



(51) International Patent Classification:

C07K 14/005 (2006.01)

G01N 33/68 (2006.01)

A61K 39/12 (2006.01)

G01N 33/569 (2006.01)

A61P 31/14 (2006.01)

(21) International Application Number:

PCT/US2020/045241

(22) International Filing Date:

06 August 2020 (06.08.2020)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/883,382

06 August 2019 (06.08.2019)

US

(71) Applicant: THE UNIVERSITY OF NORTH CAROLI-

NA AT CHAPEL HILL [US/US]; 109 Church Street, Chapel Hill, North Carolina 27516 (US).

(72) Inventors: KUHLMAN, Brian; 1009 Tallyho Tr., Chapel

Hill, North Carolina 27516 (US). KUDLACEK, Stephan T.; 24306 Volta Gardens Ct., Katy, Texas 77493 (US).

DE SILVA, Aravinda; 1906 Bearkling Place, Chapel Hill, North Carolina 27517 (US). PAYNE, Alexander; 445 E

69th St, Olin Hall #902-1, New York, New York 10021 (US). PHAN, Thanh; 112 Bim St., Apt. C, Carrboro, North

Carolina 27510 (US). METZ, Stefan; 4910 Victoria Drive, Durham, North Carolina 27713 (US).

(74) Agent: PASMAN, Lesley; MYERS BIGEL, P.A., PO Box 37428, Raleigh, North Carolina 27627 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available):

AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available):

ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

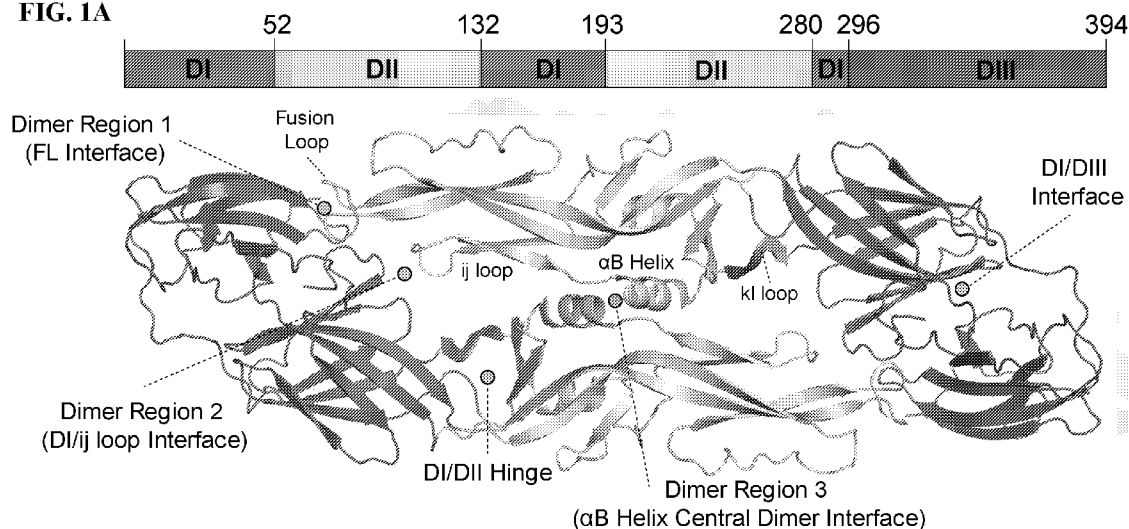
Published:

— with international search report (Art. 21(3))

— with sequence listing part of description (Rule 5.2(a))

(54) Title: METHODS AND COMPOSITIONS FOR STABILIZED RECOMBINANT FLAVIVIRUS E PROTEIN DIMERS

FIG. 1A



(57) **Abstract:** The present invention provides compositions and methods of use comprising a stabilized recombinant E glycoprotein comprising a flavivirus E glycoprotein backbone, which comprises amino acid substitutions that stabilize the E glycoprotein in dimer conformation under physiological conditions.



METHODS AND COMPOSITIONS FOR STABILIZED RECOMBINANT FLAVIVIRUS E PROTEIN DIMERS

RELATED APPLICATIONS

This application claims the benefit, under 35 U.S.C. § 119(e), of U.S. Provisional Application Serial No. 62/883,382, filed August 6, 2019, the entire contents of which are
5 incorporated by reference herein.

STATEMENT OF GOVERNMENT SUPPORT

This invention was made with government support under Grant Number W81XWH1820035 awarded by the Department of Defense. The government has certain
10 rights in the invention.

STATEMENT REGARDING ELECTRONIC FILING OF A SEQUENCE LISTING

A Sequence Listing in ASCII text format, submitted under 37 C.F.R. § 1.821, entitled
15 5470-844WO_ST25.txt, 534,075 bytes in size, generated on August 6, 2020 and filed via EFS-Web, is provided in lieu of a paper copy. This Sequence Listing is hereby incorporated herein by reference into the specification for its disclosures

FIELD OF THE INVENTION

20 The present invention is directed to recombinant stabilized flavivirus E glycoproteins that induce neutralizing antibodies against quaternary epitopes and form dimers in physiological, e.g., vaccine, conditions.

BACKGROUND OF THE INVENTION

25 Vaccine control of dengue virus (DENV), a member of the flavivirus family, has remained elusive. About 25% of the ~400 million annual DENV infections worldwide result in severe clinical manifestations, necessitating effective vaccine control of DENV. A substantial challenge in eliminating DENV infections is the prevalence of four DENV serotypes, each capable of eliciting both unique, serotype-specific and DENV cross-reactive
30 immune responses upon infection. Some responses, such as the immune response following a first or "primary" infection with one DENV serotype, can lead to lifelong protection against that serotype. However, all four DENV serotypes co-circulate in the same regions and are

transmitted by the same *A. aegypti* and *A. albopictus* mosquito vectors, which allows for infections of the same individual by a different DENV serotype. These secondary DENV infections can result in severe and sometimes lethal disease symptoms, such as dengue hemorrhagic fever and shock syndromes. A supported hypothesis for the cause of these severe dengue clinical manifestations is through increased viral burden caused by antibody-dependent enhancement (ADE), where a population of non-neutralizing cross-reactive antibodies elicited from the primary DENV infection are able to bind to the DENV serotype present in the second infection, allowing for Fc-receptor mediated endocytosis of the virus by macrophages thus enhancing the infection through increased replication of the virus. Despite these challenges, advancements have been made with multiple live-attenuated dengue vaccines including the only approved dengue vaccine, Dengvaxia (Rey et al., 2018 *EMBO Rep.* 19:206-224; Thomas and Yoon, 2019 *Hum. Vaccines Immunother.* 15:2295-2314), and several others in late stage clinical trials. Dengvaxia has proven capable of providing protection to people who have overcome a primary dengue infection against a secondary dengue infection. However, it is evidenced that vaccinating individuals who have had no prior dengue infections increases their risk of developing severe clinical manifestations of dengue, which is suggested to be caused by ADE. These observations highlight the difficulty of vaccine mediated control of dengue infection and the need for more targeted vaccination strategies to prevent DENV infections.

Characterization of antibodies elicited by DENV infected individuals reveal that the DENV envelope protein is the primary target of neutralizing antibodies, which has led to a large body of work in assessing the immunogenicity and efficacy of this protein as a subunit vaccine. While promising, E protein-based subunit vaccines have only had limited success in clinical trials. Recently, it has been appreciated that antibodies that target quaternary epitopes, present within a single E dimer and across multiple dimers in the E dimer lipid raft, are potentially neutralizing and provide protection against DENV infection.

Previous work has shown that the DENV2 soluble E protein dimer has a homodimer K_d of 12 μ M at 37°C, which is too weak to be relevant under vaccination conditions and limits its current use as a vaccine antigen by reducing the presentation of critical quaternary epitopes. The present invention overcomes shortcomings in the art by providing flavivirus E glycoproteins that retain dimer conformation at physiological conditions and can be expressed without co-expression of pr, allowing for safer vaccines.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides a stabilized recombinant flavivirus E glycoprotein, comprising a flavivirus E glycoprotein backbone and an amino acid substitution selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any combination thereof (e.g., amino acid substitutions shown in **Table 1** and/or **Table 2**), wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**.

In another aspect, the present invention provides a flavivirus E glycoprotein dimer comprising two stabilized recombinant flavivirus E glycoproteins of the present invention.

Additionally provided herein is a dengue virus particle, a flavivirus particle and/or a virus like particle (VLP) comprising the E glycoprotein of this invention.

An isolated nucleic acid molecule encoding the E glycoprotein of this invention is also provided herein, as well as an isolated nucleic acid molecule encoding the dengue virus particle, flavivirus particle or VLP of this invention.

The present invention also provides a composition comprising the E glycoprotein of this invention in a pharmaceutically acceptable carrier and also provides a composition comprising the E glycoprotein dimer of this invention, nucleic acid molecule of this invention, the vector of this invention, the particle of this invention and/or the population of this invention, in a pharmaceutically acceptable carrier.

The present invention also provides a method of producing a virus like particle (VLP) comprising the E glycoprotein of the present invention, wherein the method does not comprise co-expression of pr.

The present invention further provides the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the dengue virus particle of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the vector of this invention, the population of this invention and/or the composition of this invention, singly or in any combination, for use in the manufacture of a medicament for producing an immune response to a flavivirus in a subject, for treating a flavivirus infection in a subject in need thereof, for preventing a flavivirus infection in a subject and/or

for protecting a subject from the effects of flavivirus infection, and/or for use in any of the methods as disclosed herein.

Also provided herein is the use of the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the dengue virus particle of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the vector of this invention, the population of this invention and/or the composition of this invention, singly or in any combination, for use in producing an immune response to a flavivirus in a subject, in treating a flavivirus infection in a subject in need thereof, in preventing a flavivirus infection in a subject and/or in protecting a subject from the effects of flavivirus infection, and/or for use in any of the methods as disclosed herein.

Also provided herein is a method of producing an immune response to a flavivirus in a subject (e.g., a subject in need thereof), comprising administering to the subject an effective amount of the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the population of this invention, and/or the composition of this invention and any combination thereof.

Additionally provided herein is a method of treating a flavivirus infection in a subject (e.g., a subject in need thereof), comprising administering to the subject an effective amount of the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the population of this invention, and/or the composition of this invention and any combination thereof.

Further provided herein is a method of preventing a disorder associated with flavivirus infection in a subject (e.g., a subject in need thereof), comprising administering to the subject an effective amount of the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the population of this invention, and/or the composition of this invention and any combination thereof.

As an additional aspect, the present invention provides a method of protecting a subject from the effects of flavivirus infection, comprising administering to the subject an effective amount of the E glycoprotein of this invention, the E glycoprotein dimer of this invention, the flavivirus particle of this invention, the VLP of this invention, the nucleic acid molecule of this invention, the population of this invention, and/or the composition of this invention and any combination thereof.

In further aspects, the present invention provides methods of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising: a) administering a composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention to the subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of step (a) above under conditions whereby neutralization of the flavivirus particles can be detected; and c) detecting neutralization in step (b), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

The present invention additionally provides methods of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising: a) contacting a biological sample from a subject that has been administered an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention with flavivirus particles comprising the E glycoprotein under conditions whereby neutralization of the flavivirus particles can be detected; and b) detecting neutralization in step (a), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

In other embodiments, the present invention provides methods of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising: a) administering an immunogenic composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention to a subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of step (a) under conditions whereby neutralization of the flavivirus particles can be detected; c) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and d) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of (a).

Further provided herein are methods of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention with flavivirus particles comprising the E glycoprotein under

conditions whereby neutralization of the flavivirus particles can be detected; b) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and c) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of (a).

The present invention also provides methods of detecting an antibody to a flavivirus in a sample, comprising: a) contacting the sample with an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention under conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby detecting an antibody to the flavivirus in the sample.

The present invention also provides methods of identifying an antibody to a flavivirus in a biological sample from a subject, comprising: a) administering a composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention to the subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and c) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.

A further embodiment of the present invention includes methods of identifying an antibody to a flavivirus in a biological sample from a subject, comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.

Another embodiment of the present invention include methods of identifying an immunogenic composition that induces an antibody to a flavivirus in a subject, the method comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising an E glycoprotein of any of the present invention or an E glycoprotein dimer of the present invention with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby identifying an immunogenic composition that induces an antibody to the flavivirus in the subject.

Further aspects of the present invention include methods of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, comprising: a) administering an immunogenic composition comprising an E glycoprotein of the present invention or an E glycoprotein dimer of the present invention to a subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and c) detecting formation an antigen/antibody complex, thereby identifying an immunogenic composition that induces a neutralizing antibody to the flavivirus in the subject.

Another aspect of the present invention provides methods of producing a stabilized recombinant E glycoprotein of the present invention, comprising: introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone, wherein the one or more amino acid substitutions are selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any combination thereof (e.g., amino acid substitutions shown in **Table 1** and/or **Table 2**), wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**, thereby stabilizing the flavivirus E glycoprotein into dimer conformation.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1F show schematics of the computational design strategy for the identification of DENV2 sE dimer and monomer stabilizing mutations. **FIG. 1A** shows a schematic of the DI/DII hinge containing the structural kl loop motif, and DI/DIII linker regions, which together form the anti-parallel homodimer. The sE dimer interface can be described by three regions, Dimer Region 1, containing the fusion loop (FL) peptide (FL interface), Dimer Region 2, where the ij loop of one monomer contacts DI of the adjacent monomer, and Dimer Region 3, the central dimer interface where the α B helix joins to at the 2-fold axis of the dimer. **FIG. 1B** shows an overview of the *in silico* exhaustive site-saturation mutagenesis protocol (PM_ssm), which independently simulated mutating every residue to each of the 20 canonical amino acids (AA) at every position in the sE dimer. The

protocol walked through every residue position in primary sequence and executed an independent simulation where the residue is mutated and the design model is scored using the Rosetta scorefunction. The rosetta total score of the mutated design was subtracted by the score of the simulation where the residue is mutated to the WT residue, representing the change in rosetta score relative to WT (Δ REU), predicting the stability change upon mutation. The position being mutated and the primary sequence neighbors, residue $i+1$ and $i-1$, had no backbone (BB) constraints, allowing freedom of the backbone to accommodate the new mutation. All residues within a 10Å sphere of these residues underwent constrained BB sampling (± 2 Å deviation) and sidechain repacking to alleviate clashes introduced by the mutation. All other residues were fixed and had no backbone or sidechain sampling. The mutations with Δ REU > -2 were rejected and the remaining mutations were used as seed residues to be combined in silico using the PM_Comb protocol into entire domains, domain interfaces, or at the dimer interface. **FIG. 1C** shows the IntFc, HCat and UndPk simulations that were performed using the cluster_mut protocol to identify clusters of stabilizing mutations that form new contacts to each other and to the WT residues (**FIG. 1C, right**). All residues within 7Å the seed residue (dark) were designed together (light) allowing side chain and constrained BB sampling of residues up to 10Å away from the seed residue, excluding the designable residues, were allowed to accommodate the mutations (**FIG. 1C, top and left**). **FIG. 1D** shows a schematic of regions in the DENV2 sE dimer selected to focus the Rosetta simulations for identification of stabilizing DENV2 sE dimer and monomer mutations. **FIG. 1D, Top** shows the seed residues, represented as spheres, in the Dimer region 1, Dimer region 2, and Dimer Region 3 that were used in the IntFc simulations. Histidine-cation (HCat) clusters, involved in the low pH dissociation of the sE dimer to trimer, were targeted and used as seed residues for the HCat simulations. **FIG. 1D, Bottom** shows RosettaHoles analysis used to identify regions throughout the DENV2 sE dimer predicted to contribute to both dimer and monomer instability. Residues within the DI/DIII interface (UP Region 1), DI core (UP Region 2), DI/DII Hinge (UP Region 3) and DII core and α B helix (UP region 4) were selected as seed residues for the UndPk simulations. Hydrophobic residues normally buried in the E dimer on the virus or at the E post-fusion trimer interface, surface exposed in the sE dimer, were selected as input for the SHP simulations to be redesigned to polar residues. Sequences shown are amino acid residues in position 251-267 of SEQ ID NO:6 (WT DENV2 sE) and of SEQ ID NO:# (IntFc2), wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as SEQ ID NO:6. **FIG. 1E** shows an overview of the

DENV2 sE stability design simulations pipeline. The four representative DENV2 sE crystal structures, PDB 1oan, 1tg8, 1oke and 4utc were minimized using the FastRelax Rosetta algorithm in preparation for the simulations (Step 1). Residues representing the contacts made by quaternary epitope antibodies 2D22, EDE1 C8 and EDE1 C10 (Step 2, spheres) are selected to prevent design during the simulations. The seed residue for a given simulation is passed to the cluster_mut protocol or multiple seed residues to the PM_Comb protocol using the logic shown in **FIG. 1B & FIG. 1D**, where the designated residues are mutated to any of the 20 canonical AA, except cysteine (Step 3). After design was complete, each design was evaluated using the rosetta scorefunction and the process repeated until 100 design models per simulation were produced. After aggregating the results, the designs with $\Delta\text{REU} > -2$ were discarded and designs were manually inspected and selected for further experimental characterization (Step 4). **FIG. 1F** shows a table of cytometry data of cells displaying DENV2 sE variant proteins bound to cMyc, 1C19, 3H5, 2D22, EDE1 C8 and EDE1 C10 antibodies, represented by geometric mean fluorescence intensity ratio (Fr) of DENV2 sE variant to DENV2 sE WT displayed cells. Fr data for cells stained at RT(23°C, left) or 40°C (right) are presented. Fr values > 1 indicate improved antibody binding to DENV2 sE variants, while Fr values ≈ 1 and < 1 represent similar and reduced antibody binding, respectively. Black squares indicate antibody binding was not tested for those sE variants. Asterisks indicate DENV2 sE variants (IntFc6 and Mnmer2) were unfolded after incubation at 40°C evidenced by no observed binding of the DENV antibodies.

FIGS. 2A-2D show representative flow cytometry data of antibody binding to mammalian surface displayed DENV2 sE variants. Mammalian surface display was used to screen for improved DENV2 sE Rosetta variant quaternary epitope presentation at 37°C.

FIG. 2A shows a diagram of DENV2 sE mammalian display platform. Secreted DENV2 sE are displayed on the surface of EXPI293F cells by genetically fusing the c-terminus to the MHC Ia cytoplasmic and transmembrane domains via a GS linker. In the linker, a cMyc epitope tag is inserted for detection of successful surface display by anti-cMyc antibody binding. Quaternary epitope presentation of the DENV2 sE variants are detected via binding of representative quaternary epitope antibodies. **FIG. 2B** shows a bar graph displaying flow cytometric analysis of monomer epitope antibody 3H5 ("monomer"; left bar), and cross-reactive EDE1 C10 ("Quat.^{CR}"; center bar) and type-specific 2D22 ("Quat.^{TS}"; right bar) quaternary epitope antibody binding to surface displayed DENV2 sE WT, DENV2 sE variants (Cm2, IntFc2, IntFc8 and UndPk6) and membrane anchor negative control (MHC ctrl). The geometric mean fluorescence ratio (Fr) of sE variant to sE WT surface displayed

cells post antibody immunostaining are plotted. **FIGS. 2C** and **2D** show representative flow cytometry plots with the representative gating strategy for analysis of DENV anti-E monomer and quaternary epitope specific antibody binding to DENV2 sE proteins, represented double stained cells displaying DENV2 sE WT (**FIG. 2C**) or DENV2 sE UndPk6 (**FIG. 2D**) at 40°C.

sE surface displayed cells were stained with chicken anti-cMyc (x-axis) and detected by secondary anti-chicken antibody (Alexa-488) to discriminate cells displaying sE (Q3) from cells with no sE display (Q4) and also stained with anti-DENV E antibody (represented by EDE1 C10) and detected by fluorescently-labeled goat anti-human IgG (PerCP), to differentiate between sE proteins presenting (Q2) or lacking epitope presentation measured by antibody binding. The PerCP geometric mean fluorescence intensity of gated cMyc positive cells is recorded (Q3 & Q4) and used for Fr analysis.

FIGS. 3A-3D show representative nanoDSF measured DENV2 sE protein nanoDSF thermal melt experiments at 4μM concentration, monitoring 330nm fluorescence from 15°C to 95°C. **FIG. 3A** shows first-derivative 330nm nanoDSF thermal melt plots of DENV2 sE WT (black; 1), Mnmer2 (pink; 2), PM4 (purple; 3) and IntFc2 (blue; 4). DENV2 sE protein thermal melts contain two melting transitions, with sE dimer dissociation corresponding in the first transition (Tm1, negative first derivative), followed by complete protein unfolding occurring during the second transition (Tm2, positive first derivative). Increases in dimer stability or monomer stability were observed with increases in Tm1 or Tm2 as observed for IntFc2 and PM4 respectively. Loss of the Tm1 transition for Mnmer2 is indicative of no observed dimer dissociation. **FIG. 3B** thermal melt traces for DENV2 sE WT, IntFc2 (I2, blue; 4), IntFc8 (I8, green; 5) and PM4 (P4, purple; 3) are shown. The sE stable combination (SC) variant, SC.1 (orange; 6) containing I2, I8 and P4, had a nearly identical Tm2 as P4, and Tm1 close to the addition of I2 and I8's change in Tm1 (dimer stability) compared to WT. **FIG. 3C** shows a table of quantified absolute (Tm1 and Tm2) and relative to WT (ΔTm1 and ΔTm2) melting points for DENV2 sE proteins presented in **FIGS. 3A** and **3B**. **FIG. 3D** shows a schematic of the DENV2 sE nanoDSF experiment model, describing the sE conformations as a function of temperature. At low temperature, dimer formation is favored, with increasing temperature inducing dimer dissociation observed in the first melting transition corresponding to Tm1, followed by complete protein unfolding and aggregation occurring during the second transition (Tm2).

