distance from Trp_{231}. However, the Trp_{231} substitutions did not significantly affect the binding of any of the remaining DII mAbs, 4E5, 1A5D-1, and 10A1D-2 (DI or DII); whereas mAb 1A5D-1 reactivity was reduced or ablated by all of the fusion peptide substitutions. mAb 4E5 does not recognize native virus yet it blocks virus-mediated cell-membrane fusion, presumably by recognizing an epitope that is exposed only during or after low-pH-catalyzed conformational changes (Roehrig *et al.*, *Virology* 246:317-28, 1998). Without being bound by theory, if substitutions at Trp_{231} induced domain wide structural alterations, a loss of reactivity of mAb 1A5D-1 (and the possible exposure of the non-native-accessible mAb 4E5 epitope, resulting in an increase, or at least a change in, the reactivity of mAb 4E5 by IFA for these constructs), would be expected. Moreover, the reactivities of polyclonal MHIAF and of all of the DIII mAbs were no different for these constructs than they were for the non-mutated wild-type plasmid transfected cells (Table 3). DIII however, is reduction-denaturation stable and folds into its native IgC like conformation even when this domain is expressed alone without the remainder of the E-glycoprotein (Bhardwaj *et al.*, *J. Virol.* 75:4002-07, 2001).

Both $W_{231}F$ and $W_{231}L$ plasmids, as well as the $G_{104}H$ plasmid, failed to secrete measurable VLP antigen into tissue culture media following transient transfection of COS-1 or CHO cells. The inability of cells transfected with these plasmids to secrete VLP antigen into tissue-culture media could result from the disruption of a variety of protein maturation processes. Without being bound by theory, interference with particle maturation could occur via disruption of E-prM/M intermolecular interactions, E-glycoprotein dimer interactions, or via the disruption of dimer organization into the surface lattice covering mature particles. Although the two processes are interdependent, these substitutions may not interfere with particle formation per se, but may directly interfere with particle secretion itself. In fact, the IFA staining pattern of DEN-2 $G_{104}H$ and of $W_{231}F/L$ transfected cells was highly punctate and localized within inclusion bodies. Similar IFA staining patterns have been observed with non-secreting constructs of dengue and other flaviviruses (Chang *et al.*, *Virology* 306:170-80, 2003). Studies with TBE virus VLPs have shown that interactions between prM and E are involved in prM-mediated intracellular transport of prM-E heterodimers (Allison *et al.*, *J. Virol.* 73:5605-12, 1999). The location of Gly_{104} near the interior-lateral edge of DII puts it very close to the E-dimer "hole" where the prM/M proteins are located in the heterodimer (Kuhn *et al.*, *Cell* 108:717-25, 2002; FIG. 1). Therefore, it seems likely that $G_{104}H$ interferes with VLP secretion via disruption of the prM-E interactions necessary for intracellular transport and secretion. The identity of this residue is positively correlated with arthropod vector. The mosquito-born flaviviruses have a glycine at this position whereas the tick-borne flaviviruses have a histidine. Interestingly, Pletnev *et al.* (*J. Virol.* 67:4956-63, 1993) introduced the reverse substitution, $H_{104}G$, into the TBE virus E-glycoprotein in a TBE/DEN-4 chimeric infectious clone, and they were unable to recover virus from this mutant. The inability of $G_{104}H$ transfected cells to secrete VLP antigen similarly suggests that this too could be a lethal substitution in DEN-2 virus. Taken together, these two results are consistent with the idea that vector-specific selection has produced strong epistasis between this residue and other unidentified residue(s) elsewhere in the E- or prM/M proteins.

Example 4

Identification of flavivirus complex and sub-complex cross-reactive epitope residues

This example demonstrates the identification of flavivirus complex and sub-complex cross-reactive epitopes using a structure-based rational mutagenesis method.

Cell culture, virus strains and recombinant plasmids

CHO cells (ATCC CCL 61; Manassas, VA) were grown at 37°C with 5% CO_2 on Dulbeco's modified Eagle's minimal essential medium with F-12 nutrient mixture (D-MEM/F-12, GIBCO, Grand Island, NY) supplemented with 10% heat-inactivated fetal bovine serum (FBS, Hyclone Laboratories, Inc., Logan, UT), 110 mg/l sodium pyruvate, 0.1 mM nonessential amino acids, 2 mM L-glutamine, 2.438 g/L $NaHCO_3$, 100 U/ml penicillin, and 100 μg/ml streptomycin.

The recombinant expression plasmids pCB8SJ2 and pCBWN were used as template DNAs for both site-directed mutagenesis and for transient expression of St. Louis encephalitis virus (SLEV) and West Nile virus (WNV) recombinant antigen (see below). The pCB8SJ2 plasmid includes the human cytomegalovirus early gene promoter, Japanese encephalitis virus (JEV) signal sequence, SLEV prM and E gene region (amino-terminal 80%), JEV carboxyl terminal 20%, and bovine growth hormone poly(A) signal. The replacement of the terminal 20% of SLEV E with JEV E gene sequences dramatically increases the secretion of extracellular VLPs into the culture medium without altering the native SLEV E glycoprotein conformation (Purdy *et al.*, *J. Clin. Micro.* 42:4709-17, 2004). The pCBWN plasmid includes the human cytomegalovirus early gene promoter, JEV signal sequence, WNV prM and E gene region in its entirety, and bovine growth hormone poly(A) signal (Davis *et al.*, *J. Virol.* 75:4040-47, 2001).

Procedural algorithm

Following the identification and ablation of flavivirus group cross-reactive epitopes, flavivirus complex and sub-complex cross-reactive epitopes have been identified. Two different flavivirus complexes, the JEV complex and the DENV complex, were focused on. The DENV complex consists of the four dengue serotypes, DENV-1, DENV-2, DENV-3, and DENV-4. The large JEV complex includes JEV, WNV, Murray Valley encephalitis virus (MVEV), and SLEV.

The procedural algorithm for the identification of flavivirus complex and sub-complex cross-reactive epitopes utilizes the following optimality criteria: 1) The identification and selection of amino acid residues with ≥35% of their surface solvent accessible. These residues are identified from the published atomic structure coordinates of the DENV-2 soluble ectodomain of the envelope glycoprotein and homology models of SLEV and WNV derived from the DENV-2 structure (Modis *et al., Proc. Natl. Acad. Sci. USA* 100:6986-91, 2003). In addition to examination of amino acid residues in structural domain II, residues in domains I and III were examined, since published results indicate that some complex and sub-complex cross-reactive epitopes are mapped onto domains I and III in addition to domain II (Roehrig *et al.*, *Virology* 246:317-28, 1998). 2) Amino acids on the outer or lateral surface of the E-glycoprotein dimer, and accessible to antibody. 3) Amino acid conservation across the flavivirus complex (based upon a structural alignment of the protein sequences). Residues conserved across all member viruses of the same complex are favored. If conserved within but not across the entire complex, then residues with shared identities between WNV and SLEV are favored in the JEV complex, and residues with shared identities between DENV-2 and two or more other viruses in the DENV complex are favored over those shared with DENV-2 and only one other DENV complex virus. 4) Side chain projections exposed towards the outer surface and accessible to antibody paratopes. 5) Residues with high temperature (β-) factors should be favored, as these residues tend to be flexible and are able to conform to the antibody paratope, increasing the antibody-antigen affinity. Amino acid residues with high temperature factors are more commonly found in antigen epitopes than lower temperature factor residues. 6) Following identification of potential individual flavivirus complex and sub-complex cross-reactive epitope residues, all residues are mapped and highlighted on the same E-glycoprotein dimer structure together. With this technique, groups of potential cross-reactive epitope residues forming clusters (and hence probable epitopes) are readily identified. 7) Residues fitting all of these criteria and occurring in structural clusters approximately 20 x 30 $Å^2$ (which is the average "footprint" of an antibody Fab that interacts with an antigen epitope) are favored over residues that are more isolated in the protein structure. 8) Within an identified structural cluster of potential epitope residues, residues that more completely satisfy greater numbers of the optimality criteria are selected for the first round of mutagenesis analysis.

Site-directed mutagenesis

Site-specific mutations were introduced into the SLEV and WNV E genes using the Stratagene Quick Change® multi site-directed mutagenesis kit (Stratagene, La Jolla, CA) and pCB8SJ2 and pCBWN as DNA templates following the manufacturer's recommended protocols. The sequences of the mutagenic primers used for all constructs are listed in Table 5. Four or five colonies from each mutagenic PCR transformation were selected and grown in 5 ml LB broth cultures. DNA was mini-prepped and sequenced from these cultures. Structural gene regions and regulatory elements of all purified plasmids were sequenced entirely upon identification of the correct mutation. Automated DNA sequencing was performed using a Beckman Coulter CEQ™ 8000 genetic analysis system (Beckman Coulter, Fullerton, CA) and analyzed using Beckman Coulter CEQ™ 8000 (Beckman Coulter, Fullerton, CA) and Lasergene® software (DNASTAR, Madison, WI).

Transient expression of SLEV and WNV recombinant antigens by CHO cells

CHO cells were electroporated with pCB8SJ2 or pCBWN using the protocol described by Chang *et al.* (*J. Virol.* 74:4244-52, 2000). Electroporated cells were recovered in 50 ml DMEM, seeded into 150 cm^2 culture flasks for VLP expression and into 96-well tissue culture plates for IFA, and incubated at 37°C with 5% CO_2. Cells in 96 well plates for IFA were fixed 14-24 hours post electroporation. Tissue-culture medium and cells were harvested 48-72 hours post electroporation for antigen characterization.

Characterization of mutant pCB8SJ2 and pCBWN infected cells and secreted antigen

Fourteen to twenty four hours following electroporation, 96-well tissue culture plates (Costar® #3603 Corning, Inc., Corning, NY) containing cells transformed with the mutated pCB8SJ2 or pCBWN clones were washed twice with PBS, fixed with 3:1 acetone:PBS (v:v) for 10 minutes and air dried. E-glycoprotein-specific mAbs recognizing each of the three E-glycoprotein domains (Table 6) were used to determine affinity reductions in cross-reactive epitopes by IFA as described by Chang *et al.* (*J. Virol.* 74:4244-52, 2000).

Tissue culture medium was harvested 48-72 hours following electroporation. Cell debris was removed from tissue culture media by centrifugation for 30 minutes at 10,000 rpm. Ag-ELISA was used to detect secreted antigen from the mutagenized pCB8SJ2 and pCBWN transformed CHO cells. Secreted antigen was captured with polyclonal rabbit anti-SLEV and rabbit anti-pCBWN sera at 1:30,000 and 1:50,000 dilutions, respectively. MHIAF specific for SLEV and WNV was used at a 1:15,000 dilution to detect captured antigen, and this MHIAF was detected using horseradish peroxidase conjugated goat anti-mouse HIAF at a 1:5000 dilution.

Secreted antigen was concentrated from positive tissue culture medium by centrifugation overnight at 19,000 rpm, and resuspended in TN buffer (50 mM Tris, 100 mM NaCl, pH 7.5) to 1/100th the original volume. Alternatively, some antigens were concentrated using Millipore's Amicon® Ultra PL-100 (Millipore, Billerica, MA) centrifugal filter devices. Concentrated antigen was analyzed with a panel of anti-flavivirus mAbs in Ag-ELISA to determine mAb end point reactivities of the mutated antigens, following the protocol of Roehrig *et al.* (*Virology* 246:317-28, 1998). This Ag-ELISA protocol is the same as that used herein to detect secreted antigen, with the exception of using the specified mAbs (Table 6) instead of polyclonal MHIAF.

Antigenic characterization and MAb screening of potential cross-reactive epitope residue mutants

Using the structure-based design approach described above, candidate flavivirus complex and sub-complex cross-reactive epitope residues were narrowed down to 34 in DENV-2 and 31 each in WNV and SLEV. From these residues and with reiterative application of the optimality criteria described herein 17 DENV-2, 13 WNV, and 11 SLEV residues were chosen as most likely to be incorporated into complex and sub-complex cross-reactive epitopes (highlighted in Tables 7-9). Amino acid substitutions were modeled at these probable cross-reactive epitope residues, selecting substitutions that should potentially disrupt or ablate antibody recognition without altering E-glycoprotein structural conformation, disrupting dimer interactions, or impairing particle formation, maturation, or secretion. Stability calculations were performed for all possible amino acid substitutions of candidate residues using the PoPMuSiC server, (available on the Université Libre de Bruxelles' web site) and the DENV-2 E-glycoprotein pdb file coordinates (Modis *et al.*, *Proc. Natl.*

Acad. Sci. 100:6986-91, 2003) or homology model coordinates for WNV and SLEV. Amino acid substitutions modeled in the E-glycoprotein structures with free energies of folding equal to or less than that of the non-mutated wild-type E-glycoprotein were re-examined with the Swiss-Pdb Viewer software (available on the Swiss Institute of Bioinformatics' web site) to identify those substitutions that minimized local structural disturbances while maintaining structurally relevant biochemical interactions such as hydrogen bonding and/or charge interactions with neighboring amino acids.

Substitutions at 11 of 16 potential cross-reactive epitope residues selected for mutagenesis in pCB8SJ2 altered the reactivities of all 14 of the anti-SLE mAbs, relative to wild-type pCB8SJ2 (Table 10). Eight of the 14 MAbs were flavivirus group- or subgroup-cross-reactive (see Table 6). Substitutions at nine of the 16 residues analyzed altered the reactivity of all eight of the flavivirus group- or subgroup-cross-reactive mAbs. Substitutions at four of 16 potential cross-reactive epitope residues altered all three of the JEV complex- and subcomplex-cross reactive mAbs. Only one substitution however, affected type-specific mAb reactivities (Fig. 3). The effect of this substitution ($G_{106}Q$) on type-specific mAb reactivities was to actually increase the reactivity of these mAbs relative to that of the wild-type unaltered pCB8SJ2. Without being bound by a single theory, such increase in the reactivity of type-specific antibodies is believed to be beneficial for the development of type-specific flavivirus antigens.

Substitutions at 14 of 17 residues selected for mutagenesis in pCBWN altered the reactivities of all 10 of the anti-WNV mAbs, relative to wild-type pCBWN (Table 11). Six of the 10 anti-WNV mAbs were flavivirus group- or subgroup-cross-reactive, two were JEV complex cross-reactive and two were WNV type-specific (see Table 6). Nine of the 17 substitutions examined altered the reactivities of all six group- and subgroup-cross-reactive mAbs; 12 of these 17 substitutions affected the reactivities of both of the JEV complex cross-reactive mAbs. The $G_{106}V$ substitution in pCBWN was the only substitution to alter type-specific mAb reactivities, and, as with pCB8SJ2, this substitution actually increased the reactivity of the type-specific mAbs (Fig. 3).

The outcome that many of these substitutions altered mAb reactivities (Tables 10 and 11; Fig. 3) illustrates not only the efficiency of the described algorithms for identifying cross-reactive epitope residues, but also that these cross-reactive epitopes can be altered to ablate or appreciably interfere with the ability of an antibody to recognize these modified antigens. For example, 82% and 69% of the potential cross-reactive epitope residue substitutions examined in pCBWN and pCB8SJ2, respectively, affected all of the cross-reactive antibodies reactive to these two viruses from the antibody panel (see Fig. 3). The high percentage of residues, selected *a priori,* affecting mAb reactivities illustrates the accuracy of the cross-reactive epitope residue selection algorithms.

The mAb characterization of potential cross-reactive epitope residue mutants illustrates the importance of the E-protein fusion peptide region as a potently cross-reactive antigenic determinant. As described herein, substitutions at fusion peptide residues G_{104}, G_{106}, and L_{107} strongly affected many of the mAb reactivities for DENV-2, SLEV and WNV (see Tables 10 and 11). Without being bound by a single theory, G_{106} appears to be the most important cross-reactive antigenic determinant of these residues. Substitutions at G_{106} altered the reactivities of 7 of 10 cross-reactive mAbs recognizing SLEV, and 7 of 8 cross-reactive mAbs recognizing WNV (see Tables 10 and 11). Substitutions at fusion peptide residue G104 also affected the reactivities of many mAbs for each of these viruses. However, all substitutions examined at this position produced plasmids that were unable to efficiently secrete VLP antigen upon transient transformation into eukaryotic cells. This observation was true for all three flaviviruses examined: DENV-2, SLEV and WNV.

Substitutions at fusion peptide residue G_{106} had a variety of effects on mAb reactivities for both pCBWN and pCB8SJ2. The majority of the substitutions at this residue reduced or ablated a mAb's ability to recognize the antigen. This occurred with cross-reactive mAbs 4G2, 6B6C-1, 4A1B-9, and 2B5B-3 in G_{106}V-pCBWN and with 4G2 and 2B5B-3 for G_{106}Q-pCB8SJ2 (see Tables 10 and 11), indicating that the substituted residue is a part of the antigenic epitope recognized by these antibodies.

Example 5

Human IgM MAC-ELISA Serology

This example demonstrates the representative nature of a murine antibody response as a model of human antibody response to substitutions in the flavivirus cross-reactive epitopes.

Human sera

Well-characterized serum specimens were assembled from the Diagnostic and Reference Laboratory, Arbovirus Diseases Branch, Division of Vector-Borne Infectious Diseases, US Centers for Disease Control and Prevention. A serum panel (see Table 12) was assembled from patients infected in the US between 1999 and 2004 with either WNV (n=6) or SLEV (n=10), as determined by the standard 90% plaque-reduction neutralization (PRNT) assay. SLEV is endemic to North America, whereas WNV was first introduced into North America in 1999 and has spread epidemically since that time.

The flavivirus responsible for the most recent infection was determined as that with the highest neutralizing antibody titer, which had to be at least four-fold greater than that for any other virus tested. Because of the high level of cross-reactivity between the SLEV and WNV viruses, it is often difficult to determine the infecting virus by ELISA, thus requiring the PRNT. SLEV infected sera with measurably high levels of cross-reactivity for WNV were purposefully selected in order to maximize the ability to asses for improved discrepancy (specificity) of the pCBWN-G_{106}V versus the pCBWN wild-type antigen. SLEV infected patient sera were split into two groups based upon previously determined (Diagnostic and Reference Laboratory) positive to negative (P/N) ratios for SLEV and for WNV. 'Equivocal' SLEV sera (n=5) were those that were clear SLEV infections from the PRNT data, yet had MAC-ELISA P/N ratios that were not statistically different between SLEV and WNV. Three of these equivocal SLEV samples were negative (P/N $\leq$2.0) for both viruses, one was presumptive positive (P/N $\geq$2.0 and <3.0), and one was definitive positive (P/N >5.0) for both viruses. 'Misleading' SLEV sera (n=5) were SLEV positive in the PRNT, yet had MAC-ELISA P/N ratios that were not only positive for both viruses, but were actually greater for WNV than for SLEV. Definitive 'positive' WNV infected patient sera (*n*=6) were selected based on MAC-ELISA results from the Diagnostic and Reference Laboratory collection for use as positive control sera to assess the accuracy of the pCBWN-G_{106}V plasmid derived antigen.

IgM ELISA protocols

IgM ELISAs were performed following the protocols of Purdy *et al.* (*J. Clin. Micro.* 42:4709-17, 2004) and Holmes *et al.* (*J. Clin. Micro.* 43:3227-36, 2005). Briefly, the inner 60 wells of Immulon II HB flat-bottomed 96-well plates (Dynatech Industries Inc., Chantilly, VA) were coated overnight at 4°C in a humidified chamber with 75 µl of goat anti-human IgM (Kierkegaard & Perry Laboratories, Gaithersburg, MD) diluted at 1:2000 in coating buffer (0.015 M sodium carbonate, 0.035 M sodium bicarbonate, pH 9.6). Wells were blocked with 300 µl of InBlock blocking buffer (Inbios, Seattle, WA, L/N FA1032) for 60 minutes at 37°C in a humidified chamber. 50 µl of sera were added to each well and incubated again for 60 minutes at 37°C in a humidified chamber. Human test sera were diluted 1:400 in sample dilution buffer (Inbios, L/N FA1055). Positive control sera were diluted 1:3000 for SLEV and 1:800 for WNV. Positive and negative control VLP antigens were tested on all patient sera in triplicate by diluting appropriately in sample dilution buffer and adding 50 µl to appropriate wells for incubation overnight at 4°C in a humidified chamber. Captured antigens were detected with 50 µl/well of polyclonal rabbit anti-pCBWN diluted 1:1000 in sample dilution buffer and incubated for 60 m at 37°C in a humidified chamber. Rabbit sera was detected with horseradish peroxidase conjugated goat anti-rabbit sera diluted 1:8000 in IgM conjugate dilution buffer (Inbios, L/N FA1056) and incubated for 60 m at 37°C in a humidified chamber. Bound conjugate was detected with 75 µl of 3,3'5,5'-tetramethylbenzidine (Neogen Corp, Lexington, KY) substrate, incubated at RT for 10 min, stopped with 50 µl of 2N H_2SO_4, and then read at A_{450} using an ELx405HT Bio-Kinetics microplate reader (Bio-Tek Instruments Inc., Winooski, VT).

IgM test validation and interpretation

Test validation and P/N values were determined according to the procedure of Martin *et al.* (*J. Clin. Micro.* 38:1823-26, 2000), using internal positive and negative serum controls included in each 96-well plate. Positive (P) values for each specimen were determined as the average A_{450} for the patient serum sample incubated with positive VLP antigen. Negative (N) values were determined for each plate as the average A_{450} for the normal human serum control incubated with positive VLP antigen.

Human serology

To determine how representative the murine antibody response (mAb data) is as a model of the human antibody response (serological data) to the viral substitution antigens described herein, serological assays were performed with single substitution, prototype type-specific antigens. As the mAb screening results indicated that fusion peptide residue 106 was incorporated into multiple cross-reactive epitopes for both WNV and SLEV, this substitution was selected to conduct MAC-ELISA serum tests.

The prototype type-specific G_{106}V-WNV Ag dramatically outperformed the wild-type (wt)-WNV Ag when tested on 10 difficult to discern 'equivocal' or positively 'misleading' SLEV-infected patient sera (Table 12). Six of 10 of these SLEV infected sera were correctly diagnosed as WNV-negative by MAC-ELISA (P/N $\leq$2.0) with the G_{106}V-WNV prototype Ag, three were 'equivocal' (P/N >2.0 $\leq$3.0) and one was WNV positive. However, when these same sera were tested with the wt-WNV Ag, only four sera were correctly scored as WNV negative, one was equivocal, and five were misdiagnosed as WNV positive with this unmodified Ag. When antigens were directly compared on each individual serum sample, the G_{106}V-WNV Ag produced lower P/N ratios than did the wt-WNV Ag in nine of 10 cases on these SLEV infected sera, indicating that the G_{106}V-WNV Ag exhibits improved specificity and reduced cross-reactivity relative to the wt-WNV Ag.

The prototype type-specific G_{106}V-WNV Ag also outperformed the unaltered wt-WNV Ag in MAC-ELISA sensitivity tests on positive WNV infected human sera (Table 12). Five of six WNV infected patient sera had positive P/N ratios when tested with the G_{106}V-WNV Ag, whereas four were positive with the wt-WNV Ag. The single WNV positive serum sample that tested negative with the wt-Ag and equivocal with the G_{106}V Ag had the lowest neutralizing titers of the WNV sera in the PRNT (see Table 12), indicative of a weak antibody titer.

In addition to improved accuracy with the G_{106}V-WNV Ag, it was also more sensitive than was the wt-WNV Ag. In 5 of the 6 WNV infected sera, the MAC-ELISA P/N ratios were higher with the G_{106}V- than with the wt-WNV Ag (Table 12). Higher P/N ratios are expected from an improved type-specific Ag relative to the cross-reactive wt Ag when tested on sera infected with the same virus.

The prototype type-specific G_{106}V-WNV Ag exhibited improved specificity, accuracy, and sensitivity relative to the unmodified wt-WNV Ag. The G_{106}V-WNV Ag was more specific and accurate for WNV diagnosis than was the wt Ag, correctly diagnosing more WNV infected sera as positive and fewer SLEV infected sera as negative, than did the wt-WNV Ag. The G_{106}V-WNV Ag was also more sensitive at detecting WNV antibody in WNV infected serum than was the wt-WNV Ag. The positive signal indicating the presence of WNV antibody (P/N ratios) was greater for G_{106}V-WNV Ag than it was for the wt-Ag when testing WNV infected sera, and less than that of the wt-Ag when testing non-WNV infected sera.

Example 6

Murine Immunization

This example demonstrates the ability of prototypical type-specific flavivirus mutant compositions to generate type-specific neutralizing antibody responses in mice.

Mouse vaccination

Groups of six female outbred ICR mice were used in this study. Mice were immunized by injection with pCB8D2-2J-2-9-1, pCB8D2-2J-2-9-1-G_{106}Q, pCBWN, pCBWN-G_{106}V, pCB8SJ2, or pCB8SJ2-G_{106}Q expression plasmids as described herein. Each mouse was injected with 100 µg of Picogreen® fluorometer quantified plasmid DNA in PBS pH 7.5, at a concentration of 1 µg/µl. Mice were immunized with 50 µg of plasmid DNA injected intramuscularly into each thigh on weeks 0 and 3. Mice were bled on week six following initial vaccination.

Plaque reduction neutralization assays

Six week post-vaccination serum specimens were tested for the presence of type-specific neutralizing (Nt) antibody (Ab) by plaque reduction neutralization test (PRNT). PRNT was performed with freshly confluent Vero cell monolayers as described by Chang *et al.* (*J. Virol.* 74:4244-52, 2000) using DENV-2 (16681), WNV (NY-99), and SLEV (MSI-7) viruses.

Neutralizing antibody responses

Mice were immunized with wild-type and G_{106} substituted plasmids for WNV, SLEV, and DENV-2 to determine if there were differences between the wild-type and G_{106} prototype type-specific antigens for type-specific Nt Ab titer, cross-reactive Nt Ab titer, and protection from virus challenge. The type-specific Nt Ab titer results are shown in Table 13. There was little difference in the 75% PRNT titer between wt and G_{106} substituted plasmids for all three viruses. The 75% Nt Ab titer was greater than or equal to 1:128 for almost all of the mice immunized with both the DENV-2 and both the WNV DNA vaccines. One mouse immunized with the wt DENV-2 DNA vaccine had a 75% PRNT titer of 1:64, and two mice immunized with the pCBWN-G_{106}V DNA vaccine had 75% PRNT titers of 1:64 and 1:16.

These results demonstrate that for all three flaviviruses tested, there was little to no detectable difference in type-specific neutralizing antibody titer between the prototype type-specific G_{106} mutant vaccines and their wt counterparts. These results also illustrate that the methods described herein for ablating cross-reactive epitope residues can be used to generate type-specific flavivirus prM/E expression plasmids for use as DNA vaccines that still maintain potent type-specific neutralizing immunogenicity.

Example 7

Reduction of Cross-reactive Immunogenicity of Type-specific Genetic Vaccines

This example provides methods by which prototypical type-specific flavivirus mutant compositions can be used to generate a reduced cross-reactive neutralizing antibody response relative to the unaltered wild-type compositions.

Mouse vaccination and plaque reduction neutralization assays

Female outbred ICR mice (such as the mice in Example 6) can be used in this study. Twelve-week post vaccination serum samples from immunized mice will be tested for cross-reactive (*heterologous*) Nt antibody response by PRNT. Unlike the type-specific PRNTs performed in Example 6, the cross-reactive PRNTs will be performed by examining Nt of immunized mouse sera not only for the type-specific virus used for immunization, but also for Nt of the seven other medically important flaviviruses. Thus, all 12-week mouse sera will be tested for neutralization against eight different flaviviruses: all four dengue serocomplex viruses, DENV-1 (16007), DENV-2 (16681), DENV-3 (H87), and DENV-4 (H241); three JEV serocomplex viruses, JEV (SA14-14-2), WNV (NY-99) and SLEV (MSI-7); and the single medically important member of the yellow fever virus serocomplex, YFV (17D).

Predicted antibody response

Without being bound by theory, similar type-specific Nt Ab titers between the prototype type-specific G_{106} mutant vaccines and their wt counterparts are expected. Thus, both pCBWN and pCBWN-G_{106}V vaccinated mouse sera are predicted to have similar Nt Ab titers against WNV, and pCB8D2-2J-2-9-1 and pCB8D2-2J-2-9-1-G_{106}Q will have similar Nt Ab titers against DENV-2. However, when these same sera are tested for Nt against the heterologous flaviviruses, it is expected that significantly lower PRNT titers for prototype type-specific G_{106} mutant vaccinated mouse sera will be observed than for the counterpart wt vaccinated mouse sera. For example, mice immunized with pCBWN and pCBWN-G_{106}V will both have similar PRNT titers against WNV, whereas, pCBWN-G_{106}V immunized mice will have significantly lower PRNT titer against SLEV, JEV, YF, and the four dengue serotype viruses, than wild-type pCBWN immunized mice.

Example 8

Combining Multiple Cross-reactive Epitope Substitutions into Single Plasmid Constructs

This example provides methods by which individual substitutions affecting different flavivirus cross-reactive epitopes can be combined into a single construct.

Individual substitutions affecting different flavivirus cross-reactive epitopes (such as those disclosed herein) can be combined into a single construct based, for example, on mAb screening results disclosed herein (see, Tables 3, 10 and 11), as well as additional mAb screening studies. For example, a mutagenesis primer has been designed for SLEV to introduce both the G_{106}Q and L_{107}K substitutions into a single pCB8SJ2 plasmid (see, Table 5). This double mutation plasmid has been constructed, and its sequence confirmed.