FIGS. 4A-4D show validation of nanoDSF DENV2 sE variant dimer stability using SEC-MALS. Size-exclusion coupled with multi-angle light scattering (SEC-MALS) experiments were used to validate the improved dimer stability of DENV2 sE variants by

measuring their oligomeric state at RT and 37°C. **FIG. 4A** shows a SEC-MALS experiment using 250µg of DENV2 sE WT at 2.5mg/mL and 150µg DENV2 sE Mnmer2 at 1.5mg/mL, both independently loaded onto a GE Superdex 10/200 gL analytical size exclusion column for SEC-MALS at RT (WT and Mnmer2), or at 37°C (WT). Plotted are the protein elution
 5 volumes, on the x-axis, with the normalized absorbance at 280nm (lines) on the left x-axis and the protein molar mass (dots) calculated from MALS data on the right y-axis. **FIG. 4B** shows a SEC-MALS experiment using 250 µg of DENV2 sE WT, IntFc8 (I8), UndPk6 (U6), and PM4 (P4) at 2.5mg/mL and 160µg of DENV2 sE IntFc2 (I2) at 1.6 mg/mL (I2) as analyzed at 37°C. **FIG. 4C** shows 37°C SEC-MALS analysis of stable combination variants
 10 (SC) DENV2 sE SC.10 and SC.14 and disulfide stabilized DENV2 sE Cm1 loaded with 250µg at 2.5 mg/mL. **FIG. 4D** shows a table of theoretical (expected) and MALS measured molar masses of DENV2 sE proteins at RT or 37°C presented in **FIGS. 4A-4C**, with the Peak 1 or 2 mean molar mass $\pm$ SEM (%) of the fitted MALS data reported. The absorbance peaks at the earliest elution volume and the later elution volume corresponding to Peak 1 and 2,
 15 respectively.

FIGS. 5A-5B show schematics of DENV2 sE SC.10 crystal structure comparisons to Rosetta model and EDE1 C8/sE co-crystal structure. **FIG. 5A, Top** shows DENV2 sE SC.10 dimer conformation observed in the crystal structure, colored by domain (DI), (DII), (DIII). The red dotted line represents the DI glycan loop residues, unmodeled due to insufficient
 20 density and disorder of the loop. **FIG. 5A, Bottom** shows a comparison of IntFc8 (left) IntFc2 (middle) and UndPk6 (right) mutations observed in the crystal structure to DENV2 sE WT crystal structure (PDB 1oan), the structure used as input for design of these variants, and the Rosetta predicted model. Hydrogen bonds are represented by black dotted lines. **FIG. 5B, Left** shows the root mean square deviation (RMSD) C α alignment of the DENV2 sE SC.10
 25 dimer with the DENV2 sE WT dimer co-crystallized with EDE1 C8, a DENV broadly neutralizing quaternary epitope antibody, using PyMOL align algorithm, with surface representation of the EDE1 C8 Fabs. **FIG. 5B, Right** shows the C α alignment of the DI and DIII domains from DENV2 sE WT sE (PDB 1OAN and 4UTA) and DENV2 sE SC.10. Inset shows a closer view of the kl loop conformation observed in each structure after DI and DIII
 30 alignment.

FIGS. 6A-6F show bar graphs depicting epitope presentation of DENV2 sE proteins assessed by binding of representative DENV E monomer and quaternary epitope antibodies. ELISA antibody binding analysis at 37°C of representative DENV E monomer and quaternary epitope antibodies (**FIG. 6A**) to DENV2 sE monomers, WT (**FIG. 6B**) Mnmer2

(**FIG. 6C**), and dimers, Cm1 (**FIG. 6D**), SC.14 (**FIG. 6E**), and SC.10 (**FIG. 6F**). 100ng of sE protein at 45nM was immobilized to the nickel coated ELISA plate, and incubated with 2µg/mL of each antibody. Antibody binding was detected using AP-conjugated anti-mouse or anti-human IgG and measuring the absorbance at 405nm of converted AP substrate. Antibody binding signals of antibodies targeting DI (3F9), DII (1C19), DIII (3H5) and fusion loop (FL, 4G2 and 1M7) monomer epitopes (grayscale) and quaternary antibody epitopes (2D22, EDE1 C8 and EDE2 A11) (black) are plotted, with DENV1 specific antibody, 1F4 (white), used to as a negative control. Experiment was performed in triplicate with error bars representing the mean 405nm signal $\pm$ standard deviation of the mean (SD).

FIGS. 7A-7C show that DENV2 sE SC.14 & SC.10 stable dimers elicit DENV2 envelope dimer specific antibodies in mice. **FIG. 7A** shows a schematic representation of the experimental protocol. Serum of mice immunized 3 times with 5µg of DENV2 sE WT, Mnmer2, SC.14 or SC.10 protein was harvested 16 weeks post initial immunization. To identify if elicited antibodies target E monomer epitopes or dimer epitopes, sE monomer (DENV2 sE Mnmer2) or sE dimer (SC.14) loaded Ni-NTA beads were incubated with the mice immunized sera 37°C. Antibodies specific to sE monomer were depleted by beads loaded with either sE monomer or dimer, as monomer epitopes are presented on both proteins. Dimer specific antibodies were only depleted by sE dimer, and remained in the sera post depletion with sE monomer loaded beads. Depleted sera were analyzed in a DENV2 capture ELISA to detect the remaining antibodies present post depletion with sE monomer or sE dimer loaded beads. **FIG. 7B** shows representative DENV2 ELISA serum antibody binding data of undepleted (1), His-tagged spycatcher negative control depleted (control depletion, 2), Mnmer2 depleted (monomer depleted, 3) and SC.14 depleted (dimer depleted, 4) sera from mice immunized with DENV2 sE WT, Mnmer2, SC.14 and SC.10. Depleted sera was serially diluted 4-fold and tested for serum antibody binding to DENV2 in triplicate, with error bars reporting mean 405nm absorbance $\pm$ standard deviation of the mean (SD). **C**) ELISA analysis of antibody binding of serially diluted, Mnmer2 (monomer dep.) or SC.14 (dimer dep.) depleted serum antibody binding to DENV2 (left), sE Mnmer2 (middle) or sE SC.14 (right) of each mouse (n=5) immunized with either DENV2 sE WT (red), Mnmer2 (M2, black), SC.14 (purple) or SC.10 (blue) depleted with Mnmer2 (monomer depleted) or SC.14. Each serum dilution was performed in triplicate with error bars representing the mean 405nm absorbance $\pm$ the standard deviation of the mean (SD), which was fitted to obtain the end point dilution titer (EPD). Data is represented as the ratio of end point dilution (EPD) of monomer depleted sera to dimer depleted sera.

FIG. 8 shows a schematic of sRecE dimer stability during changes in concentration and temperature.

FIGS. 9A-9C show schematics of the modeling strategy. **FIG. 19A** shows depictions of temperature-sensitive dimer contacts and HisCat clusters. **FIG. 19B** shows depictions of Underpacked Regions and surface hydrophobics. **FIG. 19C** shows an example stabilized recombinant E glycoprotein (IntFc2) with two mutations, A259W and T262R, predicted as stabilizing by the modeling strategy described herein.

FIG. 10 shows a schematic of the E glycoprotein structure with indicated regions targeted for mutations.

FIG. 11 shows an alignment of the E glycoprotein soluble ectodomain amino acid sequence of DENV1 (SEQ ID NO:147), DENV2 (SEQ ID NO:6), DENV3 (SEQ ID NO:152), and DENV4 (SEQ ID NO:169).

FIGS. 12A-12C show ZIKV mutation experiments. **FIG. 12A** shows a diagram of the ZIKV E glycoprotein structure with an engineered disulfide. **FIG. 12B** shows protein gel analysis between the recombinant monomer and the stabilized recombinant dimer. **FIG. 12C** shows a bar graph of neutralizing antibody binding to recombinant E glycoprotein monomer and stabilized recombinant dimer.

FIGS. 13A-13B show *in vivo* ZIKV experiments. **FIG. 13A** shows ZIKV IgG levels analyzed at week 16 post infection, wherein mice were primed at week 3 and boosted at week 9 with soluble rE monomer ("rEM") or rE dimer ("rED") with or without alum adjuvant, or vehicle control. **FIG. 13B** shows neutralizing antibody titers under the same conditions as in **FIG. 13A**.

FIGS. 14A-14C show experimental results of EDIII serum depletion assays. **FIG. 14A** shows the percentage of antibodies that bound to EDIII. **FIG. 14B** shows neutralizing antibody titers in undepleted and depleted conditions. **FIG. 14C** shows % blockade of binding between recombinant E monomer and stabilized recombinant E dimer using the antibodies A9E, G9E, and C10.

FIGS. 15A-15B show *in vivo* ZIKV and DENV2 infection experiments. **FIG. 15A** shows weight loss in mice permissive to ZIKV infection following serum transfer from mice that were immunized with monomer or dimer and then challenged with ZIKV. **FIG. 15B** shows DENV2 IgG levels (left) and neutralizing antibody levels (right) in DENV2-challenged mice immunized with recombinant E monomer ("rEM"), stabilized recombinant E dimer ("rED"), plus or minus alum adjuvant.

FIGS. 16A-16C show an overview and EM results of production of VLPs. **FIG. 16A** shows a schematic of WT or stabilized E proteins that were expressed with and without pr. Cleavage sites are marked with arrows, wherein the top SS:pr and M:E arrows, and bottom SS:M and M:E arrows represent cellular signalase sites; top middle arrow (pr:M) represents a furin site. Both constructs contain a signal sequence from human serum albumin (SS), the M protein, and replace the c-terminal transmembrane region of the DENV E protein with that from Japanese encephalitis (JEV-TM). **FIG. 16B** shows a table of expression yields measured with dot blot analysis and the E protein antibody 1M7. **FIG. 16C** shows EM images from our first VLP production trial; particles incorporating the stabilized recombinant E protein, U6-I8-PM4, expressed without the pr domain (bottom) compared to commercially prepared VLPs expressed with pr (top).

FIGS. 17A-17B show sequence alignments between the E glycoprotein sequences of wildtype strains of (**FIG. 17A**) DENV2 (SEQ ID NO:182), DENV1 (SEQ ID NO: 183), DENV3 (SEQ ID NO:184), DENV4 (SEQ ID NO:185), and ZIKV (SEQ ID NO:186); and (**FIG. 17B**) DENV2 (SEQ ID NO:182), YFV (SEQ ID NO:187), JEV (SEQ ID NO:188), WNV (SEQ ID NO:189), TBEV (SEQ ID NO:190), Usutu virus (SEQ ID NO:191), and Powassan virus (SEQ ID NO:192).

DETAILED DESCRIPTION OF THE INVENTION

The present invention will now be described more fully hereinafter with reference to the accompanying drawings and specification, in which preferred embodiments of the invention are shown. This invention may, however, be embodied in different forms and should not be construed as limited to the embodiments set forth herein.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. The terminology used in the description of the invention herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention.

All publications, patent applications, patents and other references cited herein are incorporated by reference in their entireties for the teachings relevant to the sentence and/or paragraph in which the reference is presented.

As used herein, "a," "an" or "the" can mean one or more than one. For example, "a" cell can mean a single cell or a multiplicity of cells.

Also as used herein, "and/or" refers to and encompasses any and all possible combinations of one or more of the associated listed items, as well as the lack of combinations when interpreted in the alternative ("or").

The term "about," as used herein when referring to a measurable value such as an amount of dose (e.g., an amount of a non-viral vector) and the like, is meant to encompass variations of $\pm 20\%$, $\pm 10\%$, $\pm 5\%$, $\pm 1\%$, $\pm 0.5\%$, or even $\pm 0.1\%$ of the specified amount.

As used herein, the transitional phrase "consisting essentially of" (and grammatical variants) means that the scope of a claim is to be interpreted to encompass the specified materials or steps recited in the claim, "and those that do not materially affect the basic and novel characteristic(s)" of the claimed invention. Thus, the term "consisting essentially of" when used in a claim of this invention is not intended to be interpreted to be equivalent to "comprising."

As used herein, the term "nucleic acid" encompasses both RNA and DNA, including cDNA, genomic DNA, synthetic (e.g., chemically synthesized) DNA and chimeras of RNA and DNA. The nucleic acid may be double-stranded or single-stranded. The nucleic acid may be synthesized using nucleotide analogs or derivatives (e.g., inosine or phosphorothioate nucleotides). Such nucleotides can be used, for example, to prepare nucleic acids that have altered base-pairing abilities or increased resistance to nucleases.

As used herein, the term "polypeptide" encompasses both peptides and proteins (including fusion proteins), unless indicated otherwise.

In embodiments of the invention, an "immunogenically active fragment" of a flavivirus polypeptide (e.g., the E protein) comprises, consists essentially of or consists of at least about 6, 8, 10, 12, 15, 20, 30, 50, 75, 100, 125, 150, 200, 250, 300, 350, 400, 450 or more amino acids, optionally contiguous amino acids, and/or less than about 495, 475, 450, 425, 400, 350, 300, 250, 200, 150, 100, 75 or 50 amino acids, optionally contiguous amino acids, including any combination of the foregoing as long as the lower limit is less than the upper limit, and the "immunogenically active fragment" induces an immune response (e.g., IgG and/or IgA that react with the native antigen), optionally a protective immune response, against dengue virus in a host and induces the production of antibodies that specifically bind to the quaternary dengue virus epitope newly identified by the inventors.

The term "epitope" as used herein means a specific amino acid sequence that, when present in the proper conformation, provides a reactive site for an antibody (e.g., B cell epitope) or T cell receptor (e.g., T cell epitope).

Portions of a given polypeptide that include a B-cell epitope can be identified using any number of epitope mapping techniques that are known in the art. (See, e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, Glenn E. Morris, Ed., 1996, Humana Press, Totowa, N.J.). For example, linear epitopes can be determined by, e.g.,
5 concurrently synthesizing large numbers of peptides on solid supports, the peptides corresponding to portions of the protein molecule, and reacting the peptides with antibodies while the peptides are still attached to the supports. Such techniques are known in the art and described in, e.g., U.S. Pat. No. 4,708,871; Geysen et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:3998-4002; Geysen et al. (1986) *Molec. Immunol.* 23:709-715.

10 Similarly, conformational epitopes can be readily identified by determining spatial conformation of amino acids such as by, e.g., x-ray crystallography and 2-dimensional nuclear magnetic resonance. Antigenic regions of proteins can also be identified using standard antigenicity and hydrophathy plots, such as those calculated using, e.g., the Omega version 1.0 software program available from the Oxford Molecular Group. This computer
15 program employs the Hopp/Woods method (Hopp et al. *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828) for determining antigenicity profiles and the Kyte-Doolittle technique (Kyte et al. *J. Mol. Biol.* (1982) 157:105-132) for hydrophathy plots.

Generally, T-cell epitopes that are involved in stimulating the cellular arm of a subject's immune system are short peptides of about 8-25 amino acids. A common way to
20 identify T-cell epitopes is to use overlapping synthetic peptides and analyze pools of these peptides, or the individual ones, that are recognized by T cells from animals that are immune to the antigen of interest, using, for example, an enzyme-linked immunospot assay (ELISPOT). These overlapping peptides can also be used in other assays such as the stimulation of cytokine release or secretion, or evaluated by constructing major
25 histocompatibility (MHC) tetramers containing the peptide. Such immunogenically active fragments can also be identified based on their ability to stimulate lymphocyte proliferation in response to stimulation by various fragments from the antigen of interest.

A "recombinant" nucleic acid, polynucleotide or nucleotide sequence is one produced by genetic engineering techniques.

30 A "recombinant" polypeptide is produced from a recombinant nucleic acid, polypeptide or nucleotide sequence.

As used herein, an "isolated" polynucleotide (e.g., an "isolated nucleic acid" or an "isolated nucleotide sequence") means a polynucleotide at least partially separated from at least some of the other components of the naturally occurring organism or virus, for example,

the cell or viral structural components or other polypeptides or nucleic acids commonly found associated with the polynucleotide. Optionally, but not necessarily, the "isolated" polynucleotide is present at a greater concentration (i.e., is enriched) as compared with the starting material (e.g., at least about a two-fold, three-fold, four-fold, ten-fold, twenty-fold, fifty-fold, one-hundred-fold, five-hundred-fold, one thousand-fold, ten thousand-fold or greater concentration). In representative embodiments, the isolated polynucleotide is at least about 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more pure.

An "isolated" polypeptide means a polypeptide that is at least partially separated from at least some of the other components of the naturally occurring organism or virus, for example, the cell or viral structural components or other polypeptides or nucleic acids commonly found associated with the polypeptide. Optionally, but not necessarily, the "isolated" polypeptide is present at a greater concentration (i.e., is enriched) as compared with the starting material (e.g., at least about a two-fold, three-fold, four-fold, ten-fold, twenty-fold, fifty-fold, one-hundred-fold, five-hundred-fold, one thousand-fold, ten thousand-fold or greater concentration). In representative embodiments, the isolated polypeptide is at least about 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more pure.

Furthermore, an "isolated" cell is a cell that has been partially or completely separated from other components with which it is normally associated in nature. For example, an isolated cell can be a cell in culture medium and/or a cell in a pharmaceutically acceptable carrier.

The terms "immunogen" and "antigen" are used interchangeably herein and mean any compound (including polypeptides) to which a cellular and/or humoral immune response can be directed. In particular embodiments, an immunogen or antigen can induce a protective immune response against the effects of dengue virus infection.

"Effective amount" as used herein refers to an amount of a vector, nucleic acid, epitope, polypeptide, cell, particle, VLP, composition or formulation of the invention that is sufficient to produce a desired effect, which can be a therapeutic and/or beneficial effect. The effective amount will vary with the age, general condition of the subject, the severity of the condition being treated, the particular agent administered, the duration of the treatment, the nature of any concurrent treatment, the pharmaceutically acceptable carrier used, and like factors within the knowledge and expertise of those skilled in the art. As appropriate, an "effective amount" in any individual case can be determined by one of ordinary skill in the art by reference to the pertinent texts and literature and/or by using routine experimentation.

The term "immunogenic amount" or "effective immunizing dose," as used herein, unless otherwise indicated, means an amount or dose sufficient to induce an immune response (which can optionally be a protective response) in the treated subject that is greater than the inherent immunity of non-immunized subjects. An immunogenic amount or effective immunizing dose in any particular context can be routinely determined using methods known in the art.

The terms "vaccine," "vaccination" and "immunization" are well-understood in the art, and are used interchangeably herein. For example, the terms vaccine, vaccination or immunization can be understood to be a process or composition that increases a subject's immune reaction to an immunogen (e.g., by providing an active immune response), and therefore its ability to resist, overcome and/or recover from infection (i.e., a protective immune response).

By the terms "treat," "treating" or "treatment of" (and grammatical variations thereof) it is meant that the severity of the subject's condition is reduced, at least partially improved or ameliorated and/or that some alleviation, mitigation or decrease in at least one clinical symptom is achieved and/or there is a delay in the progression of the disease or disorder. In representative embodiments, the terms "treat," "treating" or "treatment of" (and grammatical variations thereof) refer to a reduction in the severity of viremia and/or a delay in the progression of viremia, with or without other signs of clinical disease.

A "treatment effective" amount as used herein is an amount that is sufficient to treat (as defined herein) the subject. Those skilled in the art will appreciate that the therapeutic effects need not be complete or curative, as long as some benefit is provided to the subject.

The term "prevent," "preventing" or "prevention of" (and grammatical variations thereof) refer to prevention and/or delay of the onset and/or progression of a disease, disorder and/or a clinical symptom(s) in a subject and/or a reduction in the severity of the onset and/or progression of the disease, disorder and/or clinical symptom(s) relative to what would occur in the absence of the methods of the invention. In representative embodiments, the terms "prevent," "preventing" or "prevention of" (and grammatical variations thereof) refer to prevention and/or delay of the onset and/or progression of viremia in the subject, with or without other signs of clinical disease. The prevention can be complete, e.g., the total absence of the disease, disorder and/or clinical symptom(s). The prevention can also be partial, such that the occurrence of the disease, disorder and/or clinical symptom(s) in the subject and/or the severity of onset and/or the progression is less than what would occur in the absence of the present invention.

A "prevention effective" amount as used herein is an amount that is sufficient to prevent (as defined herein) the disease, disorder and/or clinical symptom in the subject. Those skilled in the art will appreciate that the level of prevention need not be complete, as long as some benefit is provided to the subject.

5 The efficacy of treating and/or preventing dengue virus infection by the methods of the present invention can be determined by detecting a clinical improvement as indicated by a change in the subject's symptoms and/or clinical parameters (e.g., viremia), as would be well known to one of skill in the art.

10 Unless indicated otherwise, the terms "protect," "protecting," "protection" and "protective" (and grammatical variations thereof) encompass both methods of preventing and treating dengue virus infection in a subject, whether against one or multiple strains, genotypes or serotypes of dengue virus.

15 The terms "protective" immune response or "protective" immunity as used herein indicates that the immune response confers some benefit to the subject in that it prevents or reduces the incidence and/or severity and/or duration of disease or any other manifestation of infection. For example, in representative embodiments, a protective immune response or protective immunity results in reduced viremia, whether or not accompanied by clinical disease. Alternatively, a protective immune response or protective immunity may be useful in the therapeutic treatment of existing disease.

20 An "active immune response" or "active immunity" is characterized by "participation of host tissues and cells after an encounter with the immunogen. It involves differentiation and proliferation of immunocompetent cells in lymphoreticular tissues, which lead to synthesis of antibody or the development of cell-mediated reactivity, or both." Herbert B. Herscovitz, *Immunophysiology: Cell Function and Cellular Interactions in Antibody Formation*, in IMMUNOLOGY: BASIC PROCESSES 117 (Joseph A. Bellanti ed., 1985).
25 Alternatively stated, an active immune response is mounted by the host after exposure to immunogens by infection or by vaccination. Active immunity can be contrasted with passive immunity, which is acquired through the "transfer of preformed substances (antibody, transfer factor, thymic graft, interleukin-2) from an actively immunized host to a non-immune host." *Id.*
30

A "subject" of the invention includes any animal susceptible to dengue virus infection. Such a subject is generally a mammalian subject (e.g., a laboratory animal such as a rat, mouse, guinea pig, rabbit, primates, etc.), a farm or commercial animal (e.g., a cow, horse, goat, donkey, sheep, etc.), or a domestic animal (e.g., cat, dog, ferret, etc.). In particular

embodiments, the subject is a primate subject, a non-human primate subject (e.g., a chimpanzee, baboon, monkey, gorilla, etc.) or a human. Subjects of the invention can be a subject known or believed to be at risk of infection by a flavivirus (e.g., dengue virus and/or Zika virus). Alternatively, a subject according to the invention can also include a subject not previously known or suspected to be infected by a flavivirus or in need of treatment for flavivirus infection.

Subjects may be treated for any purpose, such as for eliciting a protective immune response or for eliciting the production of antibodies in that subject, which antibodies can be collected and used for other purposes such as research or diagnostic purposes or for administering to other subjects to produce passive immunity therein, etc.