Cells can be transformed with this double mutated plasmid (or another plasmid containing a sequence encoding an E glycoprotein having a combination of two or more mutated amino acids), and the antigen characterized. In SLEV, the G_{106}Q substitution alone alters the reactivities of many mAbs recognizing distinct cross-reactive epitopes (Table 10). However, this substitution alone has no significant effect on the flavivirus group cross-reactive epitope recognized by MAb T-23-1. The $L_{107}K$ substitution does knock out the ability of mAb T-23-1 to recognize the flavivirus cross-reactive epitope. Without being bound by theory, this suggests that L_{107} is incorporated in the cross-reactive epitope recognized by mAb T-23-1, while G_{106} is not.

Because of the generally additive effects observed when combining these substitutions into single constructs (see, Tables 10 and 11), it is expected that $G_{106}Q/L_{107}K$ antigen will combine the different effects observed from mAb screening of the individual mutants into a single, multiple substituted mutant. Upon transfection into mammalian cells, such a multiple mutant plasmid can be used to produce improved type-specific antigens. When utilized as genetic vaccines, these plasmids are expected to exhibit further reductions in cross-reactive immunogenicity while still inducing a potent type-specific immune response.

Example 9

Immune Stimulatory Compositions for the Inhibition or Treatment of a Flavivirus Infection

This example provides methods for administering substances suitable for use as immune stimulatory compositions for the inhibition or treatment of a flavivirus infection.

An immune stimulatory composition containing a therapeutically effective amount of a flavivirus polypeptide that includes at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity (particularly in an E glycoprotein) can be administered to a subject at risk for, or exposed, to a flavivirus (*e.g.*, a dengue virus, West Nile virus, etc.). Alternatively, an immune stimulatory composition containing a therapeutically effective amount of a nucleic acid vector that includes flavivirus nucleic acid molecules described herein, or that includes a nucleic acid sequence encoding at least one flavivirus cross-reactive epitope with reduced or ablated cross-reactivity (particularly in an E glycoprotein), can be administered to a subject at risk for, or exposed to a flavivirus.

Dosages and routes of administration for the immune stimulatory composition can be readily determined by one of ordinary skill in the art. Therapeutically effective amounts of an immune stimulatory composition can be determined, in one example, by *in vitro* assays or animal studies. When *in vitro* or animal assays are used, a dosage is administered to provide a target tissue concentration similar to that which has been shown to be effective in the *in vitro* or animal assays.

While this disclosure has been described with an emphasis on preferred embodiments, it will be apparent to those of ordinary skill in the art that variations and equivalents of the preferred embodiments may be used and it is intended that the disclosure may be practiced otherwise than as specifically described herein. Accordingly, this disclosure includes all modifications encompassed within the spirit and scope of the disclosure as defined by the claims below.

APPENDIX I

TABLES

Table 1. Nucleotide sequence of primers used for mutagenesis. The mismatched nucleotides causing the desired substitutions are underlined.

Sequence	SEQ ID NO:	Mutation
5'-TGTTGTTGTGTTGGTTAGGTTTGCCTCTATACAG-3'	1	K_{64}N
5'-TGGGTTCCCCTTGCATTGGGCAGCGAGATTCTGTTGTTG-3'	2	T_{76}M
5'-TTCATTTAGGCTGGGTTCCCCTCGTGTTGGGCAG-3'	3	Q_{77}R
5'-CCCTTTCCAAATAGTCCACAGTGATTTCCCCATCCTCTGTCTACC-3'	4	G_{104}H
5'-GCCTCCCTTTCCAAATAGTTGACATCCATTTCCCCA-3'	5	G_{106}Q
5'-GGTCACAATGCCTCCCTTTCCAAATTTTCCACATCCATTTCCCC-3'	6	L_{107}K
5'-AGTTTTCTGGTTGCACAACTTTTCCTGCCATGTTCTTTTTGC-3'	7	E_{126}A
5'-GTATCCAATTTGACCCTTGATTGTCCGCTCCGGGCAACC-3'	8	T_{226}N
5'-GTCTCTTTCTGTATGAAATTTGACCCTTGTGTGTC-3'	9	W_{231}F
5'-AATGTCTCTTTCTGTATCAGATTTGACCCTTGTGTGTCCGCTCC-3'	10	W_{231}L
5'-TCCTGTTTCTTCGCACGGGGATTTTTGAAAGTGACC-3'	11	H_{244}R
5'-ACAACAACATCCTGTCGCTTCGCATGGGGATTTTTG-3'	12	K_{247}R

Table 2. Stability free energy (ddG) calculations for putative domain II cross-reactive epitope substitutions based upon the published pdb coordinates for the DEN-2 virus (Modis *et al.*, *PNAS* 100:6986-91, 2003) and the TBE virus (Rey *et al.*, *Nature* 375:291-98, 1995) E-glycoprotein structures.

DEN-2 SUB	ddG (kcal/mol)	TBE SUB	ddG (kcal/mol)
K64N	-0.45	K64N	-0.15
T76M	-0.54	T76M	-0.02
Q77R	0.45	M77R	-0.10
G104H	-0.16	H104H	NA
G106Q	0.87	G106Q	-0.03
L107K	0.19	L107K	0.12
E126A	2.16	K126A	0.85
T226N	0.33	Q233N	0.03
E126A/T226N	2.49	K126A/Q233N	0.88
W231F	1.54	W235F	1.34
W231L	1.84	W235L	2.26
H244R	4.18	H248R	0.00
K247R	-0.30	K251R	-0.19

Table 3. mAb reactivities for mutant and wild-type plasmids.

mAb	D2HIAF	4G2	6B6C1	4E5	1A5D1	1B7-5	10A1D2	1B4C2	9A4D1	3H5	9A3D8	10A4D2	9D12
Epitope	polyclonal	A1	A1	A2	A3	A5	A/C	C1	C4	B1	B2	B3	B4
PRNT	+	+	+/-	+	-	+	-	-	-	+	+	+	+
SA	+	+	+	-	+/-	+	+/-	+	-	+	+	+	+
Specificity	NA	group	group	sub-comp.	type	sub-group	comp.	sub-comp.	type	type	type	sub-comp.	type
Wild Type													
IFA	4.1	3.8	3.8	2.6	4.4	4.1	≥2.9	4.4	≥2.9	>4.4	3.5	4.1	>4.4
Ag-ELISA	>6.0	>6.0	≥6.0	≥2.9	4.2	5.7	>3.8	>5.3	2.9	>6.0	>6.0	>6.0	>6.0
T76M													
IFA	-	-	-	-	-	-	-	-	-	-	nd	-	nd
Ag-ELISA	-	-	-	-	≤5%	-	-	0.8%	-	-	-	-	-
G104H													
IFA	-	<3%	6%	-	<0.8%	3%	-	-	-	-	nd	-	nd
Ag-ELISA	na	na	na	na	na	na	na	na	na	na	na	na	na
G106Q													
IFA	-	<3%	<3%	-	<0.8%	-	nd	6%	nd	-	-	-	-
Ag-ELISA	-	<0.1%	<0.1%	-	<6%	-	13%	≤0.1%	-	-	-	-	-
L107K													
IFA	-	<3%	-	-	-	-	<25%	6%	-	-	nd	-	nd
Ag-ELISA	-	<0.1%	-	-	5%	-	6%	0.2%	-	-	-	-	-
E126A													
IFA	-	-	6%	-	-	-	-	-	-	-	nd	-	nd
Ag-ELISA	-	-	-	-	10%	13%	-	-	-	-	-	-	-
E126A/T226N													
IFA	-	-	3%	-	-	3%	<25%	-	-	-	nd	-	nd
Ag-ELISA	-	-	-	-	5%	13%	-	-	-	-	-	-	-
W231F/L													
IFA	-	<3%	<3%	-	-	<2%	-	6%	-	-	-	-	-
Ag-ELISA	na	na	na	na	na	na	-	-	-	-	-	-	-

na: not applicable (these constructs did not secrete VLP antigen and thus could not be examined by Ag-ELISA); nd: not determined.

Table 4. Amino acid sequence variability for proposed cross-reactive epitope residues in domain II of the flavivirus E protein.

Virus	K64N	T76M	Q77R	G104H	G106Q	L107K	E126A	T226N	W231/F, L	H244R	K247R
DEN-2	K	T	Q	G	G	L	E	T	W	H	K
DEN-4	S	T	Q	G	G	L	T	T	W	H	R
DEN-3	K	T	Q	G	G	L	E	T	W	H	K
DEN-1	K	T	Q	G	G	L	E	T	W	H	K
Japanese Encephalitis	S	T	T	G	G	L	I	T	W	H	K
Murray Valley encephalitis	T	T	T	G	G	L	A	T	W	H	K
West Nile	T	T	M	G	G	L	I	T	W	H	K
St. Louis encephalitis	T	T	T	G	G	L	T	T	W	H	K
Ilhéus	T	T	M	G	G	L	T	E	W	H	R
Rocio	T	T	M	G	G	L	M	D	W	H	R
Bagaza	K	T	M	G	G	L	E	G	W	H	K
Iguape	E	Q	M	G	G	L	P	G	W	H	K
Bussuquara	K	A	V	G	G	L	A	S	W	H	K
Kokobera	Q	T	M	G	G	L	E	G	W	H	K
Kédougou	T	T	Q	G	G	L	K	A	W	H	K
Zika	S	T	Q	G	G	L	T	T	W	H	R
Yellow fever	V	S	T	G	G	L	S	G	W	H	T
Sepik	S	T	M	G	G	L	E	G	W	H	T
Entebbe Bat	N	T	T	G	G	L	Q	D	W	H	S
Tick-borne encephalitis	K	T	M	H	G	L	T	Q	W	H	K
Louping ill	K	T	M	H	G	L	T	P	W	H	K
Omske hemorrhagic fever	K	A	M	H	G	L	T	V	W	H	K
Langat	K	T	M	H	G	L	T	E	W	H	K
Alkhurma	K	A	M	H	G	L	T	H	W	H	K

Table 4. (cont.)

Virus	K64N	T76M	Q77R	G104H	G106Q	L107K	E126A	T226N	W231/F, L	H244R	K247R
Deer tick	K	T	T	H	G	F	V	Q	W	H	K
Powassan	K	T	T	H	G	F	V	Q	W	H	K
Montana myotis leukoencephalitis	D	T	L	G	G	L	A	H	W	H	K
Rio Bravo	S	T	Q	G	G	L	I	S	W	H	K
Modoc	E	T	Q	G	A	L	M	P	W	Y	K
Apoi	A	T	Q	G	G	L	I	K	W	H	K

DENV-2 strains containing variable amino acid sequences at these positions are indicated below with their GenBank accession numbers (all incorporated by reference as of the date of filing of this application).

64R:AF359579; **77L:**M24449, X15434, X15214; **107F**: M24446

126K:L10053, D00346, M29095, AF204178, M24450, M24451, AF410348, AF410361, AF410362, AF410365, AF204177, D10514

226K: AB111452, AY158337; **247R**: AF231718, AF231719, AF231720

Table 5. Nucleotide sequence of primers used for mutagenesis. The mismatched nucleotides causing the desired substitutions are underlined.

Primer	Sequence	SEQ ID NO:	Mutation
SLEV:			
G104H	CTCCCTTTTCCAAACAGACCACAGTGGTTACCCCATCCGC	31	Gly-His
G104N	CTCCCTTTTCCAAACAGACCACAGTTGTTACCCCATCCGC	32	Gly-Asn
G104D	CCCTTTTCCAAACAGACCACAGTCGTTACCCCATCCGC	33	Gly-Asp
G104K	CTCCCTTTTCCAAACAGACCACACTTGTTACCCCATCCGC	34	Gly-Lys
G106Q	CTCCCTTTTCCAAACAGCTGACATCCGTTACCCCATCCGC	35	Gly-Gln
G106K	CTCCCTTTTCCAAACAGCTTACATCCGTTACCCCATCCGC	36	Gly-Lys
G106V	TCCCTTTTCCAAACAGTACACATCCGTTACCCCATCCGC	37	Gly-Val
G106D	CT TTTCCAAACAGATCACATCCGTTACCCCATCCGC	38	Gly-Asp
L107F	CTCCCTTTTCCAAAGAAACCACATCCGTTACCCCATCCGC	39	Leu-Phe
G106Q/ L107F	AATGCTCCCTTTTCCAAAGAACTGACATCCGTTACCCCATCCGC	40	Gly-Gln Leu-Phe
R166Q	CGGGCTTATGGTGAATTGAGCCGCTTGGTTTTTTCC	41	Arg-Gln
T177I	TTCCATACTCGCCCATGTTGGCAATAAAGGACGGTG	42	Thr-Ile
G181S	GTAACTGTTCCATACTCGGACATGTTGGCCGTAAAGG	43	Gly-Ser
E182N	GTAACTGTTCCATAGTTGCCCATGTTGGCCGTAAAGG	44	Glu-Asn
T231N	CTCTGTTGCGCCAATCGTTTGTGGCAGGGCTCGTC	45	Thr-Asn
W233F	TTCTCTGTTGCGGAAATCAGTTGTGGCAGGGCTCGTC	46	Trp-Phe
H246R	TACTACAGTTTGCTTGGTGGCACGCGGTTCCTC	47	His-Trp
S276G	TGATTGCAAGGTTAGGGTTGATCCGCTAACAGTGGC	48	Ser-Gly
K294Y	CGTTCCCTTGATTTTGACGTAGTCAAGCTTAGCTCTGC	49	Lys-Tyr
T301A	ACACATGCCATATGCCGTTCCCTTGATTTTGACC	50	Thr-Ala
T330D	CAGGGTCCGTTGCTTCCATCATACTGCAGTTCCAC	51	Thr-Asp
A367S	CGATCATGACCTTGTTGTTCGATCCCCCTGTGC	52	Ala-Ser
N368F	TTCGATCATGACCTTGTTGAACGCTCCCCCTGTGC	53	Asn-Phe
WNV:			
G104N	TTTGCCAAATAGTCCGCAGTTGTTGCCCCAGCCCC	54	Gly-Asn
G104D	TTGCCAAATAGTCCGCAGTCGTTGCCCCAGC	55	Gly-Asp
G104K	CCTTTGCCAAATAGTCCGCACTTGTTGCCCCAGCCCC	56	Gly-Lys
G104A	TTGCCAAATAGTCCGCATGCGTTGCCCCAGC	57	Gly-Ala
G106V	TTTGCCAAATAGGACGCAGCCGTTGCCCCAGCC	58	Gly-Val
G106R	TTTGCCAAATAGCCTGCAGCCGTTGCCCCAGCC	59	Gly-Arg
G106Y	CCTTTGCCAAATAGGTAGCAGCCGTTGCCCCAGCCCC	60	Gly-Tyr
G106A	TTTGCCAAATAGAGCGCAGCCGTTGCCCCAGCC	61	Gly-Ala
L107Y	TTCCTTTGCCAAAGTATCCGCAGCCGTTGCCCCAGCC	62	Gly-Tyr
L107F	CCTTTGCCAAAGAATCCGCAGCCGTTGCCCCAGC	63	Gly-Phe
L107H	CCTTTGCCAAAATGTCCGCAGCCGTTGCCCCAGC	64	Gly-His
L107R	CCTTTGCCAAATCTTCCGCAGCCGTTGCCCCAGC	65	Gly-Arg
K118V	CTTGGTAGAGCAGGCAAATACGGCGCATGTGTC	66	Lys-Val
N154D	CCAACCTGTGTGGAGTAGTCTCCGTGCGAC	67	Asn-Asp
Y155G	CCAACCTGTGTGGAGCCGTTTCCGTGCGACTC	68	Tyr-Gly
Q158D	CTGAGTGGCTCCAACATCTGTGGAGTAGTTTCCGTGCG	69	Gln-Asp
R166Y	AGGAGTGATGCTGAAGTACCCTGCCTGAGTGG	70	Arg-Tyr
T177V	CCAAGCTTTAGTACGTATGAAGGCGCCGCAGGAG	71	Thr-Val
E182G	CCTCTCCATAGCCTCCAAGCTTTAGTGTGTATGAAGG	72	Glu-Gly
W233F	AACGTCTCTCTGTTCCTGAACACAGTACTTCCAGCAC	73	Trp-Phe
S276D	CCGACGTCAACTTGACAGTGTTGTCTGAAAATTCCACAGG	74	Ser-Asp
K294N	GTTCCCTTCAACTGCAAGTTTTCCATCTTCACTCTACAC	75	Lys-Asn

Primer	Sequence	SEQ ID NO:	Mutation
T301N	ACAGACGCCATAGTTTGTTCCCTTCAACTGCAATTTTTCC	76	Thr-Asn
T330N	CCATCCGTGCCGTTGTACTGCAATTCCAACACCACAG	77	Thr-Asn
A367V	GGACCTTAGCGTTGACCGTGGCCACTGAAAC	78	Ala-Val
N368S	ACCTTAGCGCTGGCCGTGGCCACTGAAAC	79	Asn-Ser

Table 6. E-glycoprotein-specific mAbs recognizing each of the three E-glycoprotein domains

mAb Name	Virus	Specificity	Domain
4G2	DENV-2	group	DII
6B6C-1	SLEV	group	DII
T23-1	WNV	group	DII
T23-2	JEV	group	DII
2B6B-2	SLEV	sub-grp (not WNV)	DII
4A1B-9	MVEV	group	DII
1B7-5	DENV-3	sub-grp: DEN+JE comp	
T21	DENV-3	sub-grp: DEN+JE comp	
2B5B-3	SLEV	sub-grp. JE comp + YF	
T11	DENV-3	sub-grp: DEN-2,3,4 + JE	
T5-1	JEV	sub-grp: DEN-2, JE, SLE	
T5-2	JEV	sub-grp: DEN-1,2, JE, WN*	
10A1D-2	DENV-2	sub-grp: DEN-1,2,3,4 + SLE	DI/DII
6B4A-10	JEV	JE comp.	
T16	JEV	JE comp.	
1B4C-2	DENV-2	sub-comp: DEN-2,3	DI
10A4D-2	DENV-2	sub-comp: DEN-1,2,3	DIII
1B5D-1	SLEV	sub-comp: SLE + JE	E-2
T20	DENV-2	sub-comp: DEN-2 + JEV	
4E5	DENV-2	sub-comp: DEN-1,2,3	DII
3H5	DENV-2	type	DIII
9A3D-8	DENV-2	type	DIII
9D12	DENV-2	type	DIII
1A5D-1	DENV-2	type	DII
9A4D-1	DENV-2	type	DI
T8	WNV	type	
3.91D	WNV (KUNV)	type	
3.67G	WNV (KUNV)	type	
4A4C-4	SLEV	type	
6B5A-2	SLEV	type	
1B2C-5	SLEV	type	

Table 7. Potential DENV-2 complex- and sub-complex-cross-reactive epitope residues, with residues chosen for mutagenesis highlighted

D2#	D1#	D3#	D4#	Dom?	B-f	Location	SC?	CRE?
K51	T51*	T51	K51	DI/DII	med	top outer edge	yes	yes
Q52	N52	Q52	E52	DI/DII	**high**	top outer edge **SDM in D2**	yes	yes
Q86	Q86	Q86	Q86	DII	**high**	out-mid-lat. **SDM in D2**	~yes	yes
Q131	Q131	Q131	Q131	DII/DI	**high**	out low-lat mid **SDM in D216681**	~yes	?/no
H149*	H149	H149	H149	DI	**high**	up-mid-top below CHO-153	yes	yes if no CHO
N153*	N153	N153	N153	DI	med	up-mid-top near CHO 153	yes	no
D154	E145	E154	D154	DI	**high**	up-in-top near CHO & prM	yes	YES?
T155*	T155	T155	T155	DI	**high**	up-mid-top near prM	yes	YES
E161	T161	T161	T161	DI	high	up-mid-top high.exp.	yes	yes
Q167	Q167	Q167	R167	DI	**high**	out-lat mid DI/II region	yes	pos?
S169	P169	S169	P169	DI	med+	DI/II border out-mid	yes	yes?
E172	E172	E172	E172	DI	**high**	DI/II border up-out edge	yes	yes
T176	T176	P176	P176	DI	med	DI/III up-out edge	yes	yes
G177*	D177	E177	D177	DI	med	DI/III up-out edge	yes	yes
E202	E202	K202	E202	DII	**high**	in-mid-up	YES	YES
D203	K203	N203	K203	DII	high	in-mid-up no SDM in D2	yes	yes
A224	A224	A224	A224	DII	med+	up-out-middle (SDM in D2)	yes	yes
T226	T226	T226	T226	DII	**high**	up-out-mid **SDM previous**	yes	no??
Q227	S227	K227	S227	DII	high	up-out-middle	yes	yes?
D290	D290	D290	E290	DI	high	out-up lat DI/III face	yes	maybe
K291	K291	K291	K291	DI	med+	out-up lat DI/III face, above D290	YES	yes?
M297	M297	M297	M297	DIII/I	**high**	mid-out-end DI/III **SDM D2?**	~yes	?yes?
S298	S298	S298	S298	DIII/I	med+	mid-out-end DI/III flavis=S/T	YES	**YES**
T303	T303	L303	S303	DIII	**high**	mid-out-end DI/III	YES	?yes
K310*	K310	K310	K310	DIII	low	out-up DI-DII interface	~YES	YES?
E311	E311	E311	E311	DIII	**high**	out-up DI-DII interface	YES	**YES**
E327*	E327	K327	E327	DIII	**high**	up-out-top "end" DIII	YES	**YES**
D229	T229	E229	A229	DIII	high	up-out-top "end" DIII	yes	yes
E360	D360	K360	N360	DIII	med+	tip-top-mid DIII	yes	no
K361	K361	K361	T361	DIII	**high**	tip-top-mid DIII	YES	**YES**
D362	E362	E362	N362	DIII	med	tip-top-mid DIII	yes	yes
V382*	A382	I382	V382	DIII	low	"RGD" loop up-out-lat	~yes	?pos
E383	G383	G383	G383	DIII	high	"RGD" loop up-out-lat	~?no	yes
P384	E384	D384	N384	DIII	med+	"RGD" loop up-out-lat	YES	yes?

* not identified as ≥ 35% SA in this particular structure/model
B-f: β-factor (temperature factor) a qualitative assessment of the scale (5-60Å^2).
SC?: is the amino acid side chain accessible and available for antibody binding
Ep?: might this amino acid be incorporated into an antigen epitope?
DVc: DENV1-4 complex;
Jec: JE complex (medically important clade =JE, MVE, WN, SLE)
SDM: site-directed mutagenesis

Table 8. Potential JEV complex- and sub-complex cross-reactive epitope residues from WNV, with residues chosen for mutagenesis highlighted

D2 #	SLE #	WN#	Dom.	B-f.	Location?	SC?	Conservation	Ep?
T68*	L68	L68	DII	low	top inner edge near N67 D2	~yes	WN, SLE=L	?yes
T76	T76	T76	DII	low	out-lateral-low-mid.	yes	"all" mosq.+ticks	?
Q77	T77*	M77	DII	med	outer lateral middle	no	variable, Q=DVc	?
N83	T83	D83	DII	med	out-up-lat. loop near FP	yes	variable type?	Yes
Q86	S86	A86	DII	high	out-mid-lat.	~yes	JEc=A (SLE=S)	yes
K88	P88	P88	DII	high	out-up-lat	~no?	variable	?possible
M118	K118	K118	DII	med+	up-mid-top near N67 in D2	yes	JEc=K, SDM in WN	YES
K122	K122	S122	DII	med+	up-mid-top	yes	var.	yes
Q131	L131	L131	DII/DI	high	out mid lat DI/II border	~yes	var. L=WN,SLE	?/YES
H149*	S149	V149	DI	high	up-mid-top below CHO-153	yes	H=DVc;	yes if no CHO
N153*	N154	N154	DI	med+	up-mid-top CHO on D2-153	yes	"all mosq"=N	YES
NA*	Y155	Y155	DI	na	up-mid-top near CHO 153 yes	Y=JEc	SDM in WN	YES
D154	Q158	Q158	DI	**high**	up-in-top near CHO & prM	yes	Q=Jec, SDM in WN	YES
T155*	I159*	V159	DI	**high**	up-mid-top near prM	yes	DVc=T JEc=I/V	YES
E161	R166	R166	DI	**high**	up-mid-top high exp.	yes	JEc=R, except JE=K	yes
S169	P174	P174	DI	med+	DI/II border out-mid	yes	P=mosq. (D2,3=S)	yes?
E172	T177	T177	DI	**high**	DI/II border up-out-top edge	yes	DVc=E, JEc=T	yes
E174	N179	K179	DI	high	DI/III border outer edge yes	var. JEc=K (SLE=N)		yes?
T176	G181	G181	DI	med	DI/III up-out edge	yes	DVc=var, JEc=G	yes
G177*	E182	E182	DI	med	DI/III up-out edge	yes	"all"mosq=neg.D2=G	yes
T226	T231	T231	DII	**high**	up-out-mid. SDM?	yes	DVc, JEc= T	yes?
H244*	H246	H246	DII	med	prM hole low but above P243	yes	all flavis	no?
K247	K249	K249	DII	med	prM hole low, above 243/244	yes	"all" flavis	no?
S274	S276	S276	DII/I	**high**	up-top-in **good aa JEc** YES	JEc=S,	SDM WN	YES
K291	K294	K294	DI	med+	out-up lat DI/III face	~yes	flavis=K	yes?
M297	T300	T300	DIII/I	**high**	mid-out-end DI/III	~yes	DVc=M JEc=T	?pos?
S298	T301	T301	DIII/I	med+	mid-out-end DI/III	YES	flavis=S/T	YES
E327*	T330	T330	DIII	**high**	up-out-top "end" DIII	YES	JEc=T ex JE=S	**YES**
K361	A367	A367	DIII	**high**	tip-top-mid DIII YES	JEc=A	**SDM in WN**	**YES**
D362	N368	N368	DIII	med	tip-top-mid DIII YES	JEc=N	**SDM in WN**	**YES**
V382*	R388	R388	DIII	low	"RGD" loop up-out-lat yes	JEc=R		YES
E383	G389*	G389	DIII	**high**	"RGD" loop up-out-lat ~y/na	mosq=G or E		YES

* not identified as ≥ 35% SA in this particular structure/model
B-f: β-factor (temperature factor) a qualitative assessment of the scale (5-60Å^2).
SC?: is the amino acid side chain accessible and available for antibody binding
Ep?: might this amino acid be incorporated into an antigen epitope?
DVc: DENV1-4 complex;
Jec: JE complex (medically important clade =JE, MVE, WN, SLE)
SDM: site-directed mutagenesis

Table 9. Potential JEV complex- and sub-complex cross-reactive epitope residues from SLEV, with residues chosen for mutagenesis highlighted

D2 #	SLE #	WN#	Dom.	B-f.	Location?	SC?	Conservation	Ep?
T68*	L68	L68	DII	low	top inner edge near N67 D2	~yes	WN,SLE=L	?yes
T76	T76	T76	DII	low	out-lateral-low-mid.	yes	"all" mosq. + ticks	?
Q77	T77*	M77	DII	med	outer lateral middle	no	variable, Q=DVc	?
N83	T83	D83	DII	med	out-up-lat. loop near FP	yes	variable type?	Yes
Q86	S86	A86	DII	high	out-mid-lat.	~yes	JEc=A (SLE=S)	yes
K88	P88	P88	DII	high	out-up-lat	~no?	variable	?possible
K122	K122	S122	DII	med+	up-mid-top	yes	var.	yes
Q131	L131	L131	DII/DI	high	out low lat mid	~yes	var. L=WN,SLE	?/no
H149*	S149	V149	DI	high	up-mid-top below CHO-153	yes	H=DVc;	yes if no CHO
N153*	N154	N154	DI	med+	up-mid-top CHO on D2-153	yes	"all mosq"=N	YES
NA*	Y155	Y155	DI	na	up-mid-top near CHO 153 yes	Y=JEc	SDM SLE	YES
D154	Q158	Q158	DI	**high**	up-in-top near CHO & prM	yes	Q=Jec, SDM SLE	YES
T155*	I159*	V159	DI	**high**	up-mid-top near prM	yes	DVc=T JEc=I/V	YES
E161	R166	R166	DI	**high**	up-mid-top high exp.	yes	JEc=R, except JE=K	yes
S169	P174	P174	DI	med+	DI/II border out-mid	yes	P=mosq. (D2,3=S)	yes?
E172	T177	T177	DI	**high**	DI/II border up-out-top edge	yes	DVc=E, JEc=T	YES
E174	N179	K179	DI	high	DI/III border outer edge	yes	var. JEc=K (SLE=N)	yes?
T176	G181	G181	DI	med	DI/III up-out edge	yes	DVc=var, JEc=G	yes
G177*	E182	E182	DI	med	DI/III up-out edge	yes	"all"mosq=neg D2=G	yes
T226	T231	T231	DII	**high**	up-out-mid. SDM prev.	yes	DVc, JEc=T	yes?
H244*	H246	H246	DII	med	prM hole low but above P243	yes	all flavis	yes?
K247	K249	K249	DII	med	prM hole low, above 243/244	yes	"all" flavis	no?
S274	S276	S276	DII/I	**high**	up-top-in **good aa JEc** YES	JEc=S;	SDM SLE	YES
K291	K294	K294	DI	med+	out-up lat DI/III face	~yes	flavis=K	yes?
M297	T300	T300	DIII/I	**high**	mid-out-end DI/III	~yes	DVc=M JEc=T	?pos?
S298	T301	T301	DIII/I	med+	mid-out-end DI/III	YES	flavis=S/T	YES
E327*	T330	T330	DIII	**high**	up-out-top "end" DIII	YES	JEc=T ex JE=S	YES
K361	A367	A367	DIII	**high**	tip-top-mid DIII	YES	JEc=A, **SDM in SLE**	**YES**
D362	N368	N368	DIII	med	tip-top-mid DIII	YES	JEc=N, **SDM in SLE**	**YES**
V382*	R388	R388	DIII	low	"RGD" loop up-out-lat	~yes	JEc=R	YES
E383	G389*	G389	DIII	**high**	"RGD" loop up-out-lat	~y/na	mosq=G or E	YES

* not identified as ≥ 35% SA in this particular structure/model

B-f: β-factor (temperature factor) a qualitative assessment of the scale (5-60Å^2).