Subjects include males and/or females of any age, including neonates, juvenile, mature and geriatric subjects. With respect to human subjects, in representative embodiments, the subject can be an infant (e.g., less than about 12 months, 10 months, 9 months, 8 months, 7 months, 6 months, or younger), a toddler (e.g., at least about 12, 18 or 24 months and/or less than about 36, 30 or 24 months), or a child (e.g., at least about 1, 2, 3, 4 or 5 years of age and/or less than about 14, 12, 10, 8, 7, 6, 5, or 4 years of age). In embodiments of the invention, the subject is a human subject that is from about 0 to 3, 4, 5, 6, 9, 12, 15, 18, 24, 30, 36, 48 or 60 months of age, from about 3 to 6, 9, 12, 15, 18, 24, 30, 36, 48 or 60 months of age, from about 6 to 9, 12, 15, 18, 24, 30, 36, 48 or 60 months of age, from about 9 to 12, 15, 18, 24, 30, 36, 48 or 60 months of age, from about 12 to 18, 24, 36, 48 or 60 months of age, from about 18 to 24, 30, 36, 48 or 60 months of age, or from about 24 to 30, 36, 48 or 60 months of age.

A "subject in need" of the methods of the invention can be a subject known to be, or suspected of being, infected with, or at risk of being infected with, a flavivirus (e.g., dengue virus and/or Zika virus).

The present invention is based, in part on the unexpected discovery that particular amino acid residues can be incorporated into a flavivirus E glycoprotein to stabilize the dimer conformation at physiological, e.g., vaccine, conditions. These particular amino acid residues can be transferred into the backbone amino acid sequence of multiple flavivirus E glycoproteins to create stabilized recombinant E glycoproteins, e.g., E glycoproteins which would be stabilized as dimers in physiological conditions (e.g., vaccine conditions, e.g., in low protein concentration conditions and/or at a temperature of about 37 °C).

The enveloped DENV is an enveloped virus that contains 180 copies of the envelope (E) glycoprotein on the viral surface. The E glycoprotein is the only protein presented on the

viral surface, and is arranged in a herringbone pattern as anti-parallel homodimers that pack laterally into a lipid raft containing three dimers. The E protein monomer contains three predominantly β -sheet domains referred to as DI, DII, and DIII. These domains are connected via linker regions to form the monomer, which is connected to a transmembrane domain by an amphipathic helix stem peptide. The E protein exists in multiple conformations consistent with the different stages the virus undergoes in the infection cycle, including a pre-fusion dimer at neutral pH and a post-fusion trimer that forms as the virus enters the low pH endosome. While not wishing to be bound to theory, it is believed that this requirement that the E protein transitions between different conformational states provides selective pressure during viral evolution that favors E protein sequences that are adept at transitioning between different structures and are not overly stable in a single conformation such as the pre-fusion dimer. As used herein, the term "dimer conformation" refers to the physical structure (e.g., tertiary and/or quaternary structure) of an E glycoprotein that is capable of forming dimers (e.g., homodimers). Similarly, the term "trimer conformation" refers to the physical structure (e.g., tertiary and/or quaternary structure) of an E glycoprotein that is capable of forming trimers (e.g., homotrimers), and the term "monomer conformation" refers to the physical structure (e.g., tertiary and/or quaternary structure) of an E glycoprotein that is not capable of forming higher order multimers. The present invention provides modifications, e.g., substitutions, that may stabilize an E glycoprotein into a particular preferred conformation, such as the monomer conformation, dimer conformation, and/or trimer conformation. A soluble recombinant E protein (sE, also referred to herein as sRecE), comprising the soluble ectodomain (i.e., E glycoprotein DI, DII and DIII), can form dimers at high concentrations and under crystallization conditions. These sE dimers resemble the anti-parallel E homodimer observed on the virion surface, which presents epitopes targeted by DENV neutralizing antibodies (**FIG. 1A**). Structural studies have revealed the epitope of potentially neutralizing quaternary epitope antibodies, such as 2D22 and the E dimer epitope (EDE) antibodies, are displayed within a single sE dimer (**FIG. 1D**). Dimeric sE antigens induce higher neutralizing antibody titers, thus it was hypothesized by the inventors of the present invention that dimeric sE protein could be used as an antigen to present quaternary epitopes. For example, Zika virus and dengue virus have at least one conserved quaternary epitope, recognized by the EDE neutralizing antibody. Antibodies that bind to quaternary E glycoprotein epitopes protect against dengue virus and Zika virus infection, such as EDE (a pan DENV1-4 antibody), 5J7 (DENV3), 2D22 (DENV2), and HM14c10 (DENV1). Thus, in some embodiments, the stabilized recombinant flavivirus E glycoprotein of the present

invention may comprise at least one quaternary epitope, e.g., a quaternary epitope recognized by antibodies including but not limited to 5J7, 2D22, EDE1 C8, EDE1 C10, EDE2 A11, EDE2 B7, 3F9, 1L12, DV3-290, DV3-144, DV3-415, DV3-066, D4-126, D4-131, A9E, G9E, ZKA-230, and/or ZKA-230. Recognition of the quaternary epitope may depend on the E glycoprotein being in dimer form, e.g., a recombinant flavivirus E glycoprotein stabilized in dimer conformation, e.g., stabilized in a conformation such that the E glycoprotein forms homodimers *in vitro* and/or *in vivo* such as under physiological and/or vaccine conditions. Non-limiting examples of antibodies that recognize quaternary epitopes include but are not limited to 5J7, 2D22, EDE1 C8, EDE1 C10, EDE2 A11, EDE2 B7, 3F9, 1L12, DV3-290, DV3-144, DV3-415, DV3-066, D4-126, D4-131, A9E, G9E, ZKA-230, and/or ZKA-230.

However, the DENV2 sE protein is also sensitive to environmental stresses, such as pH and temperature, similar to the native E protein. In addition, the DENV2 sE protein dimer has a homodimer K_d of 12 μM at 37°C, which is too weak to be relevant under vaccination conditions and limits its current use as a vaccine antigen by reducing the presentation of critical quaternary epitopes. Recombinant soluble E glycoprotein dimer stability is concentration and temperature dependent, wherein at physiological temperatures (e.g., 37°C), sE is predominantly monomeric. The monomer has limited presentation of broadly neutralizing epitopes (e.g., quaternary epitopes) that are important for effective immune responses. Unfolding of the sE monomer protein may start as low as about 43 °C (about 37°C for ZIKV). Dimer formation may occur at high concentration of protein, and/or at low temperature (e.g., about 23°C). Therefore, in order to use sE as a vaccine antigen, it may be beneficial to stabilize both the dimer and monomer conformation. Stabilized monomers may be useful, e.g., in the application of diagnostics, wherein the stabilized monomer may be used as control and/or depleting less broadly-neutralizing antibodies (e.g., antibodies binding non-quaternary epitopes).

Thus, in one embodiment, the present invention provides a stabilized recombinant flavivirus E glycoprotein, comprising a flavivirus E glycoprotein backbone; and one or more (e.g., one or more, two or more, three or more, four or more, etc., e.g., at least one, at least two, at least three, at least four, or more) amino acid substitution(s) selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any

combination thereof (e.g., amino acid substitutions shown in **Table 1** and/or **Table 2**), wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**.

In some embodiments, the present invention provides a stabilized recombinant flavivirus E glycoprotein, comprising a flavivirus E glycoprotein backbone; and one or more (e.g., one or more, two or more, three or more, four or more, etc., e.g., at least one, at least two, at least three, at least four, or more) amino acid substitution(s) in the flavivirus E glycoprotein backbone DI/DII hinge region, α B helix central interface, and/or fusion loop (FL) dimer interface. In some embodiments, the present invention provides a stabilized recombinant flavivirus E glycoprotein, comprising a flavivirus E glycoprotein backbone; and one or more (e.g., one or more, two or more, three or more, four or more, etc., e.g., at least one, at least two, at least three, at least four, or more) amino acid substitution(s) in the flavivirus E glycoprotein backbone DI/DII hinge region, e.g., outside of the dimer interface. Non-limiting examples of amino acid substitutions in the E glycoprotein DI/DII hinge region, e.g., outside of the E glycoprotein dimer interface, include 279W and 280P.

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone from a dengue virus (DENV, Zika virus (ZIKV), yellow fever virus (YFV), Japanese encephalitis virus (JEV), West Nile virus (WNV), tick-borne Encephalitis virus (TBEV), Powassan virus, or any combination thereof.

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a dengue virus (DENV), e.g., dengue virus serotype 1 (DENV1), dengue virus serotype 2 (DENV2), dengue virus serotype 3 (DENV3), and/or dengue virus serotype 4 (DENV4). A DENV backbone may comprise the amino acid sequence of any DENV genotype and/or strain and/or isolate currently known or as yet identified and/or isolated. Non-limiting examples of DENV1 genotypes, strains, and/or isolates include Genotypes I, II, III, IV, and V, and strains Western Pacific 1974 (SEQ ID NO:183). Non-limiting examples of DENV2 genotypes, strains, and/or isolates include DENV2 strain 16681 (SEQ ID NO:182). Non-limiting examples of DENV3 genotypes, strains, and/or isolates include Genotype I, II, III, IV, and strains such as Sri Lanka 1989, Indonesia 1982, Thailand 1995, Cuba 2002, and Puerto Rico 1977, and DENV3 strain CH53489 (SEQ ID NO:184). Non-limiting examples of DENV4 genotypes, strains, and/or isolates include DENV4 strain TVP-376 (SEQ ID NO:185). In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a chimeric virus, e.g., a chimeric dengue virus E glycoprotein such as, but not

limited to, DENV1/2, DENV 1/3, DENV 1/4, DENV 2/1, DENV 2/3, DENV 2/4, DENV 3/1, DENV 3/2, DENV 3/4, DENV 4/1, DENV 4/2, DENV 4/3.

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a Zika virus (ZIKV), e.g., ZIKV strain PF13/251013-18 (SEQ ID NO:186).

5 In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a Yellow Fever virus (YFV), e.g., YFV strain 17D (SEQ ID NO:187).

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a Japanese Encephalitis virus (JEV), e.g., JEV strain SA14-14-2 (SEQ ID NO:188).

10 In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a West Nile virus (WNV), e.g., WNV strain NY99 (SEQ ID NO:189).

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a Tick-borne Encephalitis virus (TBEV), e.g., TBEV strain Moscow B-4 (SEQ ID NO:190).

15 In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of an Usutu virus, e.g., Usutu virus strain MB119/06 (SEQ ID NO:191).

In some embodiments, the flavivirus E glycoprotein backbone comprises a backbone of a Powassan virus, e.g., Powassan virus Lineage I (SEQ ID NO:192).

20 In some embodiments, the E glycoprotein backbone comprises a full-length E glycoprotein. In some embodiments, the E glycoprotein backbone comprises a soluble ectodomain formed from E glycoprotein domains DI, DII, and DIII, e.g., soluble recombinant E protein ("sE," also referred to herein as "sRecE").

25 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise one or more (e.g., one or more, two or more, three or more, four or more, etc., e.g., at least one, at least two, at least three, at least four, or more) of the substitutions as shown in the tables of **Table 1** and/or **Table 2**, in any combination, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of dengue virus serotype 2 (DENV2) identified as SEQ ID NO:6.

30 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: R2M and E44M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MMCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFMLIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 5 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat2"; SEQ ID NO:10)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the
 10 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H27P and T48I.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise, consist essentially of, or consist of the amino acid sequence:

15 SMRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCI
 EAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKK
 NMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMEC
 SPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKK
 QDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVV
 KEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 20 PFGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat3; SEQ ID NO:12)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the
 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 25 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: R2M, E44L, D154L, and
 K246Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise, consist essentially of, or consist of the amino acid sequence:

30 SMMCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFLLIKTEAKQPATLRKYCI
 EAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKK
 NMEGKVVPENLEYTIVITPHSGEEHAVGNLTGKHGKEIKITPQSSITEAELTGYGTVTMEC
 SPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAIAK
 QDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVV
 KEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 35 PFGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat4"; SEQ ID NO:14)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the

numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: K204F and H261L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENFAWLVRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
10 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat8"; SEQ ID NO:22)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

15 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A259V and T262H.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

20 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGVMHHAALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc1"; SEQ ID NO:24)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
30 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A259W and T262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

35 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRAALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
40 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc2"; SEQ ID NO:26)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A259W, T262Y, and A263L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc3"; SEQ ID NO:28)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T262R and A263W .

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHRWLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc5"; SEQ ID NO:32)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: N8L, S29Y, and H244F.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSLRDFVEGVSGGSWVDIVLEHGYCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPFACKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc6"; SEQ ID NO:34)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T262R.

5 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

10 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHRALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc7"; SEQ ID NO:36)

15 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D.

20 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

25 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc8"; SEQ ID NO:38)

30 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: M6L and Q316M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGLSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPADTQGSNWIQKETLVTFKNPHAKKQ
 5 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETMHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM1"; SEQ ID NO:44)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the
 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: Q131I and Y299L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVIPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPADTQGSNWIQKETLVTFKNPHAKKQ
 15 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSLSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
 20 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM2"; SEQ ID NO:46)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the
 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A35M and M289W.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMMKNKPTLDFELIKTEAKQPATLRKYCIE
 30 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRWDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
 35 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM3"; SEQ ID NO:48)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the
 present invention may comprise the following amino acid substitutions wherein the
 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM4"; SEQ ID NO:50)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
20 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM4.1"; SEQ ID NO:52)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T33V and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
35 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM4.2"; SEQ ID:54)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 5 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 10 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM4.3"; SEQ ID NO:56)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H209D and G266W.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGSQEGAMHTALTWATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM5"; SEQ ID NO:58)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: V15E, F373D, and F392R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGESGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
 35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
 40 DGDSYIIIGVEPGQLKLNWRKK ("DENV2 SHP1"; SEQ ID NO:66)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, and M34L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
10 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk4"; SEQ ID NO:76)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
15 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

20 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVYEKDSPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk5"; SEQ ID NO:78)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: F279W and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk6"; SEQ ID NO:80)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
20 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk6.1"; SEQ ID NO:82)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: T48I and L277M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
35 DVVVLGSQEGAMHTALTGATEIQMSSGNMFLTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk7"; SEQ ID NO:84)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble

recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: Q256Y, G258A, A259W, and M260L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
10 DVVVLGSYEAWLHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk8"; SEQ ID NO:86)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

15 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M, G106D, A259W, and T262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

20 MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
25 DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.1 (I2-I8-P4)"; SEQ ID NO:92)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

30 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H27P, S29K, T33V, A35M, T48I, G106D, A259W, and T262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGKCVTVMMKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
10 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.2 (I2-I8-P4-H3)"; SEQ ID NO:94)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
15 G106D, H209D, A259W, T262R, G266W, F279W, F280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVYEKDSPPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.3 (I2-I8-U4-U5-U6-P5)"; SEQ ID NO:96)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, H27P,
30 S29K, T33V, M34L, A35M, T48I, A259W, T262R, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEPGKCVTVLMKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEP
10 FGDSYIIIGVEPGQLKLNWFKK

("DENV2 SC.4 (I2-I8-U4-U5-U6-P4-H3)"; SEQ ID NO:98")

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
15 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, M34L, G106D, A259W, T262R, F279W, T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
20 AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.5 (I2-I8-U4-U6)"; SEQ ID NO:100)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
30 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M, G106D, A259W, T262R, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMKKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.6 (I2-I8-U5-P4)"; SEQ ID NO:102)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D, A259W, T262R,
15 F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.7 (I2-I8-U5-U6)"; SEQ ID NO:104)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
30 G106D, A259W, T262R, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMKKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.8 (I2-I8-U5-U6-P4)"; SEQ ID NO:106)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: V15E, S29K, T33V,

5 A35M, G106D, A259W, T262R, F279W, T280P, T359Y, F373D, and F392R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

10 MRCIGMSNRDFVEGESGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRITVNPPIVYEKDSPVNIEAEP
15 DGDSYIIIGVEPGQLKLNWRKK ("DENV2 SC.9 (I2-I8-U5-U6-P4-S1)"; SEQ ID NO:108)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D, A259W, T262R,

20 F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

25 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRITVNPPIVTEKDSPVNIEAEP
30 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.10 (I2-I8-U6)"; SEQ ID NO:110)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H27P, T48I, G106D,

35 A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.11 (I2-I8-U6-H3)"; SEQ ID NO:112)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
15 G106D, A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.12 (I2-I8-U6-P4)"; SEQ ID NO:114)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
30 A259W, T262R, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVYEKDSPPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.13 (I2-U5-U6-P4)"; SEQ ID NO:116)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.14 (I2-U6)"; SEQ ID NO:118)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.15 (I8-U6)"; SEQ ID NO:120)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H27P, T48I, A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.16 (I2-U6-H3)"; SEQ ID NO:122)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
15 A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.17 (I2-U6-P4)"; SEQ ID NO:124)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, S29K,
30 T33V, M34L, A35M, G106D, A259W, T262R, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.18 (I2-I8-U4-U6-P4)"; SEQ ID NO:126)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M, G106D, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNP I VYEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.19 (I8-U5-U6-P4)"; SEQ ID NO:128)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, S29K, T33V, M34L, and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.20 (P4-U4)"; SEQ ID NO:130)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, M34L, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.21 (U4-U5-U6)"; SEQ ID NO:132)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: E13F, G14A, M34L,
15 H209D, G266W, F279W, T280P, and T359Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.22 (U4-U5-U6-P5)"; SEQ ID NO:134)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D, A259W, and
30 T262R .

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRLALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.23 (I2-I8)"; SEQ ID NO:136)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: H27P, T48I, and G258E.

5 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

10 MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.24 (M2-H3)"; SEQ ID NO:138)

15 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M, and G258E.

20 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

25 MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVM MNKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.25 (M2-P4)"; SEQ ID NO:140)

30 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G106D, A259V, T262R, A263W, F279W, and T280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
10 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.26 (I3-I8-U6)"; SEQ ID NO:142)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
15 G106D, A259V, T262R, A263W, F279W, and T280P .

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.27 (I3-I8-U6-P4)"; SEQ ID NO:144)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S29K, T33V, A35M,
30 L107C, and A313C.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGCFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EICETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 SC.28 (P4-Cm2)"; SEQ ID NO:146)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: R9V, T32V, H144Y, and
15 E368I.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNVDFVEGVSGGSWVDIVLEHGSCVVTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
20 MEGKVVQPENLEYTIVITPYSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNI IAEPP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat1"; SEQ ID NO:8)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: R2M, H27P, E44M, T48I,
30 D154M, H244Q, and K246Y.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MMCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFMLIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
35 MEGKVVQPENLEYTIVITPHSGEEHAVGNMTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPQAYKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat5"; SEQ ID NO:16)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: K204F, W206F, and

H261L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMFNFAFLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat6"; SEQ ID NO:18)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: K204F, W251F, and

H261F.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMFNFAFLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVFVLGSQEGAMFTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 HCat7"; SEQ ID NO:20)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: A259W, T262Y, and

A263L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
5 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHYLLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
10 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 IntFc4"; SEQ ID NO:30)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: D375L and N390Q.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
20 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
FGLSYIIIGVEPGQLKLQWFKK ("DENV2 PM6"; SEQ ID NO:60)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G330A.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
35 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDASPCIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 PM7"; SEQ ID NO:62)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: Y377V and K393R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
10 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
FGDSVIIIGVEPGQLKLNWFRK ("DENV2 PM8"; SEQ ID NO:64)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the

15 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: I270V and T280A.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

20 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEVQMSSGNLLFAGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
25 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk1"; SEQ ID NO:70)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
30 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: L198W.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

35 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVWLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPPIVTEKDSPVNIEAEP
40 FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk2"; SEQ ID NO:72)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: L191Y and H209D.

5 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
10 PRTGYDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("DENV2 UndPk3"; SEQ ID NO:74)

15 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: V15E, W20H, F373D, and F392R.