SC?: is the amino acid side chain accessible and available for antibody binding

Ep?: might this amino acid be incorporated into an antigen epitope?

DVc: DENV1-4 complex;

Jec: JE complex (medically important clade =JE, MVE, WN, SLE)

SDM: site-directed mutagenesis

Table 10. Inverse $\log_{10}$ end-point titers of anti-SLEV mAbs determined by the AG-ELISA for antigens expressed by wild-type pCB8SJ2 and cross-reactive reduced mutated constructs

Mutants		Mabs:	MHIAF	4G2	T-23-1	T-23-2	6B6C-1	2B6B-2	4A1B-9	1B7-5	2B5B-3	T-16	6B4A-10	1B5D-1	6B5A-2	4A4C-4	1B2C-5
		CR:	poly	grp	grp	grp	grp	grp	grp	supr comp	supr comp	JE comp	JE comp	JEV + SLE	SLEV	SLEV	SLEV
		virus:	SLEV	D2V	WNV	JEV	SLEV	SLEV	MVEV	D3V	SLEV	JEV	JEV	SLEV	MSI-7	MSI-7	MSI-7
		Secrete?															
pCB8SJ2	ELISA	+	>>4.8	>>4.5	>4.5	>6.0	>4.5	≥4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	~4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.8			
G104H	ELISA	-	>>4.8	nd	<3.0	<3.0	nd	nd	nd	nd	<3.0	nd	nd	nd	nd	nd	≥4.5
	IFA		>4.4?	≤2.3	<2.3		<2.3	<2.3	<2.3	≤2.6	<3.0	~3.5	<2.6	≤2.3			
G106Q	ELISA	+	>>4.8	<3.0	>4.5	>>6.0	>4.5	>>4.5	>4.5	>>4.5	<3.0	>>4.5	>>4.5	>>4.5	>>4.5	>>4.5	>>4.5
	IFA		>4.4	≤3.2	>4.4		<2.3	4.4	≤2.3	≥4.5	~4.1	>4.4	~4.4	~2.3			
L107K	ELISA	+	>>4.8	<3.0	≤3.0	>6.0	>4.5	>4.5	>4.5	≥4.5	<3.0	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≤2.3	~3.2		~3.8	4.4	≤4.4	≤4.1	≥4.4	>4.4	~4.4	~3.5			
R166Q	ELISA	+	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~2.2	≤4.4	≤4.1	>4.4	>4.4	~4.4	~4.1			
T177I	ELISA	+/-	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	nd	nd	nd
	IFA		>4.4	≥4.4	>4.4		>4.4	4.1	≤4.4	≤4.1	>4.4	>4.4	~4.4	~4.1			
G181S	ELISA	-/+	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	~2.3	>4.5	>4.5	nd
	IFA		>4.4	≥4.4	>4.4		>4.4	4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.5			
E182N	ELISA	-/+	>>4.8	>>4.5	≤3.0	>6.0	~3.0	>4.5	>4.5	≥4.5	<3.0	>4.5	>4.5	nd	nd	nd	nd
	IFA		>4.4	≥4.4	>4.4		~3.5	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~4.1			
T231N	ELISA	+	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	<3.0	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.8			
W233F	ELISA	-/+	>>4.8	>>4.5	nd	>6.0	>4.5	>4.5	>4.5	≥4.5	<3.0	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.5			
H246R	ELISA	++	>>4.8	>>4.5	>4.5	>6.0		>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	~2.3	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.2			
S276G	ELISA	+	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≤4.1	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~4.1			
K294Y	ELISA	-	>>4.8	>>4.5	≤3.0	4.8	>4.5	>4.5	nd	≥4.5	>4.5	>4.5	nd	nd	nd	nd	nd
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.2			
T301A	ELISA	+	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.8			

Table 10 (cont)

T330D	ELISA	+	nd	>>4.5	nd	>6.0	>4.5	>4.5	>4.5	≥4.5	nd	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~4.1			
A367S	ELISA	+/-	>>4.8	>>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		>4.4	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.5			
N368F	ELISA	-/+	>>4.8	~≤3.0	>4.5	>6.0	~4.5	>4.5	>4.5	≥4.5	>4.5	>4.5	>4.5	>3.5	>4.5	>4.5	≥4.5
	IFA		>4.4	≥4.4	>4.4		~4.1	~4.4	≤4.4	≤4.1	>4.4	>4.4	~4.4	~3.5			
G106Q/	ELISA	+	4.8	≤3.0	>4.5	>4.5	≤3.0	≥4.5	>4.5	4.5	≤3.0	>4.5	>>4.5	4.5	>4.5	>>4.5	>4.5
E182N	IFA		≥4.1	<2.3	>4.4		<2.3	<2.3	<2.3	~2.3	~2.3	3.5	~3.2	<2.3			
G106Q/	ELISA	-	nd	≤3.0	nd	nd	≤3.0	nd	nd	nd	nd	nd	≤3.0	nd	nd	nd	nd
K294Y	IFA		~4.1	<2.3	>4.4		<2.3	<2.3	<2.3	<2.3	~2.3	~2.3	~2.3	<2.3			
G106Q/	ELISA	+	4.8	≤3.0	>4.5	>4.5	>4.5	>4.5	>>4.5	>4.5	≤3.0	>4.5	>>4.5	4.5	>4.5	>>4.5	>4.5
N368F	IFA		≥4.4	<2.3	>4.4		~2.3	<2.3	<2.3	~4.4	~3.2	4.4	~4.1	<2.3			
106-182-294	ELISA	-	nd	≤3.0	nd	nd	≤3.0	nd	nd	nd	nd	nd	≤3.0	nd	nd	nd	nd
	IFA		~4.1	<2.3	~3.8		<2.3	<2.3	<2.3	<2.3	~2.3	~2.3	~2.3	<2.3			
106-182-368	ELISA	-/+	4.8	≤3.0	>4.5	>4.5	>4.5	4.2	>4.5	≥4.5	≤3.0	>4.5	>4.5	4.5	nd	>4.5	nd
	IFA		~4.4	<2.3	>4.4		<2.3	<2.3	<2.3	3.5	~2.3	3.5	~3.8	<2.3			
106-294-368	ELISA	-	nd	≤3.0	nd	nd	≤3.0	nd	nd	nd	nd	nd	≤3.0	nd	nd	nd	nd
	IFA		~4.1	<2.3	>4.4		<2.3	<2.3	<2.3	3.5	~2.3	3.8	~3.5	<2.3			
106-182	ELISA	-	nd	≤3.0	nd	nd	≤3.0	nd	nd	nd	nd	nd	≤3.0	nd	nd	nd	nd
294-368	IFA		~4.1	<2.3	>4.4		<2.3	<2.3	<2.3	<2.3	~2.3	≤2.3	~2.3	<2.3			

Shaded block: Significantly altered endpoints relative to pCB8SJ2 derived wild-type VLP antigens. Most substitutions reduced mAb reactivity, however, some mAbs reactivity increased.

Table 11. Inverse $\log_{10}$ end-point titers of anti-WNV mAbs determined by the AG-ELISA for antigens expressed by wild-type pCBWN and cross-reactive reduced mutated constructs

Mutants		Mabs: CR: virus: Secrete?	MHIAF poly WNV	4G2 grp D2V	T-23-1 grp WNV	T-23-2 grp JEV	6B6C-1 grp SLEV	4A1B-9 grp MVEV	2B5B-3 supr comp SLEV	T-16 JE comp JEV	6B4A-10 JE comp JEV	3.67G type Kun	3.91D type Kun
pCBWN	ELISA	++	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	>4.1	≥4.1	≥4.1
G104N	ELISA	-	na	na	<3.0	na	na	na	na	na	na	nd	nd
	IFA		~3.2		≤2.0	~3.2			<2.0	≤2.6	≤3.2	3.5	≥4.1
G106V	ELISA	+	5.7	<3.0	>>4.5	>6.0	<3.0	<3.0	<3.0	>>6.0	>>4.5	>>4.5	>>4.5
	IFA		≥4.1		>4.4	>4.1			<2.0	>4.1	>4.1	≥4.1	≥4.1
L107Y	ELISA	+/-	5.7	na	>4.5	>6.0	na	na	nd	>6.0	na	nd	nd
	IFA		≥4.1		<2.0	>4.1			<2.0	>4.1	>4.1	≥4.1	≥4.1
K118V	ELISA	-	5.7	>4.5	>4.5	na	na	na	na	>4.5	na	nd	nd
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	≤3.8	≥4.1	≥4.1
N154D	ELISA	++	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	4.1	≥4.1	≥4.1
Y155G	ELISA	+	5.7	>4.5	>4.5	>>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	>4.1	≥4.1	≥4.1
Q158D	ELISA	+	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	>4.1	≥4.1	≥4.1
R166Y	ELISA	++	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	>4.1	>4.1	≥4.1	≥4.1
T177V	ELISA	+	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	<2.0	4.1	≥4.1	≥4.1
E182G	ELISA	+	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	<2.0	>4.1	≥4.1	≥4.1
W233F	ELISA	++	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	<2.0	>4.1	≥4.1	≥4.1

Table 11 (cont)

S276D	ELISA	++	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	≤2.0	>4.1	≥4.1	≥4.1
K294N	ELISA	+	5.7	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	≤3.5	>4.1	≥4.1	≥4.1
T301N	ELISA	+	5.7	>>4.5	>>4.5	>>6.0	>>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	~2.9	>4.1	≥4.1	≥4.1
T330N	ELISA	+	5.7	>4.5	>>4.5	>>6.0	>>4.5	>>4.5	>4.5	>6.0	>>4.5	nd	nd
	IFA		≥4.1		>4.1	>4.1			>4.1	~2.6	>4.1	≥4.1	≥4.1
A367V	ELISA	++	5.7	>4.5	>>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	≤2.9	>4.1	≥4.1	≥4.1
N368S	ELISA	++	~6.0	>4.5	>>4.5	>6.0	>4.5	>4.5	>4.5	>6.0	>4.5	>4.5	>4.5
	IFA		≥4.1		>4.1	>4.1			>4.1	≤2.9	>4.1	≥4.1	≥4.1
G106V/T301N	ELISA	+	5.7	<3.0	>>4.5	>>4.5	<3.0		≤3.0	>>4.5	>4.5		
	IFA												
G106V/T330N	ELISA	-/+	5.7	<3.0	>>4.5	>>4.5	3.3		≤3.0	>>4.5	~4.5		
	IFA		3.8		>4.1	>4.1			≤2.0	3.8	3.8	~3.8	~3.8
G106V/T301N T330N	ELISA	-/+	5.7	<3.0	>>4.5	>>4.5	3.3		≤3.0	>>4.5	≥4.5		
	IFA		≥4.1		>4.1	>4.1			≤2.0	4.1	4.1	4.1	4.1

Shaded block: Significantly altered endpoints relative to pCB8SJ2 derived wild-type VLP antigens. Most substitutions reduced mAb reactivity, however, some mAbs reactivity increased.

Table 12. Comparative detection of human IgM antibody by MAC-ELISA with wild type (wt-) and G106V- prototype type-specific antigens.

Serum Specimen Description					**Positive/Negative Ratios[2]**			
			PRNT$_{90}$[2]		**Ref. Lab. Result**		**VLP MAC-ELISA**	
Infecting Viru	**No**	**Class[1]**	**SLEV**	**WNV**	**SLEV**	**WNV**	**wt**	**G106V**
SLEV	1	equivocal	160	20	1.10	0.81	1.12	1.02
	2	equivocal	160	20	1.17	1.20	1.11	1.16
	3	equivocal	320	40	2.10	1.30	1.83	1.15
	4	equivocal	320	80	2.40	2.90	1.74	1.34
	5	equivocal	320	20	**8.56**	**8.27**	**3.12**	1.99
	6	misleading	1280	160	**8.27**	**10.8**	**5.40**	**5.09**
	7	misleading	1280	20	**9.81**	**11.1**	**6.42**	2.35
	8	misleading	640	20	**12.4**	**14.9**	**3.76**	2.48
	9	misleading	160	40	**13.0**	**20.3**	2.02	1.47
	10	misleading	1280	10	**11.8**	**43.7**	**9.80**	2.04
No. positive					6	6	5	1
WNV	1	positive	40	160	3.37	**7.88**	1.91	2.45
	2	positive	160	2560	1.48	**5.76**	**3.12**	**4.09**
	3	positive	10	320	1.29	**8.61**	**4.21**	**3.20**
	4	positive	80	320	2.73	**8.38**	2.71	**3.04**
	5	positive	40	2560	2.12	**26.3**	**6.68**	**9.04**
	6	positive	40	1280	2.14	**28.8**	**8.27**	**10.2**
No. positives					1	6	4	5

[1] Sera were assigned to one of three classes; positive, equivocal, or misleading as described in materials and methods. Assignments were based upon previously determined P/N ratios[3] reported by the Diagnostics and Reference Laboratory, Arbovirus Diseases Branch, Division of Vector-Borne Diseases, US Centers for Disease Control and Prevention.

[2] PRNT$_{90}$, Plaque reduction neutralization test; titers represent inverse 90% plaque reduction endpoints as reported by the Diagnostics and Reference Laboratory, ADB, DVBID, CDC.

[3] Values represent ratios calculated as described in Materials and Methods. Positive ratios $\geq$3.0 are shown in bold

[4] Ratios reported by the Diagnostics and Reference Laboratory, ADB, DVBID, CDC.

[5] Ratios determined in this study comparing wild-type (wt-) WNV Ag. with prototype cross-reactivity reduced G106V-WNV Ag.

Table 13. Type-specific neutralizing antibody titers as determined by PRNT

Plasmid DNA used for immunization[1]	Mouse No.	Type-specific 75% PRNT titer[2]
pCB8D2-2J-2-9-1	1	>128
(wt DENV-2)	2	>128
	3	>128
	4	64
	5	>128
	6	>128
pCB8D2-2J-2-9-1-G106Q	1	>128
(DENV-2+G106Q)	2	>128
	3	>128
	4	>128
	5	128
	6	>128
pCBWN	1	>128
(wt WNV)	2	>128
	3	>128
	4	>128
	5	>128
	6	>128
pCBWN-G106V	1	64
(WNV+G106V)	2	>128
	3	16
	4	>128
	5	>128
	6	>128

[1]Mice were immunized intramuscularly with 100ug of plasmid DNA on weeks 0 and 3.
[2]PRNT plaque reduction neutralization test, 75% neutralization endpoint titers on mouse sera collected 6 weeks post vaccination.

CLAIMS

We claim:

1. An isolated mutant flavivirus polypeptide, comprising an amino acid sequence as shown in SEQ ID NO: 14, wherein at least one of the amino acids at position 104, 106, 107, 126, 226, or 231 is substituted compared to a wild-type flavivirus polypeptide, and wherein the polypeptide exhibits measurably reduced antibody cross-reactivity.