20 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGESGGSHVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
25 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
DGDSYIIIGVEPGQLKLNWRKK ("DENV2 SHP2"; SEQ ID NO:68)

30 In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV1 identified as SEQ ID NO:147: S29K, T33V, and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGIGNRDFVEGLSGATWVDVVLEHGKCVTVMMKDKPTLDIELLKTEVTNPAV
 LRKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGS
 5 LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPT
 SEIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAST
 SQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGH
 LKRLKMDKLTLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFS
 SQDEKGVTONGRRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 10 ("DENV1 PM4"; SEQ ID NO:148)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV1 identified as SEQ ID NO:147: A259W and S262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
 RKLCEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGS
 20 LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
 EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTS
 QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGWMHRLALTGATEIQTSGTTTIFAGHL
 KRLKMDKLTLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
 QDEKGVTONGRRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 25 ("DENV1 IntFc2"; SEQ ID NO:149)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV1 identified as SEQ ID NO:147: G106D.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
 RKLCEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCDLFGKGS
 35 LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
 EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTS
 QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGHL
 KRLKMDKLTLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
 QDEKGVTONGRRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 40 ("DENV1 IntFc8"; SEQ ID NO:150)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV1 identified as SEQ ID NO:147: F279W and A280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVIGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
 RKLCEIAKISNTTDSRCPTQGEATLVEEQDTNFCRRTFVDRGWGNGCGLFGKGS
 LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
 EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKS
 WLVHKQWFLDLPLPWTSGASTS
 QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTS
 GTTTIWPGHL
 KCRLKMDKLT
 LKGM
 SYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
 QDEKGV
 TQNGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 ("DENV1 UndPk6"; SEQ ID NO:151)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G29K, T33V, and

A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
 TLRKLCIEGKITNITDSRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
 SLVTCAKFQCLESIEGKV
 VQHENLK
 YTVIITVHTGDQHQVGNETQGVTA
 EITPQASTV
 EAILPEYGT
 LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHL
 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHG
 TILIKVEYKGEDAPCKIPFSTE
 DGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 ("DENV3 PM4"; SEQ ID NO:153)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: A257W and T260R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 5 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
 DGQGKAHNRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 10 ("DENV3 IntFc2"; SEQ ID NO:154)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G106D.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
 20 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHL
 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
 DGQGKAHNRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 25 ("DENV3 IntFc8"; SEQ ID NO:155)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: F277W and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 35 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGLH
 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
 DGQGKAHNRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 40 ("DENV3 UndPk6"; SEQ ID NO:156)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: F277W, A278P, S275L, and M205L.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWLVHRQWFFDLPLPWTSGATTET
 PTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTLIWPGLHK
 CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFSTED
 GQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 ("DENV3 UndPk6 DV2HIngemut"; SEQ ID NO:157)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G106D, A257W, T260R, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
 LK CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFST
 EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 ("DENV3 SC.10 (I2-I8-U6)"; SEQ ID NO:158)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: A257W, T260R, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 5 LVTCAKFQCLESIEGKVVQHENLK YTVIITVHTGDQH QVGNETQGVTA EITPQASTV
 EAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMH RALTGATEIQNSGGTSIWPGH
 LKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
 EDGQGKAHN GRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 10 ("DENV3 SC.14 (I2-U6)"; SEQ ID NO:159)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 20 LVTCAKFQCLESIEGKVVQHENLK YTVIITVHTGDQH QVGNETQGVTA EITPQASTV
 EAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFPGHL
 KCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
 DGQGKAHN GRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 25 ("DENV3 UndPk6.1 (A278P)"; SEQ ID NO:160)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: H27P and T48I.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTTMAKNKPTLDIELQKIEATQLATL
 RKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 35 VTCAKFQCLESIEGKVVQHENLK YTVIITVHTGDQH QVGNETQGVTA EITPQASTVE
 AILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
 TWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHLKC
 RLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTEDG
 QGKAHN GRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 40 ("DENV3 HCat3"; SEQ ID NO:161)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G29K, T33V, A35M, G106D, A257W, T260R, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
LKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
("DENV3 SC.12 (I2-I8-U6-P4)"; SEQ ID NO:162)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G29K, T33V, A35M, G106D, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
DGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
("DENV3 SC.29 (I8-U6-P4)"; SEQ ID NO:163)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: H27P, T48I, A257W, T260R, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTTMAKNKPTLDIELQKIEATQLATL
 RKLCIEGKITNITD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
 VTCAKFQCLESIEGKVQHENLKYTVIITVHTGDQHQVGNETQGVTAEITPQASTVE
 AILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
 TWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGHLK
 CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTED
 10 GQGAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 ("DENV3 SC.16 (I2-U6-H3)"; SEQ ID NO:164)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: H27P, T48I, G106D, A257W, T260R, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 20 MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTTMAKNKPTLDIELQKIEATQLATL
 RKLCIEGKITNITD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
 VTCAKFQCLESIEGKVQHENLKYTVIITVHTGDQHQVGNETQGVTAEITPQASTVE
 AILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
 TWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGHLK
 CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTED
 25 GQGAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 ("DENV3 SC.11 (I2-I8-U6-H3)"; SEQ ID NO:165)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the
 30 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G106D, F277W, and A278P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

5 MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWNGCDLFGKGS
 LVTCAKFQCLESIEGKVVQHENLK YTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGHL
 10 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
 DGQGKAHNGLRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 ("DENV3 SC.15 (I8-U6)"; SEQ ID NO:166)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G106D, A257W, and T260R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

20 MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
 LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWNGCDLFGKGS
 LVTCAKFQCLESIEGKVVQHENLK YTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
 25 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
 DGQGKAHNGLRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 ("DENV3 SC.23 (I2-I8)"; SEQ ID NO:167)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the
 30 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV3 identified as SEQ ID NO:152: G29K, T33V, A35M, G106D, A257W, and T260R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCIEGKITNITTSRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
5 SLVTCAKFQCLESIEGKVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
KCRCLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
10 DGQGKAHNRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
("DENV3 SC.1 (I2-I8-P4)"; SEQ ID NO:168)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
15 recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: G29K, T33V, and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
20 MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVA
LLRTYCIASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
25 CKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
RK ("DENV4 PM4"; SEQ ID NO:170)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the
30 numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: A259W and S262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
35 MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCIASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRALAGATEVDSGDGN
HMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGA
40 PCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHW
FRK ("DENV4 IntFc2"; SEQ ID NO:171)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: G106D.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVAL
LLRTYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVVDRGWGNGCDLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
CKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
RK ("DENV4 IntFc8"; SEQ ID NO:172)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: F279W and A280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVAL
LLRTYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MWPAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAG
APCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLH
WFRK ("DENV4 UndPk6"; SEQ ID NO:173)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: G29K, T33V, A35M, G106D, A259W, S262R, F279W, and A280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMQKPTLDFELTKTTAKEVA
 LLRTYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVVDRGWGNGCDLFGKG
 5 GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
 SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
 ADTSEVHWNKYKERMVTFKVPHAKRQDVTVLGSQEGWMHRALAGATEVDSGDGN
 HMWPAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGA
 GAPCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTL
 10 HWFRK ("DENV4 SC.12 (I2-I8-U6-P4)"; SEQ ID NO:174)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: A280P.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
 LLRTYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
 20 GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
 SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
 ADTSEVHWNKYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
 MFPGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
 CKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
 25 RK ("DENV4 UndPk6.1 (A280P)"; SEQ ID NO:175)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: H27P and T48I.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCVGVGNRDFVEGVSGGAWVDLVLEPGGCVTTMAQGKPTLDFELTKITAKEVAL
 LR TYCIEASISNITTATRCPTQGEPLYLKEEQDQQYICRRDVVDRGWGNGCGLFGKGG
 35 VVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPRSP
 SVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAGA
 DTSEVHWNKYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHM
 FAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAPC
 KVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFR
 40 K ("DENV4 HCat3"; SEQ ID NO:176)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV4 identified as SEQ ID NO:169: G29K, T33V, A35M,

5 G106D, A257W, and S262R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVAL
 LLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCDLFGKG
 10 GVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITPR
 SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
 ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRALAGATEVDSGDGN
 HMFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGA
 PCKVPIERDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHW
 15 FRK ("DENV4 SC.1 (I2-I8-P4)"; SEQ ID NO:177)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 20 recombinant glycoprotein) of ZIKV identified as SEQ ID NO:178: S29K, V33, and A35M.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

IRCIGVSNRDFVEGMSGGTWVDIVLEHGKCVTVMMQDKPTVDIELVTTTVSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDRLGWGNGCGLFGKGS
 25 LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHEVDENRAKVEI
 TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPW
 HAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDG
 AKGRLSSGHLKCRLLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGT
 DGPCCKVPAQMAVDMQTLTPVGRLLITANPVITESTENSKMMLELDPPFGDSYIVIGVG
 30 EKKITHHWHRSG ("ZIKV PM4"; SEQ ID NO:179)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 35 recombinant glycoprotein) of ZIKV identified as SEQ ID NO:178: A264W and T267R.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

IRCIGVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCGLFGKGS
 5 LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEI
 TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPW
 HAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGWVHRALAGALEAEMD
 GAKGRLSSGHLKCRLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAG
 TDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVIGV
 10 GEKKITHHWHRSG ("ZIKV IntFc2"; SEQ ID NO:180)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 15 recombinant glycoprotein) of ZIKV identified as SEQ ID NO:178: G106D.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 IRCIGVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCDLFGKGS
 20 LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEI
 TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPW
 HAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDG
 AKGRLSSGHLKCRLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGT
 DGPKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVIGVG
 25 EKKITHHWHRSG ("ZIKV IntFc8"; SEQ ID NO:181)

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble
 30 recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: S255E.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:
 MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
 35 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTG YGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGEQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
 FGDSYIIIGVEPGQLKLNWFKK ("Mnmer1"; SEQ ID NO:40)

40

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise the following amino acid substitutions wherein the numbering is based on the reference amino acid sequence of an E glycoprotein (e.g., a soluble recombinant glycoprotein) of DENV2 identified as SEQ ID NO:6: G258E.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention may comprise, consist essentially of, or consist of the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTVIRVQYEGDGSCKIPFEIMDLKRHVLGRLITVNPITVEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK ("Mnmer2"; SEQ ID NO:42)

Additional stabilized recombinant flavivirus E glycoprotein variants may include a stabilized recombinant flavivirus E glycoprotein comprising any of the amino acid substitutions as described in **Tables 1** and **2**. The present invention provides additional non limiting examples of stabilized recombinant flavivirus E glycoprotein of this invention that can be used in the compositions and methods described herein in the SEQUENCES section provided herein. Thus, further stabilized recombinant flavivirus E glycoprotein variants may also include any stabilized recombinant flavivirus E glycoprotein comprising, consisting essentially of, or consisting of any of the amino acid sequences and/or any stabilized recombinant flavivirus E glycoprotein encoded by any of the nucleic acid sequences described herein in the SEQUENCES section provided herein.

Additional stabilized recombinant flavivirus E glycoprotein variants can be made by introducing one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, etc.) substituted amino acid residues in the E glycoprotein domain sequence at any position and in any combination. Variants of this invention can also be made by insertion of amino acid residues and/or deletion of amino acid residues, with or without substitution of original amino acids residues. Amino acid residues that can be substituted include naturally occurring amino acid residues such as those shown in **Table 3**, as well as any modified amino acid residues such as those shown in **Table 4**.

In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention comprises substitutions which maintain a conformation of E glycoprotein that inhibits homodimer and/or trimer formation, e.g., monomer conformation, under physiological conditions, e.g., 37°C and/or low protein concentrations, e.g., vaccine

conditions. In some embodiments, a stabilized recombinant flavivirus E glycoprotein of the present invention comprises substitutions which maintain a conformation of E glycoprotein that allows homodimer formation, e.g., dimer conformation, under physiological conditions, e.g., 37°C and/or low protein concentrations, e.g., vaccine conditions. Thus, the present invention also provides a stabilized recombinant flavivirus E glycoprotein dimer comprising two flavivirus E glycoproteins of the present invention.

In some embodiments, the dimer has a T_m^1 melting point of about 37°C or higher, as measured at a E glycoprotein concentration of above 1 micromolar (e.g., 4 micromolar, 8 micromolar), e.g., about 37°C to about 60°C, e.g., about 37, about 38, about 39, about 40, about 41, about 42, about 43, about 44, about 45, about 46, about 47, about 48, about 49, about 50, about 51, about 52, about 53, about 54, about 55, about 56, about 57, about 58, about 59, or about 60°C or higher, as measured at a E glycoprotein concentration of above 1 micromolar. For example, some embodiments, the dimer has a T_m^1 melting point of about 37°C to about 45°C, about 45°C to about 65°C, about 37.5°C to about 50.75°C, or about 37.5°C to about 60.9°C, as measured at a E glycoprotein concentration of above 1 micromolar. In some embodiments, the dimer has a T_m^1 melting point that is equal to its t_m^2 melting point, e.g., wherein the dimer does not dissociate until such temperature that it also unfolds (e.g., until such temperature that the monomeric form unfolds).

In some embodiments, a stabilized recombinant flavivirus E glycoprotein dimer of the present invention dissociates to monomer (a T_m^1 melting point) at a temperature that is higher (e.g., about 0.5 °C to about 45 °C higher, or any value or range therein) than the temperature at which a dimer of a corresponding wildtype flavivirus E glycoprotein dissociates to monomer. In some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a T_m^1 melting point that is higher than the T_m^1 melting point of a wildtype (e.g., non-stabilized) sE glycoprotein dimer. In some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a T_m^1 melting point that is about 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 or more degrees Celsius higher than the T_m^1 melting point of a wildtype sE glycoprotein (e.g., of the corresponding backbone, e.g., of a wildtype DENV1, 2, 3, or 4 sE and/or a wildtype ZIKV sE). For example, in some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a T_m^1 melting point that is about 2°C higher than the T_m^1 melting point of a wildtype ZIKV sE, about 8°C higher than the T_m^1 melting point of a wildtype ZIKV sE, about 11°C higher than the T_m^1 melting point of a wildtype ZIKV sE, about 1.5°C

higher than the T_m^1 melting point of a wildtype DENV2 sE, about 7°C higher than the T_m^1 melting point of a wildtype DENV2 sE, about 11°C higher than the T_m^1 melting point of a wildtype DENV2 sE, about 15.5°C higher than the T_m^1 melting point of a wildtype DENV2 sE, about 10°C higher than the T_m^1 melting point of a wildtype DENV2 sE, about 22°C higher than the T_m^1 melting point of a wildtype DENV2 sE, about 16°C higher than the T_m^1 melting point of a wildtype DENV3 sE, about 20°C higher than the T_m^1 melting point of a wildtype DENV3 sE, about 21.5°C higher than the T_m^1 melting point of a wildtype DENV3 sE, about 38°C higher than the T_m^1 melting point of a wildtype DENV3 sE, about 42.5°C higher than the T_m^1 melting point of a wildtype DENV3 sE, about 40°C higher than the T_m^1 melting point of a wildtype DENV4 sE, or any value or range therein, e.g., about 4 to about 11°C, about 6 to about 10°C, or about 2 to about 45°C higher than the T_m^1 melting point of a wildtype ZIKV sE, e.g., about 2 to about 20°C, about 4 to about 25°C, or about 6 to about 18.5°C higher than the T_m^1 melting point of a wildtype DENV2 sE, e.g., about 2 to about 45°C, about 4 to about 25°C, or about 6 to about 18.5°C higher than the T_m^1 melting point of a wildtype DENV3 sE.

In some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a dimer affinity (K_d) of about 20 μ M or lower under physiological conditions (e.g., vaccine conditions, e.g., at human body temperature, e.g., as measured at 37°C). In some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a dimer affinity of about 18 μ M or lower, about 15 μ M or lower, about 10 μ M or lower, about 3 μ M or lower, about 1 μ M or lower, about 100 nM or lower, about 10 nM or lower, about 1 nM or lower, about 0.1 nM or lower, or any value or range therein, as measured at 37°C. For example, in some embodiments, a stabilized recombinant E glycoprotein dimer of the present invention has a dimer affinity of about 1 picomolar to about 20 μ M, about 100 picomolar to about 18 μ M, about 1 nM to about 3 μ M, or about 1 picomolar, about 10 picomolar, about 100 picomolar, about 1 nM, about 10 nM, about 100 nM, about 1 μ M, about 2 μ M, about 3 μ M, about 4 μ M, about 5 μ M, about 6 μ M, about 7 μ M, about 8 μ M, about 9 μ M, about 10 μ M, about 11 μ M, about 12 μ M, about 13 μ M, about 14 μ M, about 15 μ M, about 16 μ M, about 17 μ M, about 18 μ M, about 19 μ M, about 20 μ M, or any value or range therein.

The present invention also provides a flavivirus particle and a virus like particle (VLP) comprising the stabilized recombinant E glycoprotein of this invention. The flavivirus E glycoprotein of the invention can be present in an intact virus particle (e.g., a killed or live attenuated virus particle or a recombinant flavivirus vector (e.g., a recombinant dengue virus

vector)) or a virus-like particle (VLP), which may optionally be an intact dengue virus particle or dengue virus VLP.

Also provided is an isolated nucleic acid molecule encoding the E glycoprotein of this invention, an isolated nucleic acid molecule encoding the flavivirus particle or the VLP of this invention, a vector comprising the nucleic acid molecule of this invention and a population of flavivirus particles comprising the flavivirus particle this invention.

Further provided herein is a composition comprising the E glycoprotein of this invention in a pharmaceutically acceptable carrier, a composition comprising the E glycoprotein dimer of this invention in a pharmaceutically acceptable carrier, a composition comprising the nucleic acid molecule of this invention in a pharmaceutically acceptable carrier, a composition comprising the virus particle of this invention, a composition comprising the population of this invention in a pharmaceutically acceptable carrier and a composition comprising the VLP of this invention in a pharmaceutically acceptable carrier.

In some embodiments, a stabilized recombinant E glycoprotein or stabilized recombinant E glycoprotein dimer of the present invention may be used in combination (e.g., in scaffold(s) and/or conjugated with) other molecules such as, but not limited to, Fc fragments, Fc-fusion proteins, and/or nanoparticles. Fc molecules may be used, e.g., to increase serum half-life and/or serum immunogenicity. Nanoparticles may be used, e.g., as delivery devices.

Types of nanoparticles of this invention for use as delivery devices include, but are not limited to, polymer nanoparticles such as PLGA-based, PLA-based, polysaccharide-based (dextran, cyclodextrin, chitosan, heparin), dendrimer, hydrogel; lipid-based nanoparticles such as lipid nanoparticles, lipid hybrid nanoparticles, liposomes, micelles; inorganics-based nanoparticles such as superparamagnetic iron oxide nanoparticles, metal nanoparticles, platinum nanoparticles, calcium phosphate nanoparticles, quantum dots; carbon-based nanoparticles such as fullerenes, carbon nanotubes; and protein-based complexes with nanoscales. Types of microparticles of this invention include but are not limited to particles with sizes at micrometer scale that are polymer microparticles including but not limited to, PLGA-based, PLA-based, polysaccharide-based (dextran, cyclodextrin, chitosan, heparin), dendrimer, hydrogel; lipid-based microparticles such as lipid microparticles, micelles; inorganics-based microparticles such as superparamagnetic iron oxide microparticles, platinum microparticles and the like as are known in the art. These particles may be generated and/or have materials be absorbed, encapsulated, or chemically bound through known mechanisms in the art.

Production of the stabilized recombinant E glycoproteins of this invention can be carried out by introducing some (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, etc.) or all of the amino acid substitutions identified as stabilizing a flavivirus quaternary epitope and/or flavivirus E glycoprotein dimer conformation (e.g., such as in **Table 1** and **2**) into a flavivirus E glycoprotein backbone. Not every amino acid identified as stabilizing a flavivirus quaternary epitope and/or flavivirus E glycoprotein dimer conformation is required to be substituted to produce a stabilized recombinant protein of this invention. For example, in some embodiments further substitutions and/or omission of substitutions of about 1, 2, 3, 4 or 5 amino acids at either end of the contiguous amino acid sequences identified as stabilizing a flavivirus quaternary epitope and/or flavivirus E glycoprotein dimer conformation can be included in the production of a stabilized recombinant E glycoprotein of this invention. The number of substitutions necessary to produce the desired conformational epitope or dimer structure can be readily determined by one of ordinary skill in the art according to the teachings herein and according to protocols well known in the art. The amino acid residue numbering provided in the amino acid sequences set forth here is based on the unmodified (e.g., wild type) E glycoprotein amino acid sequence of the soluble recombinant DENV2 E glycoprotein (SEQ ID NO:6). However it would be readily understood by one of ordinary skill in the art that the equivalent amino acid positions in other flavivirus E glycoprotein amino acid sequences (e.g., DENV and/or ZIKV) can be readily identified, e.g., such as through alignments as shown in **FIGS. 17A-17B**, and employed in the production of the stabilized recombinant E glycoproteins of this invention..

Thus, in some embodiments the present invention provides a method of producing a stabilized recombinant E glycoprotein of the present invention, comprising: introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone, wherein the one or more amino acid substitutions are selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any combination thereof (e.g., amino acid substitutions shown in **Table 1** and/or **Table 2**), wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**, thereby stabilizing the flavivirus E glycoprotein into dimer conformation.

In some embodiments, the present invention provides a method of producing a stabilized recombinant E glycoprotein of the present invention, comprising introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone DI/DII hinge region, α B helix central interface, and/or fusion loop (FL) dimer interface, thereby stabilizing the flavivirus E glycoprotein into dimer conformation. In some embodiments, the present invention provides a method of producing a stabilized recombinant E glycoprotein of the present invention, comprising introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone DI/DII hinge region, thereby stabilizing the flavivirus E glycoprotein into dimer conformation. Non-limiting examples of amino acid substitutions in the E glycoprotein DI/DII hinge region, e.g., outside of the E glycoprotein dimer interface, include 279W and 280P. While not wishing to be bound to theory, substitutions in the E glycoprotein DI/DII hinge region outside of the dimer interface may increase dimer conformation stability through hydrophobic packing in the hinge region and/or stabilization of the kl loop. Thus, in some embodiments, the present invention provides a method of producing a stabilized recombinant E glycoprotein of the present invention, comprising introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone DI/DII hinge region, wherein the one or more amino acid substitutions hydrophobically pack the hinge region and/or to stabilize the kl loop, thereby stabilizing the flavivirus E glycoprotein into dimer conformation.

In some embodiments, a method of the present invention may comprise introducing one or more amino acid substitutions into a flavivirus E glycoprotein backbone, thereby stabilizing the flavivirus E glycoprotein into monomer conformation. Non-limiting examples of substitutions which may be introduced for monomer conformation stabilization include amino acid substitutions shown in **Table 1** and **Table 2** such as one or more substitutions comprised in the example variants Mnmer1, Mnmer2, and/or PM4, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**.

There is considerable interest in VLPs as a type of subunit vaccine for flaviviruses as the multivalent display of antigen on a particle can boost both B cell and T cell responses. To produce VLPs with the WT DENV E protein, it is necessary to co-express E with the full length prM protein. prM is one of three structural proteins in DENV, along with the E protein and capsid, and performs several functional roles during viral maturation. During secretion from the cell the pr domain binds to the fusion loop on domain DII of the E protein and prevents it from inserting into the membrane of the host cell as it passes through the ER and

the trans-Golgi network. This "chaperone" activity by the pr domain is important as the virus transports through the low-pH environment of the trans-Golgi. The E protein is dynamic and has evolved to expose the fusion loop at low pH when infecting cells. During native viral maturation, when the virus leaves the host cell pr is cleaved from M and released from the virion. However, when producing VLPs using recombinant protein the cleavage of prM is very inefficient and a large amount of pr remains attached to the particles. This presents a problem for using DENV VLPs as a vaccine because the pr domain may occlude important epitopes on the surface of the particle and pr is a dominant epitope that elicits non-neutralizing antibodies that can contribute to antibody enhancement (ADE) and severe disease symptoms. Current flavivirus subunit vaccines and live attenuated virus vaccines, e.g., dengue virus and Zika virus, use co-expression of prM and E glycoprotein to improve expression and folding of the E and sRecE protein. The present invention stabilizes the E protein dimer at neutral and low pH, thereby sequestering the fusion loop at the dimer interface and disfavoring its insertion into the host membrane during secretion, removing the need for pr during VLP production.

Therefore, in some embodiments, the present invention provides a stabilized recombinant E glycoprotein that may interact with a prM protein. In some embodiments, the present invention provides a stabilized recombinant E glycoprotein that may not require interaction with a prM protein for appropriate expression and secretion. In some embodiments, a virus like particle (VLP) comprising the E glycoprotein of the present invention is produced via a method which does not comprise co-expression of pr. The sE stabilizing mutations of the present invention do not need and are not expressed with prM and have improved expression yields. This is an advantage for use, e.g., as a vaccine, diagnostics, and/or research tool applications.

The stabilizing mutations of the present invention are in conserved positions and should also stabilize with DENV1, 2, 3, and/or 4 and ZIKV, as well as other flavivirus envelope protein monomers and dimers, as shown in **FIGS. 11** and **17A-17B**. Applications of the stabilizing mutations of the present invention include, for example, use of a stabilized recombinant E glycoprotein of the present invention in a subunit vaccine, improved DENV virus-like particle (VLP) production and stability, attenuating mutations (e.g., attenuation by stabilizing the E glycoprotein dimer conformation and reducing poorly neutralizing fusion loop (FL) epitope accessibility to antibodies *in vivo*), and/or research applications such as flavivirus (e.g., DENV, e.g., ZIKV) diagnostics and antibody epitope mapping.

It is contemplated that in some embodiments, the stabilized recombinant E glycoproteins and/or nucleic acid molecules of this invention can be used as immunogens and/or in a vaccine formulation. The stabilized recombinant E glycoproteins and/or nucleic acid molecules can be included in a pharmaceutical formulation, in any combination and/or ratio relative to one another.