2. The polypeptide of claim 1, wherein the amino acid substitution is selected from the group consisting of:

$G_{104}H$ (SEQ ID NO: 16);
$G_{106}Q$ (SEQ ID NO: 18);
$L_{107}K$ (SEQ ID NO: 20);
$E_{126}A$ (SEQ ID NO: 22);
$T_{226}N$ (SEQ ID NO: 24);
$W_{231}F$ (SEQ ID NO: 26);
$W_{231}L$ (SEQ ID NO: 28);
$E_{126}A/T_{226}N$ (SEQ ID NO: 30); or
a combination of two or more thereof.

3. An isolated mutant flavivirus polypeptide, comprising an amino acid sequence as shown in SEQ ID NO: 81, wherein at least one of the amino acids at position 106 is substituted compared to a wild-type flavivirus polypeptide, and wherein the polypeptide exhibits measurably reduced antibody cross-reactivity.

4. The polypeptide of claim 3, wherein the amino acid substitution comprises $G_{106}Q$ (SEQ ID NO: 83).

5. An isolated mutant flavivirus polypeptide, comprising an amino acid sequence as shown in SEQ ID NO: 85, wherein at least one of the amino acids at position 106 is substituted compared to a wild-type flavivirus polypeptide, and wherein the polypeptide exhibits measurably reduced antibody cross-reactivity.

6. The polypeptide of claim 5, wherein the amino acid substitution comprises $G_{106}V$ (SEQ ID NO: 87).

7. An isolated nucleic acid molecule encoding a polypeptide according to any one of claims 1, 3 or 5.

8. The nucleic acid molecule of claim 7, comprising a nucleic acid sequence as shown in any one of SEQ ID NOs: 13, 15, 17, 19, 21, 23, 25, 27, 29, 80, 82, 84, or 86.

9. A recombinant nucleic acid molecule, comprising a regulatory sequence operably linked to the nucleic acid molecule of claim 7.

10. A cell, comprising the recombinant nucleic acid molecule of claim 9.

11. The cell of claim 10, wherein the cell is a eukaryotic cell.

12. The cell of claim 11, wherein the cell is an animal cell.

13. A virus-like particle, comprising the polypeptide of any one of claims 1, 3 or 5.

14. A method for identifying a flavivirus cross-reactive epitope, comprising:

selecting a candidate epitope using a structure-based design approach;

designing a substituted epitope comprising at least one amino acid residue substitution compared to the candidate epitope;

contacting the candidate epitope with a specific binding agent under conditions whereby a candidate epitope/specific binding agent complex can form; and

contacting the substituted epitope with the specific binding agent under the same conditions used for candidate epitope/specific binding agent complex formation,

wherein a candidate epitope is identified as the flavivirus cross-reactive epitope when the substituted epitope has a substantially lower binding affinity for the specific binding agent compared to the candidate epitope.

15. The method of claim 14, wherein the specific binding agent is an antibody.

16. The method of claim 14, wherein the flavivirus cross-reactive epitope binds to a specific binding agent that binds to at least two flaviviruses selected from the group consisting of dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus.

17. The method of claim 14, wherein the structure-based design approach comprises:

identifying at least one conserved flavivirus amino acid between two or more flavivirus groups or subgroups; and

mapping the conserved flavivirus amino acid onto a structure of a flavivirus E-glycoprotein.

18. The method of claim 17, wherein the flaviviruses are selected from the group consisting of dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus.

19. The method of claim 17, wherein the conserved flavivirus amino acid exhibits two or more of the following structural characteristics:

it is located in domain II of the E-glycoprotein;

it is conserved across the flaviviruses;

it is on the outer or lateral surface of the E-glycoprotein dimer;

it has at least 35% surface accessibility potential;

its side chain projection is accessible for antibody paratopes; and

it has a high β-factor.

20. The method of claim 14, wherein the structure-based design approach comprises:

identifying at least one conserved flavivirus amino acid between two or more flavivirus complexes or subcomplexes; and

mapping the conserved flavivirus amino acid onto a structure of a flavivirus E-glycoprotein.

21. The method of claim 20, wherein the flaviviruses are selected from the group consisting of dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus.

22. The method of claim 20, wherein the conserved flavivirus amino acid exhibits two or more of the following structural characteristics:

it has at least 35% surface accessibility potential;

it is on the outer or lateral surface of the E-glycoprotein dimer;

it is conserved across the flaviviruses;

its side chain projection is accessible for antibody paratopes; and

it has a high β-factor.

23. The method of claim 14, wherein the specific binding agent is a flavivirus cross-reactive antibody.

24. The method of claim 23, wherein the flavivirus cross-reactive antibody is selected from the group consisting of 4G2, 6B6C-1, 1B7-5, 10A1D-2, 4A1B-9, and 2B5B-3.

25. A composition, comprising the polypeptide of any one of claims 1, 3 or 5 and a pharmaceutically acceptable carrier.

26. A method of eliciting an immune response against a flavivirus antigenic epitope in a subject, comprising introducing into the subject the composition of claim 25, thereby eliciting an immune response against a flavivirus antigenic epitope in the subject.

27. The method of claim 26, wherein the flavivirus antigenic epitope is selected from the group consisting of dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus.

28. The method of claim 26, wherein the subject is a mammal.

29. A composition, comprising a nucleic acid vector, wherein the vector comprises the nucleic acid molecule of claim 7, and

a pharmaceutically acceptable carrier.

30. A method of eliciting an immune response against a flavivirus antigenic epitope in a subject, comprising introducing into the subject the composition of claim 29, thereby eliciting an immune response against a flavivirus antigenic epitope in the subject.

31. The method of claim 30, wherein the flavivirus antigenic epitope is selected from the group consisting of dengue serotype 1 virus, dengue serotype 2 virus, dengue serotype 3 virus, dengue serotype 4 virus, yellow fever virus, Japanese encephalitis virus, St. Louis encephalitis virus, and West Nile virus.

32. The method of claim 30, wherein the subject is a mammal.

33. A method of detecting a flavivirus antibody in a sample, comprising:

(a) contacting the sample with the polypeptide of any one of claims 1, 3 or 5 under conditions whereby a polypeptide/antibody complex can form; and

(b) detecting polypeptide/antibody complex formation, thereby detecting a flavivirus antibody in a sample.

34. A method of diagnosing a flavivirus infection in a subject, comprising:

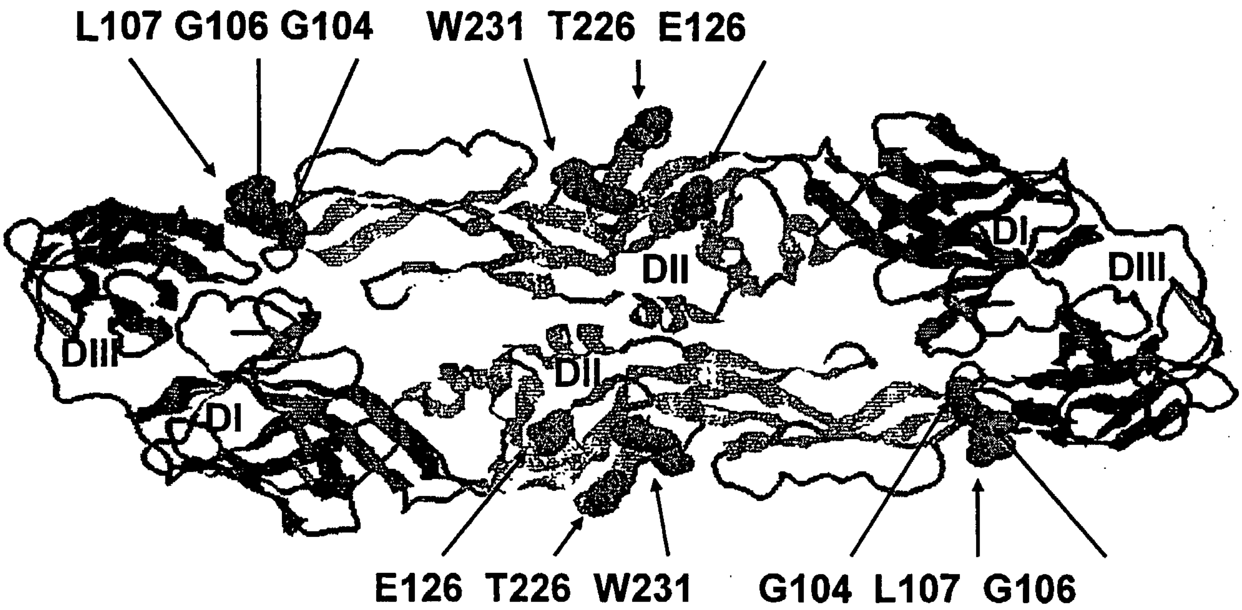
contacting a sample from the subject with the polypeptide of any one of claims 1, 3 or 5 under conditions whereby an polypeptide/antibody complex can form; and

detecting polypeptide/antibody complex formation, thereby diagnosing a flavivirus infection in a subject.

35. A flavivirus E-glycoprotein engineered to comprise at least one amino acid residue substitution according to the method of any one of claims 19 or 22.

36. A kit for detecting a flavivirus in a sample, comprising the polypeptide of any one of claims 1, 3 or 5.

FIG. 1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W231 T226 E126
DII
DI
DIII
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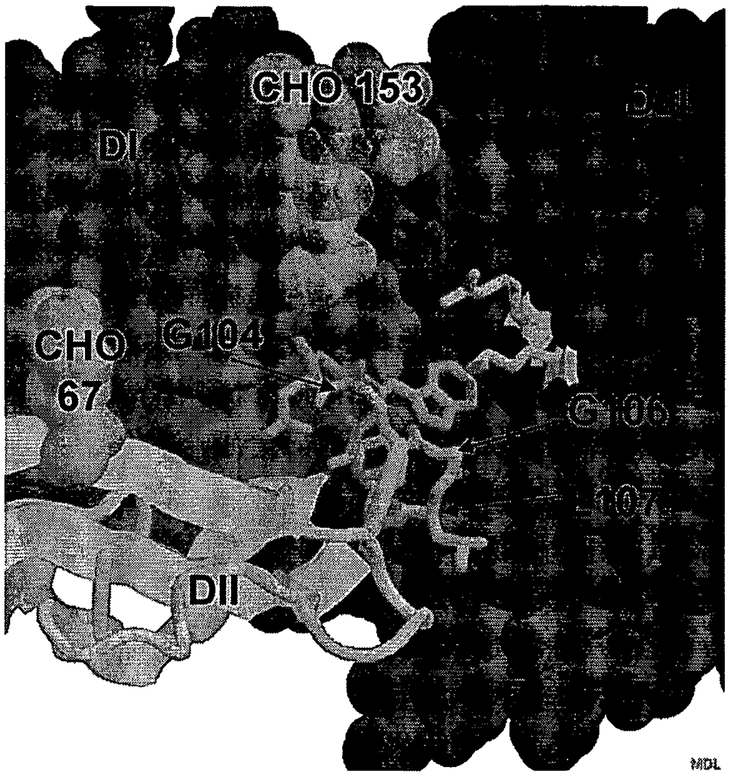
FIG. 2A.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DI
CHO
67
G104
G106
107
DII
MDL

FIG. 2B.