Thus, the present invention further provides a method of producing an immune response to a flavivirus in a subject, comprising administering to the subject an effective amount of a stabilized recombinant E glycoprotein, a stabilized recombinant E glycoprotein dimer, a flavivirus particle or VLP, a nucleic acid molecule, a population, a composition, or any combination thereof of the present invention.

In some embodiments, the present invention provides a method of treating a flavivirus infection in a subject, comprising administering to the subject an effective amount of a stabilized recombinant E glycoprotein, a stabilized recombinant E glycoprotein dimer, a flavivirus particle or VLP, a nucleic acid molecule, a population, a composition, or any combination thereof of the present invention.

In some embodiments, the present invention provides a method of preventing a disorder associated with a flavivirus infection in a subject, comprising administering to the subject an effective amount of a stabilized recombinant E glycoprotein, a stabilized recombinant E glycoprotein dimer, a flavivirus particle or VLP, a nucleic acid molecule, a population, a composition, or any combination thereof of the present invention.

In some embodiments, the present invention provides a method of protecting a subject from the effects of a flavivirus infection, comprising administering to the subject an effective amount of a stabilized recombinant E glycoprotein, a stabilized recombinant E glycoprotein dimer, a flavivirus particle or VLP, a nucleic acid molecule, a population, a composition, or any combination thereof of the present invention.

In some embodiments, the present invention provides a method of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising: a) administering a composition comprising a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention to the subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of step (a) above under conditions whereby neutralization of the flavivirus particles can be detected; and c) detecting neutralization in step (b), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

In some embodiments, the present invention provides a method of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising: a) contacting a biological sample from a subject that has been administered a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention with
5 flavivirus particles comprising the E glycoprotein under conditions whereby neutralization of the flavivirus particles can be detected; and b) detecting neutralization in step (a), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

In some embodiments, the present invention provides a method of identifying an
10 immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising: a) administering an immunogenic composition comprising a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention to a subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of
15 step (a) under conditions whereby neutralization of the flavivirus particles can be detected; c) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and d) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E
20 glycoprotein of (a).

In some embodiments, the present invention provides a method of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising a stabilized recombinant E
25 glycoprotein or E glycoprotein dimer of the present invention with flavivirus particles comprising the E glycoprotein under conditions whereby neutralization of the flavivirus particles can be detected; b) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and c) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the
30 subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of (a).

In some embodiments, the present invention provides a method of detecting an antibody to a flavivirus in a sample, comprising: a) contacting the sample with a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention under

conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby detecting an antibody to the flavivirus in the sample.

In some embodiments, the present invention provides a method of identifying an antibody to a flavivirus in a biological sample from a subject, comprising: a) administering a composition a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention to the subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and c) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.

In some embodiments, the present invention provides a method of identifying an antibody to a flavivirus in a biological sample from a subject, comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.

In some embodiments, the present invention provides a method of identifying an immunogenic composition that induces an antibody to a flavivirus in a subject, the method comprising: a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and b) detecting formation of an antigen/antibody complex, thereby identifying an immunogenic composition that induces an antibody to the flavivirus in the subject.

In some embodiments, the present invention provides a method of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, comprising: a) administering an immunogenic composition comprising a stabilized recombinant E glycoprotein or E glycoprotein dimer of the present invention to a subject in an amount effective to induce an antibody response to the E glycoprotein; b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and c) detecting formation an antigen/antibody complex, thereby identifying an immunogenic composition that induces a neutralizing antibody to the flavivirus in the subject.

The present invention can be practiced for prophylactic, therapeutic and/or diagnostic purposes. In addition, the invention can be practiced to produce antibodies for any purpose, such as diagnostic or research purposes, or for passive immunization by transfer to another subject.

5 The present invention further provides a kit comprising one or more compositions of this invention. It would be well understood by one of ordinary skill in the art that the kit of this invention can comprise one or more containers and/or receptacles to hold the reagents (e.g., antibodies, antigens, nucleic acids) of the kit, along with appropriate buffers and/or diluents and/or other solutions and directions for using the kit, as would be well known in the
10 art. Such kits can further comprise adjuvants and/or other immunostimulatory or immunomodulating agents, as are well known in the art.

 The compositions and kits of the present invention can also include other medicinal agents, pharmaceutical agents, carriers, diluents, immunostimulatory cytokines, etc. Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in
15 this art.

 Administration to a subject can be by any route known in the art. As non-limiting examples, the route of administration can be by inhalation (e.g., oral and/or nasal inhalation), oral, buccal (e.g., sublingual), rectal, vaginal, topical (including administration to the airways), intraocular, transdermal, by parenteral (e.g., intramuscular [e.g., administration to
20 skeletal muscle], intravenous, intra-arterial, intraperitoneal and the like), subcutaneous (including administration into the footpad), intradermal, intrapleural, intracerebral, and/or intrathecal routes.

 The epitopes, polypeptides, VLPs and viral vectors of the invention can be delivered *per se* or by delivering a nucleic acid (e.g., DNA) that encodes the same.

25 Immunomodulatory compounds, such as immunomodulatory chemokines and cytokines (preferably, CTL inductive cytokines) can be administered concurrently to a subject.

 Cytokines may be administered by any method known in the art. Exogenous cytokines may be administered to the subject, or alternatively, a nucleic acid encoding a
30 cytokine may be delivered to the subject using a suitable vector, and the cytokine produced *in vivo*. In particular embodiments, a viral adjuvant expresses the cytokine.

 In embodiments of the invention, multiple dosages (e.g., two, three or more) of a composition of the invention can be administered without detectable pathogenicity (e.g., Dengue Shock Syndrome/Dengue Hemorrhagic Fever).

Pharmaceutical formulations (e.g., immunogenic formulation) comprising the dengue virus epitopes, polypeptides, chimeric flavivirus VLPs or chimeric flavivirus particles, nucleic acids, vectors, cells or compositions of the invention and a pharmaceutically acceptable carrier are also provided, and can be formulated for administration in a pharmaceutical carrier in accordance with known techniques. *See, e.g., Remington, The Science and Practice of Pharmacy* (latest edition). In the manufacture of a pharmaceutical composition according to embodiments of the present invention, the composition of the invention is typically admixed with, *inter alia*, a pharmaceutically acceptable carrier. By "pharmaceutically acceptable carrier" is meant a carrier that is compatible with other ingredients in the pharmaceutical composition and that is not harmful or deleterious to the subject. The carrier may be a solid or a liquid, or both, and is preferably formulated with the composition of the invention as a unit-dose formulation, for example, a tablet, which may contain from about 0.01 or 0.5% to about 95% or 99% by weight of the composition. The pharmaceutical compositions are prepared by any of the well-known techniques of pharmacy including, but not limited to, admixing the components, optionally including one or more accessory ingredients. In certain embodiments, the pharmaceutically acceptable carrier is sterile and would be deemed suitable for administration into human subjects according to regulatory guidelines for pharmaceutical compositions comprising the carrier.

Furthermore, a "pharmaceutically acceptable" component such as a salt, carrier, excipient or diluent of a composition according to the present invention is a component that (i) is compatible with the other ingredients of the composition in that it can be combined with the compositions of the present invention without rendering the composition unsuitable for its intended purpose, and (ii) is suitable for use with subjects as provided herein without undue adverse side effects (such as toxicity, irritation, and allergic response). Side effects are "undue" when their risk outweighs the benefit provided by the composition. Non-limiting examples of pharmaceutically acceptable components include any of the standard pharmaceutical carriers such as phosphate buffered saline solutions, water, emulsions such as oil/water emulsion, microemulsions and various types of wetting agents.

In some embodiments, the compositions of the invention can further comprise one or more than one adjuvant. The adjuvants of the present invention can be in the form of an amino acid sequence, and/or in the form of a nucleic acid encoding an adjuvant. When in the form of a nucleic acid, the adjuvant can be a component of a nucleic acid encoding the polypeptide(s) or fragment(s) or epitope(s) and/or a separate component of the composition comprising the nucleic acid encoding the polypeptide(s) or fragment(s) or epitope(s) of the

invention. According to the present invention, the adjuvant can also be an amino acid sequence that is a peptide, a protein fragment or a whole protein that functions as an adjuvant, and/or the adjuvant can be a nucleic acid encoding a peptide, protein fragment or whole protein that functions as an adjuvant. As used herein, "adjuvant" describes a substance, which
5 can be any immunomodulating substance capable of being combined with a composition of the invention to enhance, improve or otherwise modulate an immune response in a subject.

In further embodiments, the adjuvant can be, but is not limited to, an immunostimulatory cytokine (including, but not limited to, GM-CSF, interleukin-2, interleukin-12, interferon-gamma, interleukin-4, tumor necrosis factor-alpha, interleukin-1,
10 hematopoietic factor flt3L, CD40L, B7.1 co-stimulatory molecules and B7.2 co-stimulatory molecules), SYNTEX adjuvant formulation 1 (SAF-1) composed of 5 percent (wt/vol) squalene (DASF, Parsippany, N.J.), 2.5 percent Pluronic, L121 polymer (Aldrich Chemical, Milwaukee), and 0.2 percent polysorbate (Tween 80, Sigma) in phosphate-buffered saline. Suitable adjuvants also include an aluminum salt such as aluminum hydroxide gel (alum),
15 aluminum phosphate, or alganmmulin, but may also be a salt of calcium, iron or zinc, or may be an insoluble suspension of acylated tyrosine, or acylated sugars, cationically or anionically derivatized polysaccharides, or polyphosphazenes.

Other adjuvants are well known in the art and include without limitation MF 59, LT-K63, LT-R72 (Pal et al. *Vaccine* 24(6):766-75 (2005)), QS-21, Freund's adjuvant (complete
20 and incomplete), aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn -glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE) and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A,
25 trealose dimycolate and cell wall skeleton (MPL+TDM+CWS) in 2% squalene/Tween 80 emulsion.

Additional adjuvants can include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL) together with an aluminum salt. An enhanced adjuvant system involves the combination of a monophosphoryl
30 lipid A and a saponin derivative, particularly the combination of QS21 and 3D-MPL as disclosed in PCT publication number WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol as disclosed in PCT publication number WO 96/33739. A particularly potent adjuvant formulation involving QS21 3D-MPL & tocopherol in an oil in water emulsion is described in PCT publication number WO 95/17210. In

addition, the nucleic acid compositions of the invention can include an adjuvant by comprising a nucleotide sequence encoding the antigen and a nucleotide sequence that provides an adjuvant function, such as CpG sequences. Such CpG sequences, or motifs, are well known in the art.

5 An adjuvant for use with the present invention, such as, for example, an immunostimulatory cytokine, can be administered before, concurrent with, and/or within a few hours, several hours, and/or 1, 2, 3, 4, 5, 6, 7, 8, 9, and/or 10 days before and/or after the administration of a composition of the invention to a subject.

10 Furthermore, any combination of adjuvants, such as immunostimulatory cytokines, can be co-administered to the subject before, after and/or concurrent with the administration of an immunogenic composition of the invention. For example, combinations of immunostimulatory cytokines, can consist of two or more immunostimulatory cytokines, such as GM/CSF, interleukin-2, interleukin-12, interferon-gamma, interleukin-4, tumor necrosis factor-alpha, interleukin-1, hematopoietic factor flt3L, CD40L, B7.1 co-stimulatory
15 molecules and B7.2 co-stimulatory molecules. The effectiveness of an adjuvant or combination of adjuvants can be determined by measuring the immune response produced in response to administration of a composition of this invention to a subject with and without the adjuvant or combination of adjuvants, using standard procedures, as described herein and as known in the art.

20 In embodiments of the invention, the adjuvant comprises an alphavirus adjuvant as described, for example in U.S. 7,862,829.

 Boosting dosages can further be administered over a time course of days, weeks, months or years. In chronic infection, initial high doses followed by boosting doses may be advantageous.

25 The pharmaceutical formulations of the invention can optionally comprise other medicinal agents, pharmaceutical agents, stabilizing agents, buffers, carriers, diluents, salts, tonicity adjusting agents, wetting agents, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

30 For injection, the carrier will typically be a liquid. For other methods of administration, the carrier may be either solid or liquid. For inhalation administration, the carrier will be respirable, and is typically in a solid or liquid particulate form.

 The compositions of the invention can be formulated for administration in a pharmaceutical carrier in accordance with known techniques. See, e.g., Remington, The

Science and Practice of Pharmacy (9th Ed. 1995). In the manufacture of a pharmaceutical composition according to the invention, the VLPs are typically admixed with, inter alia, an acceptable carrier. The carrier can be a solid or a liquid, or both, and is optionally formulated with the compound as a unit-dose formulation, for example, a tablet. A variety of

5 pharmaceutically acceptable aqueous carriers can be used, e.g., water, buffered water, 0.9% saline, 0.3% glycine, hyaluronic acid, pyrogen-free water, pyrogen-free phosphate-buffered saline solution, bacteriostatic water, or Cremophor EL[R] (BASF, Parsippany, N.J.), and the like. These compositions can be sterilized by conventional techniques. The formulations of the invention can be prepared by any of the well-known techniques of pharmacy.

10 The pharmaceutical formulations can be packaged for use as is, or lyophilized, the lyophilized preparation generally being combined with a sterile aqueous solution prior to administration. The compositions can further be packaged in unit/dose or multi-dose containers, for example, in sealed ampoules and vials.

The pharmaceutical formulations can be formulated for administration by any method
15 known in the art according to conventional techniques of pharmacy. For example, the compositions can be formulated to be administered intranasally, by inhalation (e.g., oral inhalation), orally, buccally (e.g., sublingually), rectally, vaginally, topically, intrathecally, intraocularly, transdermally, by parenteral administration (e.g., intramuscular [e.g., skeletal muscle], intravenous, subcutaneous, intradermal, intrapleural, intracerebral and intra-arterial,
20 intrathecal), or topically (e.g., to both skin and mucosal surfaces, including airway surfaces).

For intranasal or inhalation administration, the pharmaceutical formulation can be formulated as an aerosol (this term including both liquid and dry powder aerosols). For example, the pharmaceutical formulation can be provided in a finely divided form along with a surfactant and propellant. Typical percentages of the composition are 0.01-20% by weight,
25 preferably 1-10%. The surfactant is generally nontoxic and soluble in the propellant.

Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute
30 0.1-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, if desired, as with lecithin for intranasal delivery. Aerosols of liquid particles can be produced by any suitable means, such as with a pressure-driven aerosol nebulizer or an ultrasonic nebulizer, as is known to those of skill in the art. *See*, e.g., U.S. Patent No. 4,501,729. Aerosols of solid particles can likewise

be produced with any solid particulate medicament aerosol generator, by techniques known in the pharmaceutical art. Intranasal administration can also be by droplet administration to a nasal surface.

Injectable formulations can be prepared in conventional forms, either as liquid
5 solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. Alternatively, one can administer the pharmaceutical formulations in a local rather than systemic manner, for example, in a depot or sustained-release formulation.

Extemporaneous injection solutions and suspensions can be prepared from sterile
10 powders, granules and tablets of the kind previously described. For example, an injectable, stable, sterile formulation of the invention in a unit dosage form in a sealed container can be provided. The formulation can be provided in the form of a lyophilizate, which can be reconstituted with a suitable pharmaceutically acceptable carrier to form a liquid composition suitable for injection into a subject. The unit dosage form can be from about 1 μ g to about 10
15 grams of the formulation. When the formulation is substantially water-insoluble, a sufficient amount of emulsifying agent, which is pharmaceutically acceptable, can be included in sufficient quantity to emulsify the formulation in an aqueous carrier. One such useful emulsifying agent is phosphatidyl choline.

Pharmaceutical formulations suitable for oral administration can be presented in
20 discrete units, such as capsules, cachets, lozenges, or tablets, as a powder or granules; as a solution or a suspension in an aqueous or non-aqueous liquid; or as an oil-in-water or water-in-oil emulsion. Oral delivery can be performed by complexing a compound(s) of the present invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers include plastic capsules or tablets, as known in the art.
25 Such formulations are prepared by any suitable method of pharmacy, which includes the step of bringing into association the protein(s) and a suitable carrier (which may contain one or more accessory ingredients as noted above). In general, the pharmaceutical formulations are prepared by uniformly and intimately admixing the compound(s) with a liquid or finely divided solid carrier, or both, and then, if necessary, shaping the resulting mixture. For
30 example, a tablet can be prepared by compressing or molding a powder or granules, optionally with one or more accessory ingredients. Compressed tablets are prepared by compressing, in a suitable machine, the formulation in a free-flowing form, such as a powder or granules optionally mixed with a binder, lubricant, inert diluent, and/or surface

active/dispersing agent(s). Molded tablets are made by molding, in a suitable machine, the powdered protein moistened with an inert liquid binder.

Pharmaceutical formulations suitable for buccal (sub-lingual) administration include lozenges comprising the compound(s) in a flavored base, usually sucrose and acacia or tragacanth; and pastilles in an inert base such as gelatin and glycerin or sucrose and acacia.

Pharmaceutical formulations suitable for parenteral administration can comprise sterile aqueous and non-aqueous injection solutions, which preparations are preferably isotonic with the blood of the intended recipient. These preparations can contain antioxidants, buffers, bacteriostats and solutes, which render the composition isotonic with the blood of the intended recipient. Aqueous and non-aqueous sterile suspensions, solutions and emulsions can include suspending agents and thickening agents. Examples of nonaqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

Pharmaceutical formulations suitable for rectal administration are optionally presented as unit dose suppositories. These can be prepared by admixing the active agent with one or more conventional solid carriers, such as for example, cocoa butter and then shaping the resulting mixture.

Pharmaceutical formulations suitable for topical application to the skin preferably take the form of an ointment, cream, lotion, paste, gel, spray, aerosol, or oil. Carriers that can be used include, but are not limited to, petroleum jelly, lanoline, polyethylene glycols, alcohols, transdermal enhancers, and combinations of two or more thereof. In some embodiments, for example, topical delivery can be performed by mixing a pharmaceutical formulation of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Pharmaceutical formulations suitable for transdermal administration can be in the form of discrete patches adapted to remain in intimate contact with the epidermis of the subject for a prolonged period of time. Formulations suitable for transdermal administration can also be delivered by iontophoresis (*see, for example, Pharmaceutical Research* 3:318

(1986)) and typically take the form of a buffered aqueous solution of the compound(s). Suitable formulations can comprise citrate or bis/tris buffer (pH 6) or ethanol/water and can contain from 0.1 to 0.2M active ingredient.

In embodiments of the invention, the dosage of a virus particle of this invention can be in a range of about 10^4 to about 10^7 plaque forming units (PFUs). In embodiments of this invention, the dosage of a VLP of this invention can be in a range of about 500 micrograms to about 5 milligrams. In embodiments of this invention, the dosage of a protein of this invention can be in a range of about 10^0 to about 10^4 micrograms +/- adjuvant.

Further, the composition can be formulated as a liposomal formulation. The lipid layer employed can be of any conventional composition and can either contain cholesterol or can be cholesterol-free. The liposomes that are produced can be reduced in size, for example, through the use of standard sonication and homogenization techniques.

The liposomal formulations can be lyophilized to produce a lyophilizate which can be reconstituted with a pharmaceutically acceptable carrier, such as water, to regenerate a liposomal suspension.

The immunogenic formulations of the invention can optionally be sterile, and can further be provided in a closed pathogen-impermeable container.

EXAMPLES

EXAMPLE 1: Computational design identifies DENV2 sE dimer and monomer stabilizing mutations

Four crystal structures of the DENV2 sE dimer, each similar while containing differences that represent the conformations available to the DENV2 sE dimer., were used as input for design simulations. The structures were prepared for the design simulations by energy minimizing them with the FastRelax algorithm in Rosetta . Notably, this protocol only makes small structural perturbations ($\text{RMSD} < 0.5\text{\AA}$), but lowers the calculated energy of the model as specific contacts are optimized according to the Rosetta energy function.

Two different computational protocols were used to identify DENV2 sE stabilizing mutations: PM_ssm and cluster_mut. PM_ssm is an exhaustive site-saturation mutagenesis protocol which identifies point mutations (PMs) predicted to stabilize the sE dimer and/or monomer. The protocol starts at the first residue in the protein and walks through the entire primary sequence, one position at a time, mutating the WT AA to each of the 20 AA in independent simulations. Since the sE homodimer was being modeled, mutations were simultaneously placed on both chains. After mutating a residue, the conformation of the

mutated residue and surrounding residues were energy optimized with iterative rounds of rotamer-based side chain sampling and gradient-based minimization of side chain and backbone torsion angles. To minimize noise in the energy optimization simulations, residues distant from the site of mutation were constrained to remain in their initial conformation while residues immediately adjacent to the site of the mutation were energy optimized without constraints. The calculated energy of mutating to the same amino acid (AA) as wildtype (WT) was used as reference to calculate the change in rosetta energy (Δ REU, rosetta energy units) upon mutation, a Δ REU > -2 cutoff was used to select the best scoring mutations (**FIG. 1B**). The PM_ssm protocol produced predictions for 7880 mutations at the 394 residues in DENV2 sE, with 879 mutations (~11%) remaining after filtering mutations based on the Δ REU cutoff. Next, Rosetta was used to create designs containing combinations of the predicted PMs. These PM_comb simulations used the same selection logic from the PM_ssm simulations but allowed multiple residues to mutate in an entire sE protein domain, domain-domain interface, or dimer interface.

The Cluster_mut protocol was used to identify small numbers of favorable mutations (about 2 to about 4) in close proximity with each other. The protocol incorporated a "design sphere" in which all residues within 7Å of, and including, a seed residue were allowed to mutate to any AA except cysteine (**FIG. 1C**). Surrounding the design sphere was a 3Å layer in which side chains could adopt new conformations during the simulation, but their AA identities were fixed. Outside of the two spheres side chains were fixed. The design simulation was performed using the FastDesign protocol in Rosetta which iterates between rotamer-based sequence design and gradient-based optimization of backbone and side chain torsion angles. Only torsion angles within the design and repacking sphere were allowed to adjust during the minimization. To favor small numbers of mutations and only include mutations predicted to have a large impact on stability, a bonus was placed on WT amino acid during the simulations.

To focus the cluster_mut design simulations, seed residues in regions within the DENV2 sE protein were identified that were hypothesized to contribute to protein dimer and/or monomer instability. First, regions at the DENV2 sE dimer interface were selected to increase dimer stability. Three regions were identified with residues making contacts at the sE dimer interface at the central "αB helix" interface, the DI/ij-loop interface and the fusion loop (FL) interface (**FIG. 1D**). In addition to targeting interface residues, multiple reports indicate that conserved histidine residues in the flavivirus E protein are "pH sensing" residues that mediate the E conformational change from pre-fusion dimer to post-fusion trimer. These

histidine residues are close in proximity with cationic residues such as arginine and lysine and have been implicated in contributing to E dimer destabilization. These histidine-cation (herein referred to as "HisCat") interactions are energetically weak at neutral pH and highly repulsive at low pH, resulting in protonation of the histidine side chain and repulsion from the neighboring cationic residue. The sE dimer was analyzed for residue clusters containing histidines near at least one cationic residue in local space. Three main clusters were identified: 1) at the DI/DIII domain interface, 2) near the DI/ij loop dimer interface and 3) the central α B helix dimer interface. The residues involved in the sE dimer interface contacts and the histidine-cation cluster residues were used as seed residues for the IntFc and HCat cluster_mut simulations, respectively.

We also sought to stabilize the dimer by stabilizing the sE monomer. The DENV has evolved the E protein to have conformational instability to adopt the multiple conformations necessary for the virus life cycle. While not wishing to be bound to theory, the dimer and monomer instability of sE may be linked to the inherent flexibility and dynamic structure of the E glycoprotein, and that stabilizing the E monomer in the conformation observed in the dimer could improve dimer affinity. The DENV2 sE dimer was analyzed using the RosettaHoles protocol to identify underpacked regions present in the core, domain-domain interface or dimer interface. Underpacked regions contain small voids and have been shown to contribute to protein instability. RosettaHoles identified four main underpacked regions: 1) the DI/DIII domain interface known as the DI/DIII linker; 2) the DI/DII domain interface, also known as the hinge region; 3) the core of DI; and 4) at the central α B helix and FL dimer interfaces (**FIG. 1D**). Three of the underpacked regions, the DI/DIII linker, DI/DII hinge region and DI, all change conformation to allow for transition of the E pre-fusion dimer conformation to the post-fusion trimer conformation. The residues defining these underpacked regions were used as seed residues input for the "UndPk" cluster_mut simulations.

Assessment of the DENV2 sE protein also revealed a large number of surface exposed hydrophobic residues that are buried either on the viral surface or at the post-fusion trimer interface. These hydrophobic residues were manually selected for input for the surface hydrophobic to polar (SHP) simulations, using a modified PM_comb protocol, where only polar amino acids were allowed to be assessed during the design at these positions.

After performing the various design simulations, eight designs were selected from each of the protocols: PM_Comb (PM), UndPk, HCat and IntFc, and two designs from the SHP simulations for experimental studies. Recent studies have also demonstrated that the sE

protein dimer can be stabilized recombinant by introducing disulfides across the dimer interface. Two of these variants, Cm1 (A259C) and Cm2 (L107C, A313C), were used in these studies. For negative control experiments, two mutants (Mnmer1 and Mnmer2) from the PM_ssm results were used that were predicted to destabilize the dimer with the goal of creating sE protein that would remain monomer even at higher concentrations and low temperature.

Mammalian surface display screen identifies Rosetta sE designs with improved quaternary antibody epitope presentation at 37°C. To ensure the mutations allowed for sE dimer formation and to compare the ability of the variants to present quaternary epitopes at 37°C relative to WT sE, it was investigated if known quaternary epitope antibodies can bind to the designed Rosetta sE variants. To do this the transmembrane and cytoplasmic domains of MHC-I alpha chain (SEQ ID NO:3) were fused to the c-terminus of the DENV2 sE protein using a GS linker (SEQ ID NO:2), allowing for surface display of the protein on EXPI293 cells. The construct was further modified by a cMyc epitope tag inserted within the GS linker for independent detection of sE surface display (**FIG. 2A**) and an n-terminal human serum albumin signal peptide (SEQ ID NO:1), instead of co-expression of prM, was used to export the protein to the cell surface. After transfection of the plasmid containing the DENV2 sE/MHC-Iα fusion, the cells were enhanced to increase protein expression for 24 hours and harvested for immunostaining. DENV2 sE variant epitope presentation was assessed by measuring DENV2 type-specific (2D22) and cross reactive (EDE1 C8 and C10) neutralizing quaternary epitope antibody binding (PerCP positive fluorescence) to cells displaying sE protein, detected through cMyc antibody binding (Alexa488 fluorescence) (**FIGS. 2A, 2C, 2D**). We also probed for binding of simple-domain epitope antibodies including 3H5 (DIII) and 1C19 (DII/bc-loop) as a readout for proper folding of DENV2 sE variants (**FIG. 2B**). Consistent with previously observed dimerization of the DENV2 sE WT protein at lower temperatures, binding of both 2D22 and EDE1 C8 to WT sE was observed at room temperature (~23°C). Surprisingly, all antibodies tested were able to bind to all DENV2 sE Rosetta variants, albeit at different amounts relative to WT, indicating that all the variants expressed were folded properly, and able to form dimers similar to WT on the cell surface at ~23°C.

Retention of quaternary epitopes at >37°C was tested by staining the surface-displayed sE Rosetta variants with 2D22 or EDE1 C10 at 40°C. In contrast to the 23°C screen, minimal binding of 2D22 and EDE1 C10 to DENV2 sE WT was observed (**FIG. 1F** and **FIG. 2C**), while increased binding of the quaternary antibodies to both Cm1 and Cm2

was observed, consistent with stable dimer formation even at the increased temperature. Out of the 34 variants, two variants, IntFc6 and Mnmer1, showed complete unfolding as indicated by complete loss of 3H5 and 1C19 binding, and seven variants showed reduced binding of the quaternary antibodies, including Mnmer2, designed as a negative control for the experiment. Improvements ($Fr > 2$) in quaternary antibody binding to 12/34 of the sE Rosetta variants were observed. Similar to the Cm2 control, eight Rosetta sE variants, (HCat3, IntFc2, IntFc8, UndPk6, PM2, PM4, SHP1 and SHP2) had greater than 3-fold higher Fr values for either 2D22 or EDE1 C10 and > 2 -fold higher Fr values for both antibodies, indicating these variants stably present of quaternary antibody epitope at $>37^{\circ}\text{C}$ (**FIGS. 2B & 2D**).

DENV2 sE Rosetta variants increase expression and improve both sE dimer and monomer stability: Direct measuring of the stability of the DENV2 sE Rosetta variants was performed using nanoscale Differential Scanning Fluorimetry (nanoDSF). 22 selected variants and Mnmer2, Cm1, and Cm2 were cloned into a mammalian expression plasmid without prM containing a c-terminal His_{8x} tag (SEQ ID NO:4) for Ni-affinity purification and n-terminal human serum albumin (HSA) signal peptide (SEQ ID NO:1) for extracellular secretion. It has been indicated that prM co-expression is not necessary for sE expression and folding, therefore the expression construct was designed to eliminate potential problems with co-expressing prM with variants containing mutations near the pr/E binding site and to prevent additional purification steps needed to ensure removal of pr, important for preventing unwanted anti-prM antibody elicitation in future vaccine experiments. The constructs were transiently transfected into EXPI293F cells at a 60-120mL scale, after which the His-tag proteins secreted in the media were directly affinity purified using a penta-Ni resin (Marvelgent). Despite the low yields observed with DENV2 sE WT ($\sim 0.2\text{mg/L}$), this protocol yielded high purity directly from the nickel resin, eliminating the further loss of protein through multiple purification steps and allowing direct performance of nanoDSF measurements with no additional preparation. Out of the 22 variants tested, one variant (IntFc6) did not express, consistent with 40°C surface display data, five variants had lower than WT expression, eight variants had WT expression level, as well as Mnmer2, and eight had yields greater than 2-fold with drastic improvements in expression observed for DENV2 sE Rosetta variants PM4 (10-fold), IntFc8 (19.1-fold) and UndPk6 (22.5-fold) (**Table 1**). While Mnmer2 had WT expression yields, Cm1 and Cm2 both had below detectable yields when expressed at the same scale.

Dimer and monomer stability of these variants was assessed using nanoDSF. DENV2 sE dimer dissociation (T_m^1) and protein unfolding (T_m^2) can be detected in a single thermal melt experiment (**FIGS. 3A, 3D**). Performing nanoDSF thermal melts with increasing protein concentrations results in dimer dissociation occurring at higher melting transitions (T_m^1), which can be used to quantify the homodimer affinity of the DENV2 sE dimer at 37°C. Single concentration nanoDSF thermal melts were performed and compared the DENV2 sE Rosetta variant dimer and monomer stabilities to WT (**FIG. 3A** and **Table 1**). Analysis of DENV2 sE WT at 4μM revealed two thermal melt transitions, the first at 34.2°C (T_m^1) corresponding to the dissociation of sE dimer to monomer, and the second at 51.0°C corresponding to the unfolding of the sE monomer. Out the 20 selected variants that expressed with sufficient yield for analysis, five variants had lower T_m^1 values than WT, including the Mnmer2 reference variant, which showed no transition at T_m^1 . Taken with the reduction of EDE1 C10 and 2D22 binding to Mnmer2 in the surface display experiment at 40°C, this suggested that the protein is a monomer in solution. Among the four variants that had dimer stabilities similar to WT, three of them had improved monomer stabilities of > +3.5°C, including HCat3 (**Table 1**). One of these variants, PM4, which contains three mutations S29K, T33V, and A35M within the core of DI, had no improvement in dimer stability (T_m^1), but had a striking +11.4°C improvement in monomer stability (T_m^2) (**FIGS. 3A** and **3C**). DENV2 sE containing the point mutants A35M (PM4.1), S29K (PM4.3), and a double mutant containing T33V and A35M (PM4.2) all improved sE monomer stability with the addition of their respectively measured T_m^2 matching the measured T_m^2 for PM4 (T33V/A35M = +6.9°C, S29K = +4.6°C, Total = +11.5°C, PM4 = +11.4°C) (**Table 1**). Testing A35M yielded a T_m^2 of +1.5°C, which suggested that T33V provides a +5.4°C improvement. S29 and T33 make important contacts in the post-fusion trimer, suggesting that the sub-optimal contributions to stability of these residues may be related to functional selective pressure. The remaining 11 designs all had improved dimer stability, with T_m^1 transitions greater than 2.0°C over WT, with three variants (IntFc2, IntFc8 and UndPk6) all having a > 8.0°C improvements in dimer stability. The most stabilizing variant, IntFc2, had a +11.4°C improvement in T_m^1 . IntFc2 was predicted to create a new pi cation interaction across the αB helix central dimer interface, where the M protein natively interfaces with the E protein on the virus surface (**FIG. 1C** and **FIG. 5A**). IntFc8 has a single point mutation in the fusion loop (G106D) which was predicted to have more favorable torsion energies and to create a salt-bridge with K310, stabilizing a critical interaction with W101 at the FL dimer interface (**FIG. 5A**). UndPk6, which stabilized the dimer and monomer simultaneously (+8.7

T_m^1 and $+5.9 T_m^2$), contains 2 mutations buried in the DI/DII interface known as the hinge region. The model predicted increased hydrophobic packing in the hinge region with the F279W mutation and mutated the T280 residue at the base of the kl loop to proline (**FIG. 5A**). As prolines have been shown to stabilize loop conformations, similar to PM4, the point mutation T280P (UndPk6.1) was tested and showed a T_m^1 of $+6.4$ and T_m^2 of $+2.6$, indicating T280P accounts for the majority of the increased dimer stability and about half of the added monomer stability, likely due to stabilizing the kl loop.

The homodimer affinity of the most stable dimer variants was quantified by performing nanoDSF at concentrations ranging from 2-16 μ M, allowing measurement of variant sE dimer affinity (K_d) using a Van't Hoff Analysis. All variants and WT showed increasing T_m^1 values with increasing concentration, with a measured K_d of 12.9 μ M for DENV2 sE WT at 37°C (**Table 1**). Consistent with the improvements in T_m^1 , IntFc2 had an extrapolated K_d of 8nM at 37°C, a >1000 fold increase in dimer affinity over WT. Similarly, IntFc8 and UndPk6 showed an improved extrapolated K_d at 37°C of 219 nM and 238nM, respectively (a ~ 50 fold improvement over WT). To further validate the improved dimer stability of these variants, exclusion chromatography coupled with multi-angle light scattering (SEC-MALS) was used to measure these variants oligomeric state at 37°C. Consistent with the previous characterization at RT, WT eluted with two peaks, the first at ~ 14 mL with a molar mass of 91 kDa, and the second at ~ 15 mL with a molar mass (MM) of 58 kDa, consistent with the previous characterization that the WT is in a monomer-dimer equilibrium, favoring the dimer conformation at lower temperature and high concentration (**FIG. 4A**). However, at 37°C, WT almost entirely eluted at ~ 15 mL with a MALS measured MM of 61 kDa, consistent with the protein eluting predominantly as a monomer (**FIGS. 4A, 4D**). The 37°C MALS measured WT MM at the beginning of the peak was higher than the middle suggesting a minor fraction of dimers may be present. Consistent with the absence of a T_m^1 transition during nanoDSF analysis, Mnmer2 eluted as two peaks both with measured MM nearly identical to the theoretical monomer Mnmer2 MM. Monomeric DENV3 and DENV4 sE have also been observed to elute as two fractions in SEC, and may be due to the exposed FL peptide interacting with the size exclusion matrix. PM4, which had no improvement in dimer stability relative to WT, eluted at the same volume and had a nearly identical measured MM as sE WT at 37°C, while IntFc2, IntFc8 and UndPk6 eluted at the volume and with MALS-measured MM consistent with the WT sE dimer observed at RT, consistent with the improved T_m^1 (**FIGS. 4B, 4D**). The MALS MM for IntFc8 and UndPk6 were slightly lower than IntFc2, suggesting that while stabilized, partial dimer dissociation of

the IntFc8 and UndPk6 protein variants may occur at 37°C which is consistent with the Kds measured by nanoDSF (**FIG. 4D**). The nanoDSF and SEC-MALS experiments indicated that both computational protocols, PM_Comb and Cluster_mut, were successful at identifying dimer and monomer stabilizing mutations, some of which had greatly improved dimer stability (e.g., IntFc2) and monomer stability (e.g., PM4).

Combining stabilizing mutations further increases DENV2 sE dimer stability and expression levels: The SEC-MALS analysis suggested that, while the initial designs had improved dimer stability at 37°C, they may not have sufficient stability to remain dimers under vaccination conditions (e.g., 37°C and low protein concentrations). To find combinations of mutations that would boost dimer stability even further, 28 stable combination (SC) variants were tested that were built from the most stabilizing designs: IntFc2, IntFc8, UndPk6, PM4 and HCat3 (**Table 1**). The SC variants were expressed, purified, and tested for dimer and monomer stability using nanoDSF thermal melts. All SC variants had improved expression levels compared to WT, with some increasing yield >70 fold (**Table 1**). Except for SC.20, all the SC variants containing dimer stabilizing mutations had at least an 8°C increase in T_m^1 . The most stable dimer variant, SC.4, which contained 13 mutations, had a T_m^1 of 56.7°C, which is a 22.5 °C increase over wild type (**FIGS. 3B, 3C** and **Table 1**). All SC variants had ΔT_m^2 values ranging from +4°C (SC.23, 55.4°C) to +18.2°C (SC.9, 69.3°C). SC.24 and SC.25, which incorporated Mnmer2 and either HCat3 or PM4, respectively, both had nearly identical T_m^2 improvements as the HCat3 and PM4 variants without Mnmer2, however, both had no measurable T_m^1 , similar to Mnmer2 alone. Likewise, the combination of PM4 with the disulfide mutant, Cm2 resulted in a +11.4°C increase in T_m^2 and successful disulfide formation, indicated by the protein migrating as a dimer in a non-reducing SDS-PAGE gel (**Table 1**). It was not possible to recover Cm2 post purification at the 120mL scale, however, addition of PM4 with Cm2 resulted in a 3.2-fold improvement in expression over WT with an ~1mg/L expression yield (**Table 1**). Taken together, these results indicate the utility of combining these mutations to tune the sE protein to the desired expression yield and dimer and monomer stabilities.

The homodimer Kd at 37°C of the SC variants was measured by performing nanoDSF at varying protein concentrations, measuring T_m^1 and using a Van't Hoff analysis to estimate binding affinity at 37°C. Consistent with the large improvements in T_m^1 , all SC variants containing dimer stabilizing mutations had Kds at 37°C with nM affinity and 16 out of 28 SC variants had extrapolated Kds <100pM. One variant SC.14 was able to raise T_m^1 by 16.1°C and lowered the Kd at 37°C to 1nM with only four mutations from two of the best stabilizing

dimer mutation sets, IntFc2 and UndPk6. Just adding one additional mutation, G106D (IntFc8), to SC.14 to make SC.10 raised T_m 19.8°C and lowered the homodimer K_d further to < 100 pM (**Table 1**). While not wishing to be bound to theory, the exceptional stability of the SC.10 dimer may be likely due to simultaneously stabilizing the central dimer interface (IntFc2), the hinge (U6) and the FL dimer interface (IntFc8), all critical regions that regulate dimer stability. Consistent with the nanoDSF data, both SC.14 and SC.10 eluted as a single peak upon analysis with SEC-MALS at 37°C with MM of 99.5 and 102.2 kDa, respectively, similar to the disulfide stabilized sE dimer, Cm1 (**FIGS. 4C and 4D**). Taken together, combining the Rosetta variant stabilizing mutations resulted in large increases in monomer stability and dimer stability and revealed that the dimer stability is dependent on interactions in the DI/DII hinge region and at the α B helix central and FL dimer interfaces.

DENV2 sE SC.10 adopts the same dimer conformation as the EDE1 C8 bound sE dimer. The crystal structure of SC.10 was solved in order to determine if SC.10 maintained a dimer structure similar to WT sE and check the accuracy of the Rosetta design models. SC.10 was concentrated to 3.25mg/mL, and buffer exchanged into a low salt Tris buffer prior to crystallization. SC.10 hexagonal crystals formed after three days using the sitting drop method at 21°C in 15% PEG 3350 pH 4.4, 0.1M sodium acetate and 0.1M sodium iodide, that diffracted to a final resolution of 3.42Å. The diffraction data was processed and the phases were obtained by molecular replacement (MR) by using chain A of PDB 1OAN, the DENV2 sE crystal structure used for the design of IntFc2, IntFc8 and UndPk6. Successful MR required input of two models from the sE monomer chain of 1OAN, one model containing DI/DII and the second containing DIII. The model obtained from MR was refined to a Rfree/Rwork of 33.7/31.8, with the asymmetric unit containing a single sE monomer. Despite the low pH crystal condition, SC.10 adopted the biological DENV2 sE dimer conformation (**FIG. 5A**). This in contrast to the DENV1 sE protein crystallizing as the post-fusion trimer in a similar crystal condition and low pH (pH 4.5) and is consistent with the increased dimer stability observed by adding the IntFc2, IntFc8 and UndPk6 mutations (**Table 1**). The SC.10 dimer had an overall C α RMSD of 3.5Å in comparison to 1OAN, the DENV2 sE dimer crystal structure solved at pH 9.0, and is consistent with the failed MR when using the entire monomer chain from 1OAN. Despite using domains from unliganded WT DENV2 (!OAN) for MR, the SC.10 dimer conformation closely matched the DENV2 sE dimer conformation when co-crystallized with EDE1 C8 (PDB 4UTA), a DENV broadly neutralizing quaternary epitope antibody, with a C α RMSD of 1.69Å (**FIG. 5B**). With this observation, MR was successful when repeated using the PDB 4UTA full-length chain A as input.

Analysis of multiple DENV2 sE crystal structures has revealed that the DI/DII hinge angle is variable, consistent with the intrinsic dynamics and multiple conformations the E protein can adopt. To see if the changes in the SC.10 dimer conformation were dependent on the hinge angle, the DI and DIII of the sE monomer from 1OAN and 4UTA were aligned to the DI and DIII of the SC.10 monomer. Both had nearly identical DI/DIII conformations when aligned to DI and DIII of SC.10, with a C α RMSD of only 1.0Å (1OAN) and 0.8Å (4UTA). In contrast there was a larger difference in the conformation of DII relative to DI and DIII for the sE monomer in 4UTA and SC.10 compared to 1OAN (**FIG. 5B**). The kl loop in the DI/DII hinge region was nearly identical for 4UTA and SC.10, with the loop facing away from the hinge and towards the adjacent monomer in the dimer. However, in 1OAN the kl loop conformation was packed within the DI/DII hinge, suggesting the kl loop conformation may play a role in regulating the hinge angle. Also, the glycan loop in both the SC.10 and 4UTA sE structures was disordered, unlike the previously published apo DENV2 sE dimer structures, suggesting that stabilizing the sE dimer in this conformation through mutation or antibody binding may destabilize this loop.

Electron density was observed for all of the mutations, IntFc2, IntFc8, and UndPk6, in the SC.10 crystal structure. Both UndPk6 mutations are present on the kl loop. F279W fills an underpacked region in the hinge. T280P is at the base of the kl loop, and with the mutation the loop was shifted so that a backbone-side chain hydrogen bond is formed between the P280 carbonyl to the T189 sidechain hydroxyl in the adjacent loop. This hydrogen bond was not observed in either 1OAN or 4UTA. In the SC.10 structure, the density for the kl loop was well defined, suggesting that adding P280 at the base of the kl loop stabilized the observed kl conformation, which is similarly stabilized by interactions between the EDE1 C8 Fab and the kl loop when it is bound to sE in 4UTA. This was consistent with the observation that loop conformations can be stabilized with the insertion of proline at the loop ends, and that the T280P mutation contributed the most to dimer stability increase in UndPk6 (**Table 1**). On the underside of the central dimer interface, both IntFc2 mutations are present on the α B helix with T262R making two new dimer contacts: a pi-cation interaction directly with A259W and a new side chain hydrogen bond to the backbone carbonyl of P218. These are both present on adjacent monomer in the sE dimer and both observed in the IntFc2 Rosetta model (**FIG. 5A**). Aligning the UndPk6 and IntFc2 mutations in the Rosetta models to the SC.10 crystal structure revealed that both the Rosetta model and the crystal structure were in high agreement. However, IntFc8 deviated from the predicted salt bridge with K310 in the Rosetta model and formed a hydrogen bond with the side chain of Q77, which changes sidechain

conformation and forms a hydrogen bond with the backbone amide of C74 (**FIG. 5A**).

Surprisingly, while the density is weaker, a change was also observed in the W101 and K310 rotamers (**FIG. 5A**). This may be a consequence of the low pH crystallization, as the ij loop and the n-terminus observed in the SC.10 crystal structure had conformational changes near the FL that matched more closely to the DENV sE structures also solved at low pH. Also, while not wishing to be bound to theory, the low pH condition would likely favor protonation of the Asp106, (typical pKa of 4.0) and hydrogen bonding to Q77 over formation of the salt bridge with K101. However, a similar W101 rotamer observed in the SC.10 crystal structure is also observed in the crystal structure of ZIKV sE when bound to a neutralizing antibody at the DI/DIII linker, indicating this rotamer can be formed at neutral pH (PDB 6NIU, chain A). Overall the SC.10 crystal structure retains the native sE dimer conformation, even under low pH conditions crystal conditions.