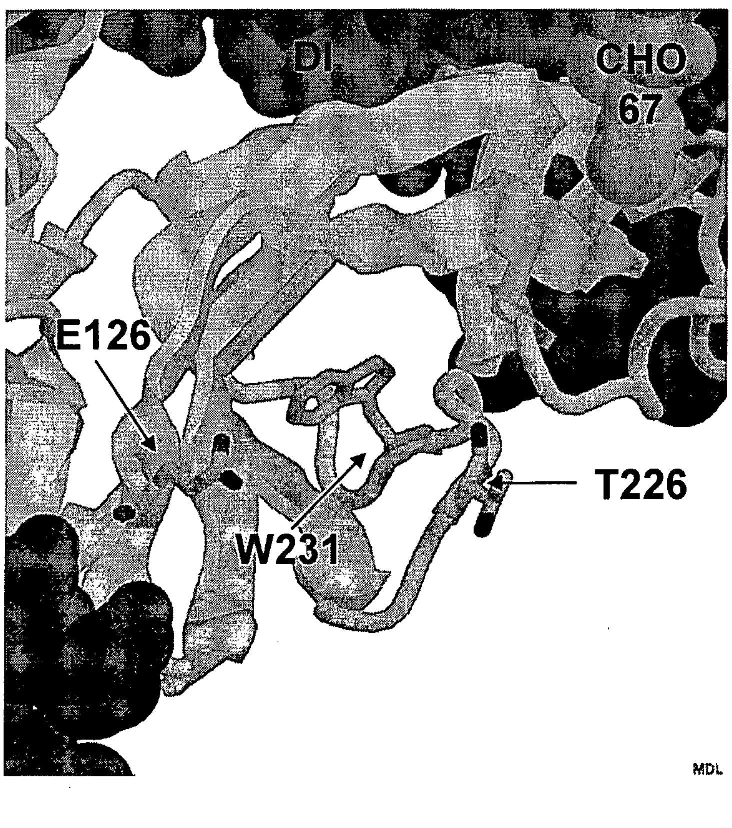

DI
CHO
67
E126
W231
T226
MDL

FIG. 2C

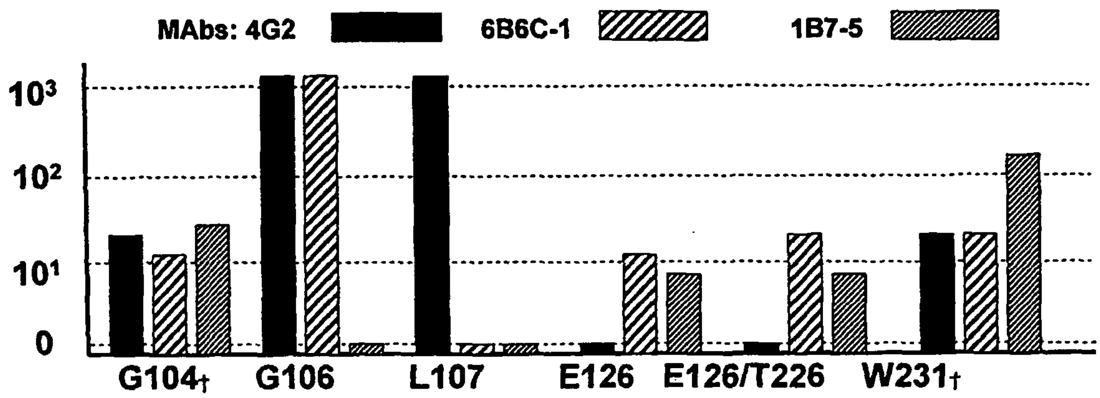
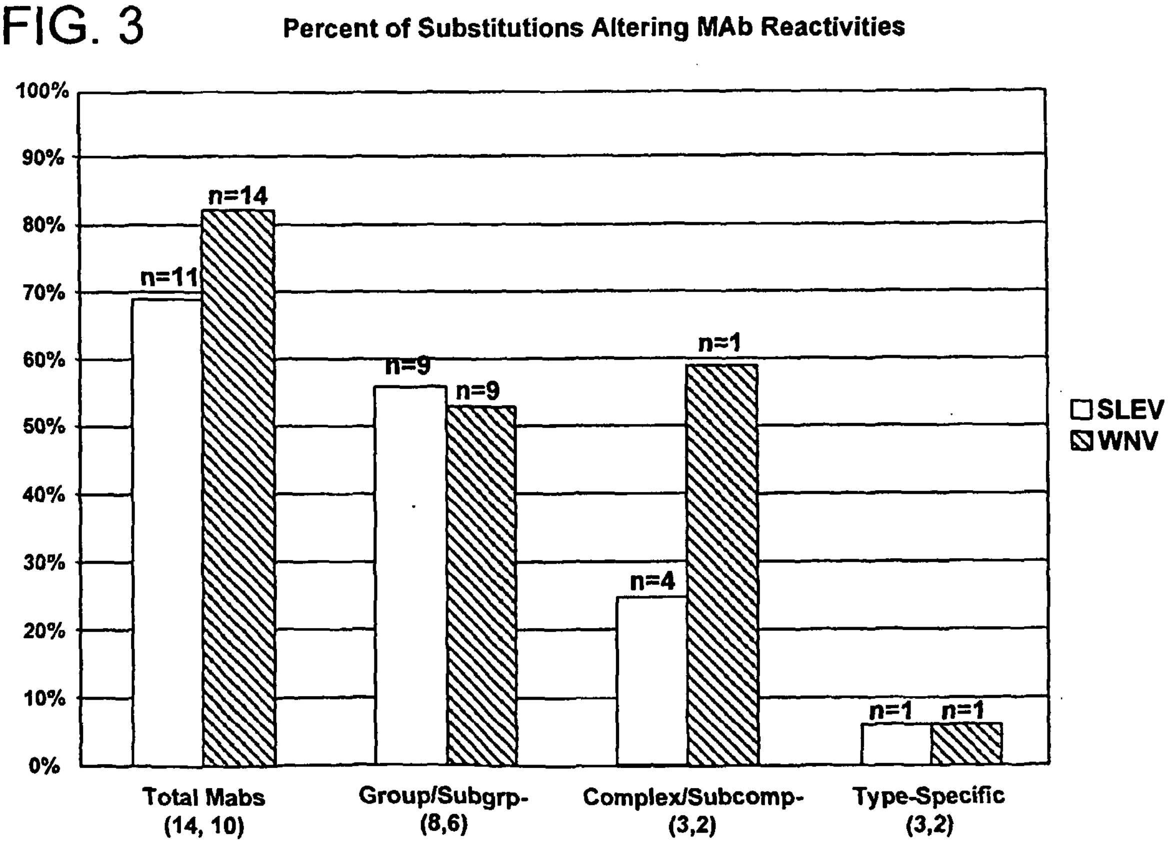

MAbs: 4G2
6B6C-1
1B7-5
10³
10²
10¹
0
G104†
G106
L107
E126
E126/T226
W231†

FIG. 3


Percent of Substitutions Altering MAb Reactivities
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
n=11
n=14
n=9
n=9
n=4
n=1
n=1
n=1
SLEV
WNV
Total Mabs (14, 10)
Group/Subgrp- (8,6)
Complex/Subcomp- (3,2)
Type-Specific (3,2)

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION
Chang, Gwong-Jen J.
Crill, Wayne D.

<120> LOCALIZATION AND CHARACTERIZATION OF FLAVIVIRUS ENVELOPE GLYCOPROTEIN CROSS-REACTIVE EPITOPES AND METHODS FOR THEIR USE

<130> 6395-66689-02

<150> US 60/591,898
<151> 2004-07-27

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Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80
```

```
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg        288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc        336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa        384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac        432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag        480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca        528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac        576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg        624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg        672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc        720
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa        768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg        816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga        864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga        912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata        960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320
```

```
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct      1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att      1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa      1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg      1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag      1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc      1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata      1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt      1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc      1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


&lt;210&gt;  14
&lt;211&gt;  495
&lt;212&gt;  PRT
&lt;213&gt;  Artificial Sequence

&lt;220&gt;
&lt;223&gt;  Synthetic Construct

&lt;400&gt;  14

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15


Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
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            20                  25                  30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

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

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
```

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                260                 265                 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 15

<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus G104H envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 15
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atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca        48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg        96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca       144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag       192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc       240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg       288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat cac tgt gga cta ttt gga aag gga ggc       336
Val Asp Arg Gly Trp Gly Asn His Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa       384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac       432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag       480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca       528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac       576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
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180 185 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg 624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg 672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc 720
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225 230 235 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa 768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
245 250 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg 816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
260 265 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga 864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
275 280 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga 912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
290 295 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata 960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305 310 315 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct 1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
325 330 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att 1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
340 345 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa 1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
355 360 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg 1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
370 375 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag 1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385 390 395 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc 1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
405 410 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata 1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile

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            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt      1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc      1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


<210>  16
<211>  495
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  16

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15


Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30


Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45


Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60


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


Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95


Val Asp Arg Gly Trp Gly Asn His Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110


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

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225 230 235 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
260 265 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
275 280 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
290 295 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305 310 315 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
325 330 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
340 345 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
355 360 365

```
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 17
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus G106Q envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 17

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atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca       48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45
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gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg      288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat gga tgt caa cta ttt gga aag gga ggc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gln Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa      384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca      528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac      576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg      624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg      672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc      720
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285
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atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct     1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att     1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa     1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg     1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag     1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc     1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata     1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt     1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc     1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta     1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa     1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


<210>  18
<211>  495
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct
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<400> 18

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

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

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gln Leu Phe Gly Lys Gly Gly
100 105 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
115 120 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
130 135 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe

225 230 235 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
260 265 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
275 280 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
290 295 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305 310 315 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
325 330 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
340 345 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
355 360 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
370 375 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385 390 395 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
405 410 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
420 425 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
435 440 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu

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465                 470                 475                 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


<210>  19
<211>  1488
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Dengue virus-2/Japanese encephalitis virus L107K envelope
       chimera.


<220>
<221>  CDS
<222>  (1)..(1485)

<400>  19
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca       48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg      288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat gga tgt gga aaa ttt gga aag gga ggc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Lys Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa      384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
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145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca       528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac       576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg       624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg       672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc       720
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa       768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg       816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga       864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga       912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata       960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct      1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att      1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa      1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg      1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag      1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
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385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc      1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata      1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt      1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc      1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


<210>  20
<211>  495
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  20

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15


Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30


Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45


Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60


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


Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95
```

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Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Lys Phe Gly Lys Gly Gly
            100                 105                 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
            260                 265                 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335
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Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
340 345 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
355 360 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
370 375 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385 390 395 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
405 410 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
420 425 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
435 440 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465 470 475 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
485 490 495

<210> 21
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus E126A envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 21
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca 48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

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gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg      288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gca gga aaa      384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Ala Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca      528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac      576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg      624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg      672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc      720
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255
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gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct     1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att     1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa     1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg     1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag     1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc     1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata     1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt     1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc     1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta     1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa     1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 22
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

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Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

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

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Ala Gly Lys
        115                 120                 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
```

```
        195                 200                 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
            260                 265                 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
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435 440 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465 470 475 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
485 490 495

<210> 23
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus T226N envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 23
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca 48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg 96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca 144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag 192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc 240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg 288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc 336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
100 105 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa 384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys

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        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac       432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag       480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca       528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac       576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg       624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg       672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aat caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc       720
Asp Asn Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa       768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg       816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga       864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga       912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata       960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct      1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att      1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa      1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
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355 360 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg 1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
370 375 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag 1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385 390 395 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc 1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
405 410 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata 1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
420 425 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt 1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
435 440 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc 1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta 1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465 470 475 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa 1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
485 490 495

<210> 24
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

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

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
100 105 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
115 120 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
130 135 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

Asp Asn Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225 230 235 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
260 265 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
275 280 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
290 295 300

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Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 25
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus W231F envelope chimera.

<220>

<221> CDS
<222> (1)..(1485)

<400> 25
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca 48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg 96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca 144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag 192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc 240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg 288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc 336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
100 105 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa 384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
115 120 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac 432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
130 135 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag 480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca 528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac 576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg 624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg 672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

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gac aca caa ggg tca aat ttc ata cag aaa gag aca ttg gtc act ttc      720
Asp Thr Gln Gly Ser Asn Phe Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct     1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att     1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa     1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg     1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag     1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc     1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata     1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt     1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc     1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460
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tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


<210>  26
<211>  495
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  26

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15


Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30


Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45


Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60


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


Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95


Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110


Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125


Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140


Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160


Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
```

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                165                 170                 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

Asp Thr Gln Gly Ser Asn Phe Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
            260                 265                 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
```

405 410 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
420 425 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
435 440 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465 470 475 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
485 490 495

<210> 27
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus W231L envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 27
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca 48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg 96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca 144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag 192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc 240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg 288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met

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                85                  90                  95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa      384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca      528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac      576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg      624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg      672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aca caa ggg tca aat ctg ata cag aaa gag aca ttg gtc act ttc      720
Asp Thr Gln Gly Ser Asn Leu Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct     1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
```

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                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att      1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa      1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg      1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag      1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc      1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata      1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt      1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc      1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 28
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

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Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30
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Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

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

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
100 105 110

Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys
115 120 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
130 135 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