DENV2 sE SC.14 & SC.10 elicit DENV2 envelope dimer specific antibodies in mice:

The data indicated that SC.14 and SC.10 are stable dimers at 37°C and efficiently present quaternary antibody epitopes at low concentrations. In order to determine if these stable dimers could elicit E protein dimer-specific antibodies in mice, female Balb/c mice (n=5) were immunized on day 0 with 5µg of DENV2 sE Mnmer2, WT, SC.14, and SC.10 formulated in isotonic sucrose/H₂O and boosted with 5µg of each protein on days 21 and 56, with blood collected on day 112 to harvest serum for analysis. The study was designed without adjuvant to measure the innate immune response to each protein antigen and eliminate adjuvant bias. To test total anti-DENV2 IgG titers sera was diluted 1:50 and a 6-fold serial dilution performed for each immunization group's five mice and tested for serum IgG binding against DENV2 in a capture ELISA. All of the groups immunized with DENV2 sE Mnmer2, WT, SC.14, and SC.10 produced similar levels of antibodies that bind to DENV2, with SC.10 having a slightly lower, but not statistically significant, mean titer.

Depletion experiments were used to assess if dimer specific antibodies were being elicited by mice immunized with DENV2 sE monomers (Mnmer2 and WT) or DENV2 sE dimers (SC.14 & S C.10). Two sets of magnetic beads were generated, one loaded with DENV2 sE monomers, using DENV2 sE Mnmer2 which remains monomeric in solution, and the other set of beads loaded with DENV2 sE dimers, using the stable dimer DENV2 sE SC.14, onto Ni-NTA magnetic beads via both protein's c-terminal 8x Histidine-tag (**FIG. 7A**). It was hypothesized that antibodies targeting E monomer epitopes would equally bind and be depleted by both the sE monomer loaded beads and the sE dimer loaded beads, as E monomer epitopes will be present on both sE monomer and dimers, as observed with the

monomer epitope antibodies via direct ELISA analysis (**FIG. 6B, 6E**). Elicited antibodies that recognize E protein dimer-specific quaternary epitopes only bind to sE dimer loaded beads and are depleted from the sera, and similar to the direct ELISA experiment, these quaternary epitope antibodies would not bind to sE monomer and thus remain in the sera after
5 depletion with sE monomer loaded beads (**FIG. 7A**). The relative change in signal in the DENV2 capture ELISA between the sE monomer depleted sera and the sE dimer depleted sera indicates whether mice, immunized with a particular DENV2 sE protein, elicited E dimer specific antibodies.

To validate the depletion protocol, sE monomer loaded beads or sE dimer loaded
10 beads were incubated with 3H5, a DIII epitope antibody that binds monomer, and 2D22, a dimer-specific quaternary epitope antibody, to see if sE monomer or sE dimer beads could deplete these antibodies. Undepleted 3H5 bound to both sE monomer and sE dimer in a direct ELISA coated with either Mnmer2 or SC.14. In contrast, and similar to the antibody binding
15 direct ELISA experiments, only sE dimer beads were able to deplete 2D22, confirming that the depletion strategy can differentiate between E monomer and E dimer-specific quaternary epitope antibodies.

The sera from all four DENV2 sE protein mouse immunized groups (Mnmer2, WT, SC.10, and SC.14) 1:50 were diluted and depleted for 2-3 rounds with either sE monomer loaded magnetic beads (monomer depleted) or sE dimer loaded magnetic beads (dimer
20 depleted) for 1hr at 37°C, with the beads magnetically removed after each round and the sera supplemented with new sE loaded beads for each subsequent round of depletion. As a negative control, sera were depleted with beads loaded with His-tagged Spycatcher protein (control depleted) to account for non-specific antibody depletion. Undepleted and depleted sera were titrated against DENV2 in a capture ELISA to assess binding of serum antibodies
25 post-depletion. As expected, both undepleted and control depleted sera gave similar ELISA signals against DENV2 (**FIG. 7B**). For the Mnmer2 and WT immunized mice sera, both the sE monomer and dimer were able to equally deplete the mice sera from both of these groups, producing nearly identical signals against DENV2 (**FIG. 7B & 7C**). For SC.14 and SC.10, sE monomer was capable of partially depleting both sera, indicating that E monomer epitope
30 antibodies are elicited by these proteins. However, unlike WT and Mnmer2 sE dimer depleted sera, sE dimer was capable of depleting both SC.14 and SC.10 mice immunized sera, reducing DENV2 ELISA signal to near background signal, particularly for SC.10 (**FIG. 7B**). Taking the ratio of the end point dilution (EPD) for the monomer and dimer depleted sera, about 13 and about 19-fold mean improvement was observed for SC.14 and SC.10

respectively, suggesting that both SC.14 and SC.10, but not Mnmer2 or WT, elicit dimer specific antibodies (**FIG. 7C**). To confirm this result, the monomer and dimer depleted sera from all four DENV2 sE protein mouse immunized groups were tested in a direct ELISA coated with either DENV2 sE Mnmer2 (sE monomer) or DENV2 sE SC.14 (sE dimer) and the difference in the monomer depleted sera to the dimer depleted sera was compared using the EPD ratio. Similar to the DENV2 ELISA, Mnmer2, WT, SC.14 and SC.10 depleted sera had low EPD ratios of 0.7, 0.9, 1.5, and 3.5, respectively, when tested against Mnmer2, indicating similar levels of monomer specific antibodies remained in both monomer and dimer depleted sera for all four groups (**FIG. 7C**). Similar to the DENV2 ELISA, when tested against SC.14, both Mnmer2 and WT had EPD ratios close to 1, while SC.14 and SC.10 had EPD ratios of 15.9 and 20.5, confirming the DENV2 ELISA that mice immunized with these proteins elicit dimer specific antibodies.

In the DENV2 ELISA analysis of both SC.14 and SC.10, the signal for the monomer-depleted sera at the lowest dilutions was higher than the undepleted sera (**FIG. 7B**). This result can be explained if there were a mixture of low affinity (LA) and high affinity (HA) antibodies elicited during the immunization. In the undepleted sera, if the LA antibodies were more abundant compared to the HA antibodies, then the LA antibodies were able to outcompete the lower abundant HA antibody during initial binding to virus on the ELISA plate. However, during the subsequent wash and incubation steps the LA antibodies are more likely to release from the virus and lower the ELISA signal. In contrast, if in the monomer depleted serum there was a higher ratio of HA to LA antibodies, then more of the HA antibodies would bind to the virus and remain bound during the wash steps, thus leading to a higher ELISA signal. It was also predicted that this scenario would result in an increase of ELISA signal at the low dilutions that rapidly decreases, as the concentration of the HA antibodies would be low, thus binding would only be observed at the highest serum concentrations (e.g., low dilutions). To support this hypothesis, a competitive binding model was created in Matlab that simulated LA ($K_d = 10\text{nM}$) and HA ($K_d = 1\text{nM}$) antibody populations binding to virus and then unbinding during subsequent wash and incubation steps. Both populations of antibodies were given the same association rate constants typically observed with antibody-antigen binding, but the HA antibody population was assigned an off-rate that was 10-fold slower. When incorporating into the model association times (T_A) and dissociation times (T_D) that match the incubation times and wash times used in the ELISA protocol, the model was able to reproduce the trends observed in the DENV2 ELISA. This suggested that the E dimer specific antibodies elicited by SC.14 and SC.10, although

lower in abundance, may be higher affinity antibodies, and compete for binding to similar regions on the virus as the more abundant LA E monomer specific antibodies. Overall, the data indicated that the stabilized DENV2 sE SC.14 and DENV2 sE SC.10 dimers are capable of eliciting E dimer-specific quaternary epitope antibodies.

5 This study was able to computationally predict multiple DENV2 sE dimer and monomer stabilizing mutations. The most stable variants have homodimer Kds less than 100 pM at 37°C, compared to 12 μ M for WT, and overall protein thermostability was raised by more than 18°C. Strikingly, adding only 1-2 mutations increased expression by up to ~20-fold and by combining these mutations, >70-fold. This increase in expression was also observed
10 without co-expression of prM, which reduced additional purification steps and testing required to ensure no prM is present in the final sE vaccine formulation prior to immunization, as prM presents non-neutralizing epitopes that can elicit antibodies that cause ADE. Taken together, these stability and expression improvements aid in the practical consideration of producing these proteins at the scale that would be needed to create subunit
15 vaccines.

Furthermore, this study demonstrated that alternate combinations of the mutations can be used to select for desired stability, expression and oligomerization properties. For example, the affinity of the DENV2 sE dimer was tunable by combining the dimer stabilizing mutations IntFc2, IntFc8 and UndPk6 at different regions of the sE protein to create the
20 SC.10 stable dimer. Combining Mnmer2 with PM4 (SC.25) retained the protein as a monomer while increasing expression and improving protein stability (**Table 1**). These mutations can also be combined with the previously published cysteine mutations, to increase the stability and expression of the covalently stabilized dimers (**Table 1**, SC.28). While this study focused on DENV2 sE, the computationally targeted DENV2 sE regions are largely
25 conserved in other DENV serotype and flavivirus E proteins, including Zika, suggesting that this strategy can be applied to improve the stability and expression of other flavivirus E protein.

The most stabilizing mutation sets (IntFc2, IntFc8, UndPk6 and PM4) all targeted regions of the E protein that are important for the DENV infection cycle. IntFc2 creates new
30 contacts on the "underside" of the E dimer that would natively be interacting with the M protein on the DENV envelope. UndPk6 stabilized the DI/DII hinge, a region where mutations have been shown to affect the pH threshold for viral infection. UndPk6 stabilized the sE dimer without any new contacts at the dimer interface (FIG. 5A). Structural analysis suggested that these mutations stabilize the sE dimer by reducing the entropic cost of forming

the sE dimer by stabilizing the monomer in a dimer-favored monomer conformation, as this region has been shown to be inherently flexible in the sE WT protein. Additionally, mutating T280 to proline eliminated a native E contact with the M protein on the virus, which is lost in the context of sE. Comparison of the hinge angle in the SC.10, EDE1 C8 bound sE and apo sE crystal structures suggested that the kl loop conformation affects the E dimer stability (FIG. 5B). This provides insight into the structural regulation of E protein conformational changes during virus infection. On the virus, the M protein makes contacts with T280 on the kl loop in E, which may stabilize the prefusion E dimer conformation. Loss of this E-M contact during virus endocytosis would destabilize the kl loop, thus favoring the new hinge loop conformation observed in the post-fusion trimer. The UndPk6 mutations also stabilized the kl loop through increased hydrophobic packing in the hinge and mutation to proline at the position 280 at the base of the kl loop, which restricts the conformational space of the kl loop by forming a new hydrogen bond with T189 on the adjacent hinge loop (FIG. 5A). It was also observed that a mutation L277M, present in the DI/DII hinge, destabilized the dimer that also was observed to allow for more infection at higher pH, lending support to the hypothesis that the mutation destabilized the dimer through changes in the DI/DII hinge region, allowing for trimer formation at a less stringent pH.

Rosetta predicted only a small number of unique mutations in near the FL that would still preserve native sE dimer formation that would be favorable, one being G106D, the IntFc8 variant, suggesting that the FL dimer interface is already largely optimized with favorable contacts. IntFc8 stabilizes the sE dimer, reduces FLE presentation, and drastically improves expression (FIG. 3A-3C, Table 1 and FIG. 6F). Furthermore, quaternary epitope antibody binding appeared unaffected by the mutation (FIG. 6F). Another mutation set, PM4, contains three mutations in the DI core. The analysis of underpacked regions implicated the DI core as a large underpacked region, consistent with the changes within DI required for the E dimer to transition to the post-fusion trimer. PM4 mutates the suboptimal buried polar residues, S29 and T33, that form contacts to DIII in the low pH postfusion trimer conformation. Mutating both residues drastically improved the stability of the protein, by +4.6°C and by the additive property +5.4°C, respectively, suggesting the WT amino acids have been selected to stabilize the E protein post fusion trimer conformation as opposed to maximizing the thermostability of DI.

To validate the analysis that these mutations affect E regions important for the virus life cycle, the PM4, IntFc8 and UndPk6 mutations were cloned into the E gene of the DENV2 16681 RNA genome and transfected the RNA into C6/36 cells. Only propagation of DENV2

16681 WT was observed and no propagation of the mutated viruses, indicating that these mutations either prevent virus production or render the virus non-infectious. The same results were observed when transfecting the RNA genome of DENV2 16681 WT and DENV2 16681 PM4 virus into Vero-81, confirming the lack of mutated virus propagation was not cell line dependent. This data was also consistent with the DENV2 sE SC.10 stable dimer, which contains IntFc2, IntFc8 and Undpk6, crystallizing as the biological sE dimer under low pH conditions that typically favor the E trimer, supporting the long-standing notion that stabilizing the dimer, whether with antibodies or, in this case, dimer stabilizing mutations, renders the virus non-infectious. These results suggest that the virus has evolved the E protein to contain these local instability regions for functional purposes, allowing for adoption of multiple E conformations required for infection.

The improvements in the dimer stability for sE variants also provided improved quaternary epitope presentation at 37°C. Enhanced binding of both type-specific (2D22) and cross-reactive (EDE1 C8 & EDE2 A11) known neutralizing quaternary epitope antibodies to both DENV2 sE SC.14 & SC.10 variants are consistent with the improved dimer stability and stable epitope presentation at 37°C. Additionally, SC.10 crystallized in the same sE dimer conformation that WT E adopts when bound by EDE1 C8, consistent with the improved binding of EDE1 C8 to SC.10 observed in the ELISA experiment (**FIG. 5B** and **6F**). While the focus of this work was to improve sE quaternary epitope presentation, SC.14 and SC.10 also efficiently present the 3F9 DI epitope, an epitope known to be targeted by neutralizing antibodies elicited in natural DENV2 infected individuals. This indicates that in addition to presenting quaternary epitope antibodies, SC.14 and SC.10 also present other important neutralizing antibody epitopes observed to be elicited by the human immune response during natural infection.

A primary purpose of designing stabilized DENV2 sE dimers was to assess if these stabilized dimers can elicit quaternary epitope antibodies that target the E dimer. This study provides the first evidence that stabilized DENV2 sE dimers can elicit E dimer-specific antibodies *in vivo*. It was observed that these antibodies are low in abundance and in competition for similar monomer specific antibody epitope regions. This has also been observed during natural infection, as the monomer-specific FLE and dimer-specific EDE antibodies elicited compete for similar epitope regions on the DENV E protein. Furthermore, it has been shown that the EDE antibodies have a higher affinity to DENV and are more potently neutralizing than the FLE antibodies. A similar trend was observed in this study,

with the E dimer-specific antibodies having increased binding to DENV2 after depletion of the mouse serum monomer-specific antibodies with Mnmer2.

While quaternary epitope antibodies were observed in SC.10 and SC.14 mouse immunized sera, a substantial fraction of elicited IgG was able to be depleted by the DENV2 sE Mnmer2 protein, suggesting both of these proteins still also antibodies that target epitopes within the DENV2 sE monomer. These monomer epitope antibodies may represent both potentially neutralizing antibodies, such as 3H5 (DIII) and 3F9 (DI) for DENV2, and poorly neutralizing antibody epitopes including FLE antibodies such as 4G2 and 1M7, which have been shown to play a role in causing ADE.

Cell Lines and Viruses: EXPI293F (ThermoFisher, Cat: A14527) cells were maintained in EXPI293 expression media at 37°C, 8% CO₂ at 250rpm without antibiotics, until passage 25 to improve batch-to-batch reproducibility. Insect C6/36 (CRL-1660) cells were grown at 32° C with 5% CO₂ in minimal essential medium (MEM) media supplemented with 5% fetal bovine serum (FBS) and 100 U/mL penicillin, 100 mg/mL streptomycin. Vero-81 (CCL-81) cells were obtained from ATCC. Vero cells were grown at 37° C with 5% CO₂ in Dulbecco's Modified Eagle's Medium (DMEM) 5% fetal bovine serum (FBS), 100 U/mL penicillin, 100 mg/mL streptomycin, 1% GlutaMax, 1% Sodium Bicarbonate, 1% non-essential amino acids. The RNA genome of DENV2 strain 16681 was used for cloning of stabilizing mutations for transfection into C6/36 for virus induction.

DENV2 sE protein construct design, cloning and plasmid preparation for cell surface display and soluble expression: DNA encoding the DENV2 (strain 16681) soluble envelope protein, sE (res1-394), lacking the stem and transmembrane domains, was cloned into the modified PαH mammalian expression vector, originally derived from pHLSec vector by substitution of an alternative multiple cloning site containing a CAG promoter and human serum albumin signal peptide, replacing the original PTPα signal sequence. DENV2 sE was expressed for both mammalian cell surface display and soluble expression using the same pαH vector backbone and plasmids were renamed to differentiate function. For mammalian surface display, sE genes were cloned into the pD2sE_Dsp display vector, which genetically fuses a GS_{6x}-cMyc-GS_{7x} linker and the MHC Iα transmembrane/cytoplasmic domains to the c-terminus of sE; for membrane anchoring, a cMyc epitope tag was added for independent detection of sE surface display; for soluble expression, sE genes were cloned into the pD2sE_EV8 expression vector containing a c-terminal GS_{6x}-His_{8x} tag for nickel affinity purification. All DENV2 sE Rosetta variant and SC variant cloning was performed by Twist

Biosciences. DENV2 sE cloned plasmids were heat-shock transformed into *E. coli* DH5 α cells for amplification, miniprep or midiprep using DNA endotoxin-free kits and stored in endotoxin-free H₂O at -20°C.

Mouse immunizations: Female Balb/c mice were inoculated at 6 weeks of age. Each mouse was immunized subcutaneously with 5 μ g of either DENV2 rE monomer (n=5), rE wild type (n=5), rE disulfide dimer (n=5), rE Rosetta dimer (n=5), rE Rosetta dimer FLmut (n=5), all formulated in isotonic 9.25% sucrose/H₂O, or vehicle alone (n=3). All groups received 3 immunizations (day 0, 21 and 56) and serum samples were collected on day 21, 28, 63 and 112 by submandibular bleed.

Cloning, transfection and immunostaining of DENV2 16681 containing stabilizing mutations: Dengue virus 2 (DENV2) infectious clones were designed by subdividing the DENV2 genome into a plasmid system. Wild type and mutant DENV2 pre membrane and envelope sequences were synthetically derived and introduced into a four-plasmid infectious clone system utilizing the DENV2 16681 strain. Plasmids were transformed, miniprep, digested, and analyzed by gel electrophoresis for accuracy. Digested DENV2 fragments were then ligated together and purified by a chloroform extraction. DENV2 full-length genomic RNA was then generated using T7 RNA polymerase. Infectious genome-length DENV2 RNA transcripts were electroporated into C6/36 (CRL-1660) cells. Four days later, cell supernatants were harvested and cells were immunostained to confirm virus recovery. The recovered viruses were sequenced to confirm sequence identity. Four days after viral RNA electroporation, cells were washed with 1X PBS and fixed with 10% Formalin for 20 min at room temperature. Fixed cells were then permeabilized by washing twice with 5ml of 1X Permeabilization buffer (ThermoFisher). Fixed and permeabilized cells were then blocked for 10 minutes at room temperature with blocking buffer (1X Permeabilization buffer containing 5% non-fat dry milk). Fixed and permeabilized cells were stained with anti-prM hybridoma, 2H2, and anti-E hybridoma, 4G2, at 1:1000 diluted in blocking buffer for 30 min at 37° C. Fixed and permeabilized cells were then washed three times with 1X PBS and were stained with an anti-mouse horseradish peroxidase (HRP)-labeled secondary antibody for 30 min at 37° C. After washing three times with 1X PBS, foci were visualized with TrueBlue substrate compared to cells electroporated with 1X PBS.

EXAMPLE 2: Mutations stabilizing ZIKV E glycoprotein dimer

Using computational modeling of the DENV2 soluble recombinant envelope protein (sRecE), amino acid mutations were identified that were capable of (1) stabilizing the DENV2 sRecE dimer conformation at human body temperature (e.g., 37 °C) while retaining human DENV neutralizing antibody epitopes; (2) improving total protein stability by up to 18 °C (to a temperature of about 69.3 °C) compared to the wildtype parent protein; and (3) improving expression levels and final production yield by up to 72.9 fold compared to the wildtype parent protein. These mutations stabilized the dimer by targeting distinct instability regions throughout the sRecE protein.

A modeling strategy was implemented that targeted regions of instability at the sRecE dimer interface, as shown in **FIGS. 9A-9C**. Targets included temperature sensitive interface regions caused by a high fraction of polar residues, HisCat clusters that weaken the dimer to form trimer at low pH, fixing UnderPacked defects to improve stability, and surface hydrophobics which can reduce aggregation and increase stability in solution. For example, the mutant IntFc2, comprising A259W and T262R mutations, had a $\Delta\Delta G_{\text{monomer/res}}$ score of -2.767 REU (methods as described in Example 1). Lower $\Delta\Delta G$ Scores indicated stabilizing mutations. Identified mutants, the mutations comprised therein, and the dimer affinity (nM K_D), protein unfolding (T_m), expression data (mg/L yield) and location of mutations are shown in **Table 2** and **FIG. 10**.

The Fusion Peptide (also referred to as the Fusion Loop) is an immunodominant epitope. Antibodies that target this region are poorly neutralizing and may lead to enhancement of disease. The fusion loop epitope is buried in the sRecE dimer, thus a stabilized dimer (e.g., comprising stabilizing mutations of the present invention) may prevent exposure of the fusion loop epitope, thereby not eliciting disease enhancing fusion loop antibodies during vaccination. For example, a stabilized E glycoprotein of the present invention, IntFc8, is stabilized in dimer conformation as compared to the WT sRecE and comprises a G106D mutation in the fusion loop. Mutating this position prevents binding of fusion loop binding antibodies, and this study shows that this mutation also helps with dimer stability, suggesting that this mutation may prevent elicitation of these disease enhancing antibodies in a vaccine application.

The quaternary epitopes as described in Example 1 are conserved in other flaviviruses such as ZIKV, as shown in **FIGS. 11** and **17A-17B**. To engineer disulfide interactions for the expression of stable ZIKV rE dimers, an A264C mutation was introduced into the EDII dimer interphase (**FIG. 12A**). Expression of stable dimers was confirmed by protein gel analysis

showing a protein band twice the size of the monomer (**FIG. 12B**). On ELISA, the stabilized dimer was shown to be bound by highly neutralizing antibodies that recognize epitopes of quaternary structure, including C8, C10, A9E, G9E, ZKA-230, and ZKA-230 (**FIG. 12C**).