Asp Thr Gln Gly Ser Asn Leu Ile Gln Lys Glu Thr Leu Val Thr Phe
225 230 235 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
260 265 270

```
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495
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<210> 29
<211> 1488
<212> DNA

<213> Artificial Sequence

<220>
<223> Dengue virus-2/Japanese encephalitis virus E126A/T226N envelope chimera.

<220>
<221> CDS
<222> (1)..(1485)

<400> 29
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atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca       48
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15

gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg       96
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30

acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca      144
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45

gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag      192
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc      240
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro
65                  70                  75                  80

agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg      288
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95

gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110

att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gca gga aaa      384
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Ala Gly Lys
        115                 120                 125

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac      432
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
    130                 135                 140

tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag      480
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca      528
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac      576
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190
```

```
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg      624
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg      672
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

gac aat caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc      720
Asp Asn Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa      768
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
                245                 250                 255

gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg      816
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
            260                 265                 270

tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga      864
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga      912
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata      960
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct     1008
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att     1056
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa     1104
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg     1152
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
    370                 375                 380

gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag     1200
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385                 390                 395                 400

gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc     1248
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
                405                 410                 415

gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata     1296
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
            420                 425                 430
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gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt      1344
Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
        435                 440                 445

ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc      1392
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
    450                 455                 460

tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta      1440
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465                 470                 475                 480

gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa      1488
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
                485                 490                 495


&lt;210&gt;  30
&lt;211&gt;  495
&lt;212&gt;  PRT
&lt;213&gt;  Artificial Sequence

&lt;220&gt;
&lt;223&gt;  Synthetic Construct

&lt;400&gt;  30

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1               5                   10                  15


Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr
            20                  25                  30


Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
        35                  40                  45


Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
    50                  55                  60


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


Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
                85                  90                  95


Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
            100                 105                 110


Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Ala Gly Lys
        115                 120                 125


Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
```

```
    130                 135                 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145                 150                 155                 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
                165                 170                 175

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
            180                 185                 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
        195                 200                 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
    210                 215                 220

Asp Asn Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225                 230                 235                 240

Lys Asn Pro His Ala Lys Lys Gln Asp 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 Met
            260                 265                 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
        275                 280                 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
    290                 295                 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305                 310                 315                 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
                325                 330                 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
            340                 345                 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
        355                 360                 365

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
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370 375 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys
385 390 395 400

Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly
405 410 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile
420 425 430

Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe
435 440 445

Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu
450 455 460

Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu
465 470 475 480

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
485 490 495

<210> 31
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<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 31
ctccctttc caaacagacc acagtggtta ccccatccgc 40

<210> 32
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 32
ctccctttc caaacagacc acagttgtta ccccatccgc 40

<210> 33
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 33
ccctttcca aacagaccac agtcgttacc ccatccgc 38

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 34
ctccctttc caaacagacc acacttgtta ccccatccgc 40

<210> 35
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 35
ctccctttc caaacagctg acatccgtta ccccatccgc 40

<210> 36
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 36
ctccctttc caaacagctt acatccgtta ccccatccgc 40

<210> 37
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 37
tccctttcc aaacagtaca catccgttac cccatccgc 39

<210> 38
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 38
cttttccaaa cagatcacat ccgttacccc atccgc 36

<210> 39
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 39
ctccctttc caaagaaacc acatccgtta ccccatccgc 40

<210> 40
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 40
aatgctccct tttccaaaga actgacatcc gttaccccat ccgc 44

<210> 41
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 41
cgggcttatg gtgaattgag ccgcttggtt ttttcc 36

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 42
ttccatactc gcccatgttg gcaataaagg acggtg 36

<210> 43
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 43
gtaactgttc catactcgga catgttggcc gtaaagg 37

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 44
gtaactgttc catagttgcc catgttggcc gtaaagg 37

<210> 45
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 45
ctctgttgcg ccaatcgttt gtggcagggc tcgtc 35

<210> 46
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 46
ttctctgttg cggaaatcag ttgtggcagg gctcgtc 37

<210> 47
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 47
tactacagtt tgcttggtgg cacgcggttc ctc 33

<210> 48
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 48
tgattgcaag gttagggttg atccgctaac agtggc 36

<210> 49
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 49
cgttcccttg attttgacgt agtcaagctt agctctgc 38

<210> 50
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 50
acacatgcca tatgccgttc ccttgatttt gacc 34

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 51
cagggtccgt tgcttccatc atactgcagt tccac 35

<210> 52
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 52
cgatcatgac cttgttgttc gatcccctg tgc 33

<210> 53
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 53
ttcgatcatg accttgttga acgctccccc tgtgc 35

<210> 54
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 54
tttgccaaat agtccgcagt tgttgcccca gcccc 35

<210> 55
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 55
ttgccaaata gtccgcagtc gttgccccag c 31

<210> 56
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 56
cctttgccaa atagtccgca cttgttgccc cagcccc 37

<210> 57
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 57
ttgccaaata gtccgcatgc gttgccccag c 31

<210> 58
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 58
tttgccaaat aggacgcagc cgttgcccca gcc 33

<210> 59
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 59
tttgccaaat agcctgcagc cgttgcccca gcc 33

<210> 60
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 60
cctttgccaa ataggtagca gccgttgccc cagcccc 37

<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 61
tttgccaaat agagcgcagc cgttgcccca gcc 33

<210> 62
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 62
ttcctttgcc aaagtatccg cagccgttgc cccagcc 37

<210> 63
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 63
cctttgccaa agaatccgca gccgttgccc cagc 34

<210> 64
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 64
cctttgccaa aatgtccgca gccgttgccc cagc 34

<210> 65
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 65
cctttgccaa atcttccgca gccgttgccc cagc 34

<210> 66
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 66
cttggtagag caggcaaata cggcgcatgt gtc 33

<210> 67
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 67
ccaacctgtg tggagtagtc tccgtgcgac 30

<210> 68
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 68
ccaacctgtg tggagccgtt tccgtgcgac tc 32

<210> 69
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 69
ctgagtggct ccaacatctg tggagtagtt tccgtgcg 38

<210> 70
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 70
aggagtgatg ctgaagtacc ctgcctgagt gg 32

<210> 71
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 71
ccaagcttta gtacgtatga aggcgccgca ggag 34

<210> 72
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 72
cctctccata gcctccaagc tttagtgtgt atgaagg 37

<210> 73
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 73
aacgtctctc tgttcctgaa cacagtactt ccagcac 37

<210> 74
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 74
ccgacgtcaa cttgacagtg ttgtctgaaa attccacagg 40

<210> 75
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 75
gttcccttca actgcaagtt ttccatcttc actctacac 39

<210> 76
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 76
acagacgcca tagtttgttc ccttcaactg caatttttcc 40

<210> 77
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 77
ccatccgtgc cgttgtactg caattccaac accacag 37

<210> 78
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 78
ggaccttagc gttgaccgtg gccactgaaa c 31

<210> 79
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutagenic oligonucleotide primer.

<400> 79
accttagcgc tggccgtggc cactgaaac 29

<210> 80
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> St. Louis encephalitis virus/Japanese encephalitis virus envelope chimera.

<220>
<221> CDS
<222> (1)..(1503)

<220>
<221> misc_feature
<222> (316)..(318)
<223> Mutagenesis of GGT codon to CAG codon produces a G106Q substitution.

<400> 80
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ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc agt      48
Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser
1               5                   10                  15

ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc aca      96
Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr
            20                  25                  30

gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag atg     144
Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met
        35                  40                  45

gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca acc     192
Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr
    50                  55                  60

ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa gct     240
Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala
65                  70                  75                  80
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cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat gtt      288
His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val
                85                  90                  95

gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg agc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
            100                 105                 110

att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg aag      384
Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys
        115                 120                 125

acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg cat      432
Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
    130                 135                 140

ggt tca acg gac tct acg tca cat ggc aat tac ttt gag cag att gga      480
Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Phe Glu Gln Ile Gly
145                 150                 155                 160

aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc ttt      528
Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe
                165                 170                 175

acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa gca      576
Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala
            180                 185                 190

aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag gag      624
Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu
        195                 200                 205

aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt cca      672
Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro
    210                 215                 220

tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg gtg      720
Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val
225                 230                 235                 240

gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta gga      768
Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly
                245                 250                 255

tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca gcc      816
Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala
            260                 265                 270

act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa tgc      864
Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys
        275                 280                 285

aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc atg      912
Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met
    290                 295                 300

tgt gac tct gcc ttc acc ttc agc aag aac cca gct gac aca ggg cac      960
Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Ala Asp Thr Gly His
305                 310                 315                 320
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ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc tgc 1008
Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys
325 330 335

cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg gtt 1056
Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val
340 345 350

gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg aac 1104
Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn
355 360 365

aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac atc 1152
Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile
370 375 380

gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa gag 1200
Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu
385 390 395 400

gga agc acg ctg ggc aag gcc ttt tca aca act ttg aag gga gct caa 1248
Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln
405 410 415

aga ctg gca gcg ttg ggc gac aca gcc tgg gac ttt ggc tct att gga 1296
Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
420 425 430

ggg gtc ttc aac tcc ata gga aaa gcc gtt cac caa gtg ttt ggt ggt 1344
Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly
435 440 445

gcc ttc aga aca ctc ttt ggg gga atg tct tgg atc aca caa ggg cta 1392
Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
450 455 460

atg ggt gcc cta ctg ctc tgg atg ggc gtc aac gca cga gac cga tca 1440
Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser
465 470 475 480

att gct ttg gcc ttc tta gcc aca ggg ggt gtg ctc gtg ttc tta gcg 1488
Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala
485 490 495

acc aat gtg cat gct taa 1506
Thr Asn Val His Ala
500

<210> 81
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81

Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser

1 5 10 15

Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr
20 25 30

Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met
35 40 45

Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr
50 55 60

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

His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys
115 120 125

Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
130 135 140

Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Phe Glu Gln Ile Gly
145 150 155 160

Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe
165 170 175

Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala
180 185 190

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

Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro
210 215 220

Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val
225 230 235 240

Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly

245 250 255

Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala
260 265 270

Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys
275 280 285

Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met
290 295 300

Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Ala Asp Thr Gly His
305 310 315 320

Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys
325 330 335

Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val
340 345 350

Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn
355 360 365

Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile
370 375 380

Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu
385 390 395 400

Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln
405 410 415

Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
420 425 430

Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly
435 440 445

Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
450 455 460

Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser
465 470 475 480

Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala

                485   490   495

Thr Asn Val His Ala
            500

<210> 82
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> St. Louis encephalitis virus/Japanese encephalitis virus G106Q
envelope chimera.

<220>
<221> CDS
<222> (1)..(1503)

<400> 82
ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc agt 48
Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser
1   5   10   15

ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc aca 96
Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr
            20   25   30

gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag atg 144
Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met
        35   40   45

gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca acc 192
Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr
    50   55   60

ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa gct 240
Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala
65   70   75   80

cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat gtt 288
His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val
                85   90   95

gtg gac cgc gga tgg ggt aac gga tgt cag ctg ttt gga aaa ggg agc 336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gln Leu Phe Gly Lys Gly Ser
            100   105   110

att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg aag 384
Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys
        115   120   125

acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg cat 432
Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
    130   135   140

ggt tca acg gac tct acg tca cat ggc aat tac ttt gag cag att gga 480
Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Phe Glu Gln Ile Gly

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145                 150                 155                 160

aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc ttt      528
Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe
                165                 170                 175

acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa gca      576
Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala
            180                 185                 190

aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag gag      624
Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu
        195                 200                 205

aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt cca      672
Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro
    210                 215                 220

tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg gtg      720
Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val
225                 230                 235                 240

gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta gga      768
Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly
                245                 250                 255

tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca gcc      816
Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala
            260                 265                 270

act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa tgc      864
Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys
        275                 280                 285

aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc atg      912
Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met
    290                 295                 300

tgt gac tct gcc ttc acc ttc agc aag aac cca gct gac aca ggg cac      960
Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Ala Asp Thr Gly His
305                 310                 315                 320

ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc tgc     1008
Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys
                325                 330                 335

cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg gtt     1056
Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val
            340                 345                 350

gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg aac     1104
Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn
        355                 360                 365

aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac atc     1152
Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa gag     1200
Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu
```

```
385                 390                 395                 400

gga agc acg ctg ggc aag gcc ttt tca aca act ttg aag gga gct caa      1248
Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

aga ctg gca gcg ttg ggc gac aca gcc tgg gac ttt ggc tct att gga      1296
Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
            420                 425                 430

ggg gtc ttc aac tcc ata gga aaa gcc gtt cac caa gtg ttt ggt ggt      1344
Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445

gcc ttc aga aca ctc ttt ggg gga atg tct tgg atc aca caa ggg cta      1392
Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
    450                 455                 460

atg ggt gcc cta ctg ctc tgg atg ggc gtc aac gca cga gac cga tca      1440
Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser
465                 470                 475                 480

att gct ttg gcc ttc tta gcc aca ggg ggt gtg ctc gtg ttc tta gcg      1488
Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala
                485                 490                 495

acc aat gtg cat gct taa                                              1506
Thr Asn Val His Ala
            500
```

<210> 83
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 83

```
Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser
1               5                   10                  15

Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr
            20                  25                  30

Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met
        35                  40                  45

Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr
    50                  55                  60

Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala
65                  70                  75                  80
```

```
His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val
                85                  90                  95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gln Leu Phe Gly Lys Gly Ser
            100                 105                 110

Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys
        115                 120                 125

Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
    130                 135                 140

Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Phe Glu Gln Ile Gly
145                 150                 155                 160

Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe
                165                 170                 175

Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala
            180                 185                 190

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

Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro
    210                 215                 220

Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val
225                 230                 235                 240

Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly
                245                 250                 255

Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala
            260                 265                 270

Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys
        275                 280                 285

Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met
    290                 295                 300

Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Ala Asp Thr Gly His
305                 310                 315                 320
```

```
Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys
                325                 330                 335

Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val
            340                 345                 350

Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn
        355                 360                 365

Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu
385                 390                 395                 400

Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly
            420                 425                 430

Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445

Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
    450                 455                 460

Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser
465                 470                 475                 480

Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala
                485                 490                 495

Thr Asn Val His Ala
            500
```

<210> 84
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> West Nile virus envelope gene region.

<220>
<221> CDS

<222> (1)..(1503)

<220>
<221> misc_feature
<222> (316)..(318)
<223> Mutagenesis of GGA codon to GTC codon produces a G106V substitution.

<400> 84
ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga gtg tct 48
Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser
1 5 10 15

gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc gtg act 96
Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr
20 25 30

atc atg tct aag gac aag cct acc atc gat gtg aag atg atg aat atg 144
Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met
35 40 45

gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg gct acc 192
Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr
50 55 60

gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga gaa gct 240
Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala
65 70 75 80

cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa gga gtg 288
His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val
85 90 95

gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa gga agc 336
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata gga aga 384
Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg
115 120 125

acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt gtc cat 432
Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
130 135 140

gga cca act act gtg gag tcg cac gga aac tac tcc aca cag gtt gga 480
Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly
145 150 155 160

gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct tca tac 528
Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr
165 170 175

aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt gaa cca 576
Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro
180 185 190

cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt gga aca 624
Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr
195 200 205

```
aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac ctc cct      672
Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro
    210                 215                 220

tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg tta atg      720
Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met
225                 230                 235                 240

gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca ttg ggc      768
Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly
                245                 250                 255

tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att cct gtg      816
Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val
            260                 265                 270

gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg aag tgt      864
Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys
        275                 280                 285

aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat ggc gtc      912
Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val
    290                 295                 300

tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca ggt cac      960
Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His
305                 310                 315                 320

ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga cct tgc     1008
Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys
                325                 330                 335

aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg cca gtg     1056
Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
            340                 345                 350

ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg gcc aac     1104
Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn
        355                 360                 365

gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca tac ata     1152
Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac aag tct     1200
Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser
385                 390                 395                 400

gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga gcg cag     1248
Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca gtt gga     1296
Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
            420                 425                 430

ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc gga gga     1344
Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445
```

gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa gga ttg 1392
Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
450 455 460

ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat agg tcc 1440
Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser
465 470 475 480

ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc ctc tcc 1488
Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser
485 490 495

gtg aac gtg cac gcc tga 1506
Val Asn Val His Ala
500

<210> 85
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85

Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser
1 5 10 15

Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr
20 25 30

Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met
35 40 45

Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr
50 55 60

Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala
65 70 75 80

His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg
115 120 125

Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
130 135 140

Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly
145 150 155 160

Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr
165 170 175

Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro
180 185 190

Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr
195 200 205

Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro
210 215 220

Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met
225 230 235 240

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

Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val
260 265 270

Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys
275 280 285

Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val
290 295 300

Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His
305 310 315 320

Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys
325 330 335

Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
340 345 350

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn
355 360 365

```
Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser
385                 390                 395                 400

Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
            420                 425                 430

Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445

Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
    450                 455                 460

Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser
465                 470                 475                 480

Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser
                485                 490                 495

Val Asn Val His Ala
            500


<210>  86
<211>  1506
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  West Nile virus envelope gene region with G106V substitution.


<220>
<221>  CDS
<222>  (1)..(1503)

<400>  86
ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga gtg tct      48
Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser
1               5                   10                  15

gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc gtg act      96
Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr
            20                  25                  30

atc atg tct aag gac aag cct acc atc gat gtg aag atg atg aat atg     144
Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met
```

```
        35                  40                  45

gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg gct acc      192
Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr
    50                  55                  60

gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga gaa gct      240
Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala
65                  70                  75                  80

cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa gga gtg      288
His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val
                85                  90                  95

gtg gac agg ggc tgg ggc aac ggc tgc gtc cta ttt ggc aaa gga agc      336
Val Asp Arg Gly Trp Gly Asn Gly Cys Val Leu Phe Gly Lys Gly Ser
            100                 105                 110

att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata gga aga      384
Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg
        115                 120                 125

acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt gtc cat      432
Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
    130                 135                 140

gga cca act act gtg gag tcg cac gga aac tac tcc aca cag gtt gga      480
Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly
145                 150                 155                 160

gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct tca tac      528
Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr
                165                 170                 175

aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt gaa cca      576
Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro
            180                 185                 190

cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt gga aca      624
Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr
        195                 200                 205

aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac ctc cct      672
Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro
    210                 215                 220

tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg tta atg      720
Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met
225                 230                 235                 240

gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca ttg ggc      768
Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly
                245                 250                 255

tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att cct gtg      816
Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val
            260                 265                 270

gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg aag tgt      864
Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys
```

```
        275                 280                 285

aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat ggc gtc        912
Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val
    290                 295                 300

tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca ggt cac        960
Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His
305                 310                 315                 320

ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga cct tgc       1008
Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys
                325                 330                 335

aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg cca gtg       1056
Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
            340                 345                 350

ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg gcc aac       1104
Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn
        355                 360                 365

gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca tac ata       1152
Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac aag tct       1200
Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser
385                 390                 395                 400

gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga gcg cag       1248
Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca gtt gga       1296
Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
            420                 425                 430

ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc gga gga       1344
Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445

gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa gga ttg       1392
Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
    450                 455                 460

ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat agg tcc       1440
Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser
465                 470                 475                 480

ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc ctc tcc       1488
Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser
                485                 490                 495

gtg aac gtg cac gcc tga                                               1506
Val Asn Val His Ala
            500


<210>  87
```

<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 87

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Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser
1               5                   10                  15

Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr
            20                  25                  30

Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met
        35                  40                  45

Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr
    50                  55                  60

Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala
65                  70                  75                  80

His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val
                85                  90                  95

Val Asp Arg Gly Trp Gly Asn Gly Cys Val Leu Phe Gly Lys Gly Ser
            100                 105                 110

Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg
        115                 120                 125

Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
    130                 135                 140

Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly
145                 150                 155                 160

Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr
                165                 170                 175

Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro
            180                 185                 190

Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr
        195                 200                 205
```

```
Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro
    210                 215                 220

Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met
225                 230                 235                 240

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

Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val
            260                 265                 270

Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys
        275                 280                 285

Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val
    290                 295                 300

Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His
305                 310                 315                 320

Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys
                325                 330                 335

Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
            340                 345                 350

Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn
        355                 360                 365

Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile
    370                 375                 380

Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser
385                 390                 395                 400

Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln
                405                 410                 415

Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
            420                 425                 430

Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly
        435                 440                 445
```

Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
450 455 460

Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser
465 470 475 480

Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser
485 490 495

Val Asn Val His Ala
500