To test *in vivo* efficacy, mice were primed and boosted on week 3 and week 9 with soluble rE monomer ("rEM") and rE dimer ("rED"), and ZIKV IgG levels and neutralizing antibody levels were analyzed at week 16 (**FIGS. 13A and 13B**). ZIKV rE dimers induced higher levels of IgG antibodies and the serum also had higher levels of neutralizing antibodies. rEM did not induce any neutralizing antibodies, while rED did, suggesting that the oligomeric state of the protein is important for the induction of neutralizing antibodies.

The percentage of antibodies that bind to EDIII was evaluated by performing EDIII serum depletion assays, as shown in **FIG. 14A**. ZIKV monomer induced a very EDIII-targeted response, while ZIKV dimer had a low percentage of EDIII binding antibodies. The dimer induced neutralizing activity of the mouse serum did not change when EDIII antibodies were depleted, in contrast to monomers plus alum, where the EDIII antibodies were mainly responsible for neutralization (**FIG. 14B**). A blockade of binding assay was used to show that dimer induced immune sera was able to block binding of ZIKV specific antibodies with a quaternary footprint, where monomers were unable to do so (**FIG. 14C**).

Sera from mice that were immunized with monomers or dimers were transferred to mice that were permissive to ZIKV infection. Mice that received monomer sera lost significant amounts of body weight and were not protected against ZIKV viral challenge, while mice that were inoculated with dimer induced mouse sera were able to protect (**FIG. 15A**). Similar studies performed with DENV2 also show that dimers induced higher levels of IgG and neutralizing antibodies than monomers (**FIG. 15B**).

EXAMPLE 3: Production of DENV VLPs without co-expression of pr, an antigen implicated in antibody dependent enhancement.

Current approaches for producing flavivirus VLPs require co-expression of full length prM to promote secretion from the cell and boost production yields. A downside of this approach is that pr is inefficiently cleaved from the particles and remains as a dominant epitope that elicits non-neutralizing antibodies implicated in antibody dependent enhancement. As shown in Example 1, by stabilizing the E dimer with the stabilizing mutations it was possible to create DENV VLPs without co-expression of pr. This strategy may result in particles that more closely resemble mature DENV and are safer to use as vaccines.

To establish the feasibility of producing DENV VLPs without pr, expression experiments were performed with four DENV2 constructs: (1) prM along with WT E, (2) M along with WT E, (3) prM along with the E protein stabilized with the mutations sets I8-U6-PM4, and (4) M along with the E protein stabilized with I8-U6-PM4 (**FIGS. 16A-16B**). The genes for the constructs were cloned into a mammalian expression vector (PaH) and transiently transfected into Expi293 cells. Following expression, low speed centrifugation was used to clear the culture media of the cells and the amount of E protein in the media was quantified with dot blot analysis and the DENV2 antibody 1M7. A dramatic boost in expression was observed with both VLP constructs containing the stabilizing mutations, while with WT E we were not able to detect any E protein in the case where pr was not included. To verify that the proteins were forming VLPs, sucrose gradient centrifugation was used to separate soluble protein from particles. Similar analysis was performed with the soluble E protein dimer for comparison. Dot blot analysis of the fractions collected from the sucrose gradient showed that while soluble E remained at the top of the sucrose gradient, the stabilized E VLP construct without pr was present in similar sucrose fractions as commercial VLPs (native antigen company) that was purchased for control experiments. The commercial VLPs were produced with the co-expression of pr. Negative stain EM confirmed that particles were being formed, which showed they are larger on average (about 35-40 nm versus about 25-30 nm) than the commercial VLPs produced using pr and WT E (**FIG. 16C**). Western blot analysis was used to characterize the amount of uncleaved prM on the commercial VLPs and found that in many cases more than 50% of the prM was uncleaved.

The foregoing is illustrative of the present invention, and is not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

All publications, patent applications, patents, nucleotide sequences, amino acid sequences, GenBank accession numbers and other references cited herein are incorporated by reference in their entireties for the teachings relevant to the sentence and/or paragraph in which the reference is presented.

Table 1

NanoDSF Analysis																														
DENV2 sE Variant Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis		Expression Analysis																			
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)														
WT	-	-	-	8.0	35.9	-	50.3	-	0.994	12958.6	-74.1	-67.1	-6.9	-	0.2	-														
Rosetta Design Variants																	HCat1 (H1)	DI/DIII Interface	R9V, T32V, H144Y, E368I	4	8.0	33.3	-4.1	52.2	2.0				0.3	1.5
																	HCat2 (H2)	DI/DIII Interface	R2M, E44M	2	4.0	34.0	-0.2	55.1	4.1				1.0	4.3
																	HCat3 (H3)	DI	H27P, T48I	2	8.0	35.9	0.0	53.8	3.6				0.2	0.9
																	HCat4 (H4)	Dimer Region 2	R2M, E44L, D154L, K246I	4	8.0									
																	HCat5	Dimer	R2M,	7										

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis				Dimer Dissociation (T _m ¹) Van't Hoff Analysis						Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
(H5)	Region 2	H27P, E44M, T48I, D154M, H244Q, K246Y														
HCat6 (H6)	Dimer Region 3	K204F, W206F, H261L	3													
HCat7 (H7)	Dimer Region 3	K204F, V251F, H261F	3													
HCat8 (H8)	Dimer Region 3	K204F, H261L	2													
IntFc1 (I1)	Dimer Region 3	A259V, T262H	2	4.0	38.4	4.2	50.2	-0.8	0.998	2042.7	-93.9	-85.8	-8.1	-1.1	0.2	0.9
IntFc2 (I2)	Dimer Region 3	A259W, T262R	2	4.0	45.6	11.4	52.9	1.8	0.943	8.0	-147.3	135.8	-11.5	-4.6	0.9	3.8
IntFc3 (I3)	Dimer Region 3	A259V, T262R	3	4.0	43.4	9.2	51.6	0.6	0.958	191.0	-96.2	-86.7	-9.5	-2.6	0.3	1.3

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
		A263W														
IntFc4 (I4)	Dimer Region 3	A259W, T262Y, A263L	3													
IntFc5 (I5)	Dimer Region 3	T262R, A263W	2	4.0	40.0	5.8	51.3	0.3							0.3	1.1
IntFc6 (I6)	Dimer Region 2	N8L, S29Y, H244F	3												N.D	N.D
IntFc7 (I7)	Dimer Region 3	T262R	1	4.0	38.8	4.7	51.3	0.3	0.974	2162.7	-68.9	-60.8	-8.0	-1.1	0.5	1.9
IntFc8 (I8)	Dimer Region 1	G106D	1	4.0	42.9	8.7	51.8	0.8	0.948	219.3	-103.5	-94.1	-9.4	-2.5	4.6	19.1
PM1 (P1)	Dimer Region 1	M6L, Q316M	2	4.0	28.5	-5.6	49.9	-1.1							0.1	0.3
PM2 (P2)	DI/DIII Interface & DI/DII Hinge	Q131I, Y299L	2												0.1	0.5
PM3	DI	A35M,	2	4.0	36.5	2.4	47.6	-3.4							0.1	0.4

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis				Dimer Dissociation (T _m ⁻¹) Van't Hoff Analysis			Expression Analysis					
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
(P3)		M289W														
PM4 (P4)	DI	S29K, T33V, A35M	3	4.0	34.5	0.3	62.4	11.4	0.989	11506.7	-72.5	-65.5	-7.0	-0.1	2.5	10.5
PM4.1	DI	A35M	1	4.0	35.0	0.8	52.5	1.5	0.995	9350.8	-79.8	-72.7	-7.1	-0.2	1.3	5.3
PM4.2	DI	T33V, A35M	2	4.0	34.5	0.4	57.9	6.9	0.997	10845.3	-78.5	-71.4	-7.0	-0.1	1.8	7.5
PM4.3	DI	S29K	1	4.0	34.9	0.8	55.6	4.6	0.998	9567.7	-81.0	-73.8	-7.1	-0.2	0.8	3.4
PM5 (P5)	DII	H209D, G266W	2	4.0	36.9	2.7	50.9	-0.1							0.1	0.4
PM6 (P6)	DIII	D375L, N390Q	2													
PM7 (P7)	DIII	G330A	1													
PM8 (P8)	DIII	Y377V, K393R	2													
UndPk1 (U1)	DI/DII Hinge	I270V, T280A	2													
UndPk2 (U2)	DI/DII Hinge	L198W	1													

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis				Dimer Dissociation (T _m ¹) Van't Hoff Analysis						Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
UndPk3 (U3)	DI/DII Hinge	L191Y, H209D	2													
UndPk4 (U4)	DI/DIII Interface	E13F, G14A, M34L	3	4.0	37.3	3.1	50.1	-0.9							0.1	0.5
UndPk5 (U5)	DI/DIII Interface	T359Y	1	4.0	36.2	2.0	51.0	-0.1							0.2	1.0
UndPk6 (U6)	DI/DII Hinge	F279W, T280P	2	4.0	42.9	8.7	56.9	5.9	0.998	238.2	-94.0	-84.6	-9.4	-2.5	5.4	22.5
UndPk6 (U6)	DI/DII Hinge	T280P	1	4.0	40.5	6.4	53.6	2.6	0.989	590.0	-103.1	-94.3	-8.8	-1.9	1.5	6.3
UndPk7 (U7)	DI/DII Hinge	T481L, L277M	2	4.0	31.0	-1.1	52.8	0.8							1.0	4.3
UndPk8 (U8)	Dimer Region 3	Q256Y, G258A, A259W, M260L	4	4.0	31.2	-4.7	53.9	3.6							0.2	0.9
SHP1 (S1)	DI & DIII	V15E, F373D, F392R	3	4.0	35.1	0.9	51.9	0.9							0.5	2.0

NanoDSF Analysis																	
DENV2 sE Variant Information				Melting Point Analysis				Dimer Dissociation (T _m ¹) Van't Hoff Analysis						Expression Analysis			
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)	
Disulfide	SHP2 (S2)	DI & DIII	V15E, W20H, F373D, F392R	4													
	Mnmer1 (M1)	Dimer Region 3	S255E	1													
	Mnmer2 (M2)	Dimer Region 3	G258E	1	4.0	N/A	51.2	0.2	N/A	N/A	N/A	N/A	N/A	N/A	0.2	0.7	
	Cm1 ^a	Dimer Region 3	A259C	1	4.0	N/A	51.0	0.0	N/A	N/A	N/A	N/A	N/A	N/A	B.D	B.D	
Combination (SC)	Cm2 ^b	Dimer Region 1	L107C, A313C	2													
	SC.1	DR 1 & 3, DI	I2-I8-P4	6	4.0	52.4	18.2	62.5	11.5	0.990	< 0.1	-150.3	135.6	-14.7	-7.8	12.5	51.8
	SC.2	DR 1 & 3, DI	I2-I8-P4-H3	8	4.0	52.1	17.9	65.2	14.2	0.996	< 0.1	-149.0	134.5	-14.5	-7.6	13.5	56.0
	SC.3	DR 1 & 3,	I2-I8-U4-U5-U6-P5	11	4.0	53.8	19.7	59.0	8.0	0.993	< 0.1	-323.1	298.1	-24.3	-17.4	7.4	30.8

NanoDSF Analysis									
DENV2 sE Variant Information				Melting Point Analysis			Dimer Dissociation (T_m^{-1}) Van't Hoff Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μ M)	T_m^{-1} ($^{\circ}$ C) (Dimer Dissociation)	ΔT_m^{-1} ($^{\circ}$ C) (Var - WT)	T_m^{-2} ($^{\circ}$ C) (Protein Unfolding)	ΔT_m^{-2} ($^{\circ}$ C) (Var - WT)	Expression Analysis
SC.4	DI/DIII, DI/DII, DII	I2-I8-U4- U5-U6- P4-P5-H3	1 3	4.0	56.7	22.5	65.5	14.4	R ²
									Kd (nM) (at 37 $^{\circ}$ C)
									ΔH°_{bind} (kcal/mol)
									$T\Delta S^{\circ}_{bind}$ (kcal/mol*K) (at 37 $^{\circ}$ C)
									ΔG°_{bind} (kcal/mol)
									$\Delta\Delta G^{\circ}_{bind}$ (kcal/mol) (Var-WT)
SC.5	DR 1 & 3, DI/DIII, DI/DII	I2-I8-U4- U6	8	4.0	54.0	19.8	59.4	8.4	0.998
SC.6	DR 1 & 3, DI/DIII, DI	I2-I8-U5- P4	7	4.0	52.3	18.2	63.7	12.7	0.995
SC.7	DR 1 & 3, DI/DIII, DI/DII	I2-I8-U5- U6	6	4.0	54.2	20.1	59.3	8.3	0.986
									<0.1
									-299.7
									-133.2
									-276.5
									-20.0
									-13.1
									50.7
									12.2
									31.1
									48.7
									24.2

NanoDSF Analysis									
DENV2 sE Variant Information				Melting Point Analysis			Dimer Dissociation (T_m^{-1}) Van't Hoff Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μ M)	T_m^{-1} ($^{\circ}$ C) (Dimer Dissociation)	ΔT_m^{-1} ($^{\circ}$ C) (Var - WT)	T_m^{-2} ($^{\circ}$ C) (Protein Unfolding)	ΔT_m^{-2} ($^{\circ}$ C) (Var - WT)	Expression Analysis
SC.8	DR 1 & 3, DI/DIII, DI/DII, DI	I2-I8-U5- U6-P4	9	4.0	55.6	21.5	66.6	15.6	Yield (mg/L)
SC.9	DR 1 & 3, DI/DIII, DI/DII, DI, DIII	I2-I8-U5- U6-P4-S1	1 2	4.0	56.1	22.0	69.3	18.2	Yield Fold Change (Var/WT)
SC.10	DR 1 & 3, DI/DII	I2-I8-U6	5	4.0	53.9	19.8	59.3	8.3	12.8
SC.11	DR 1 & 3, DI/DII, DI	I2-I8-U6- H3	7	4.0	56.5	22.3	61.4	10.4	16.9
SC.12	DR 1 & 3, DI/DII,	I2-I8-U6- P4	8	4.0	55.3	21.2	65.9	14.9	14.3
									59.3
									44.7
									43.6

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis				Dimer Dissociation (T _m ¹) Van't Hoff Analysis						Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
	DI															
SC.13	DR 3, DI/DIII, DI/DII, DI	I2-U5- U6-P4	8	4.0	49.3	15.1	66.4	15.4	0.999	5.4	-107.2	-95.5	-11.7	-4.8	18.4	76.5
SC.14	DR 3, DI/DII	I2-U6	4	4.0	50.2	16.1	57.8	6.8	0.941	1.3	-125.9	-113.3	-12.6	-5.7	11.4	47.3
SC.15	DR 1, DI/DII	I8-U6	3	4.0	50.6	16.4	57.2	6.2	0.989	<0.1	-307.4	-286.9	-20.5	-13.5	13.4	55.7
SC.16	DR 3, DI/DII, DI	I2-U6-H3	6	4.0	53.8	19.7	60.1	9.1	0.978	<0.1	-1004.0	-944.6	-59.4	-52.5	10.1	41.8
SC.17	DR 3, DI/DII, DI	I2-U6-P4	7	4.0	48.7	14.5	66.4	15.4	0.998	11.8	-99.5	-88.2	-11.2	-4.3	15.1	62.8
SC.18	DR 1 & 3, DI/DII	I2-I8-U4- U6-P4	11	4.0	54.2	20.1	64.5	13.5	0.990	<0.1	-119.8	-105.9	-13.9	-7.0	12.1	50.3

NanoDSF Analysis																
DENV2 sE Variant Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
	DI/DIII, DI															
SC.19	DR 1, DI/DII, DI/DIII, DI	I8-U5-U6-P4	7	4.0	49.8	15.6	66.6	15.6	0.997	1.8	-120.7	-108.3	-12.4	-5.5	14.9	62.0
SC.20	DI/DIII, DI	P4-U4	6	4.0	33.4	-0.8	59.5	8.5	0.998	16137.4	-70.6	-63.8	-6.8	0.1	4.5	18.9
SC.21*	DI/DIII, DI/DII	U4-U5-U6	6	4.0	43.1	8.9	56.7	5.6	0.997	242.4	-91.3	-81.9	-9.4	-2.5	5.1	21.3
SC.22*	DI/DIII, DI/DII, DII	U4-U5-U6-P5	8	4.0	43.1	8.9	55.2	4.2	0.988	46.0	-146.2	-135.8	-10.4	-3.5	3.0	12.4
SC.23	DR 1 & 3	I2-I8	3	4.0	50.1	15.9	55.1	4.1	0.990	<	-490.9	-463.5	-27.4	-20.5	9.5	39.4
SC.24	DR 3, DI	M2-H3	3	4.0	N/A	N/A	55.4	4.4	N/A	N/A	N/A	N/A	N/A	N/A	0.9	3.7
SC.25	DR 3, DI	M2-P4	4	4.0	N/A	N/A	62.6	11.6	N/A	N/A	N/A	N/A	N/A	N/A	1.8	7.4
SC.26	DR 1 & 3, DI/DII	I3-I8-U6	6	4.0	53.1	18.9	58.7	7.7	0.999	<0.1	-320.5	-297.1	-23.4	-16.5	17.2	71.4

NanoDSF Analysis									
DENV2 sE Variant Information	Melting Point Analysis		Dimer Dissociation (T _m ⁻¹) Van't Hoff Analysis		Expression Analysis				
			Yield Fold Change (Var/WT)						
			Yield (mg/L)						
			ΔΔG° _{bind} (kcal/mol) (Var-WT)						
			ΔG° _{bind} (kcal/mol)						
			TΔS° _{bind} (kcal/mol*K) (at 37°C)		1	116.7			
	ΔH° _{bind} (kcal/mol)			-131.0					
	Kd (nM) (at 37°C)			<0.1					
	R ²			0.999					
			Yield Fold Change (Var/WT)		Yield (mg/L)	64.8			
ΔΔT _m ⁻² (°C) (Var - WT)									
T _m ⁻² (°C) (Protein Unfolding)									
ΔT _m ⁻¹ (°C) (Var - WT)									
T _m ⁻¹ (°C) (Dimer Dissociation)									
Concentration (μM)			4.0	2.0					
# of Mutations			9	5					
Mutations			I3-I8-U6-P4	P4-Cm2					
Region			DR 1 & 3, DI/DII, DI	DR1, DI					
Name			SC.27	SC.28					

Table 2

NanoDSF Analysis																
DENV/ZIKV sE Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
WT	-	-	-	4.0	34.2	-	51.0	-	0.994	12958.6	-74.1	-67.1	-6.9	-	0.2	-
PM4 (P4)	DI	S29K, T33V, A35M	3	4.0	34.5	0.3	62.4	11.4	0.989	11506.7	-72.5	-65.5	-7.0	-0.1	2.5	10.5
IntFc2 (I2)	Dimer Region 3	A259W, T262R	2	4.0	45.6	11.4	52.9	1.8	0.943	8.0	-147.3	-135.8	-11.5	-4.6	0.9	3.8
IntFc8 (I8)	Dimer Region 1	G106D	1	4.0	42.9	8.7	51.8	0.8	0.948	219.3	-103.5	-94.1	-9.4	-2.5	4.6	19.1
UndPk6 (U6)	DI/DII Hinge	F279W, T280P	2	4.0	42.9	8.7	56.9	5.9	0.998	238.2	-94.0	-84.6	-9.4	-2.5	5.4	22.5
WT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N.D	N.D
PM4 (P4)	DI	S29K, T33V, A35M	3	4.0	44.9	-	66.0	-	-	-	-	-	-	-	0.2	-
DENV2																
DENV1																

NanoDSF Analysis																
DENV/ZIKV sE Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
IntFc2 (12)	Dimer Region ₃	A259W, S262R	2	1.0	N/A	-	56.5	-							0.01	-
IntFc8 (18)	Dimer Region ₁	G106D	1	1.0	N/A	-	57.2	-							0.01	-
UndPk6 (U6)	DI/DII Hinge	F279W, A280P	2												N.D	N.D
WT	-	-	-	4.0	<15	0.0	52.6								0.01	-
PM4 (P4)	DI	G29K, T33V, A35M	3	4.0	<15	0.0	64.8	12.2							2.9	287.2
IntFc2 (12)	Dimer Region ₃	A257W, T260R	2	4.0	42.1	27.1	54.1	1.5	0.999	772.0	-64.5	-55.8	-8.7	-	0.3	33.4
IntFc8 (18)	Dimer Region ₁	G106D	1	4.0	36.3	21.3	53.1	0.5	0.998	4843.0	-49.0	-41.4	-7.5	-	0.8	80.4
			DENV3													

NanoDSF Analysis				Expression Analysis	
DENV/ZIKV sE Information		Melting Point Analysis			Dimer Dissociation (T_m) Van't Hoff Analysis
		Concentration (μ M)	T_m^1 ($^{\circ}$ C) (Dimer Dissociation)	ΔT_m^1 ($^{\circ}$ C) (Var - WT)	T_m^2 ($^{\circ}$ C) (Protein Unfolding)
Dimer Dissociation (T_m) Van't Hoff Analysis		ΔT_m^2 ($^{\circ}$ C) (Var - WT)	R^2	Kd (nM) (at 37 $^{\circ}$ C)	ΔH°_{bind} (kcal/mol)
		ΔG°_{bind} (kcal/mol)	$T\Delta S^{\circ}_{bind}$ (kcal/mol*K) (at 37 $^{\circ}$ C)	ΔG°_{bind} (kcal/mol)	$\Delta\Delta G^{\circ}_{bind}$ (kcal/mol) (Var-WT)
Yield Fold Change (Var/WT)		Yield (mg/L)			
Name		Region	Mutations	# of Mutations	
UndPk6 (U6)	DI/DII Hinge	F277W, A278P	2		
UndPk6_DV2 Hingemut	DI/DII Hinge	F277W, A278P, S275L, M205L	4		
SC.10	DR 1,3 and DI/DII Hinge	I2-I8-U6	5		
SC.14	DR 3	I2-U6	4		
UndPk6.1	DI/DII Hinge	A278P	1		
HCat3	DR 2	H27P, T48I	2		
SC.12	DL, DI/DII Hinge, DR 1 &	I2-I8-U6-P4	8		

NanoDSF Analysis																
DENV/ZIKV sE Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
	3															
SC.29	DI, DI/DII Hinge, DR 1	I8-U6-P4	6	8.0	42.7	27.7	63.7	11.1							0.3	26.4
SC.16	DI/DII Hinge, DR 1,2	I2-U6-H3	6												0.1	12.0
SC.11	DI/DII Hinge, DR 1,2,3	I2-I8-U6-H3	7												0.4	38.1
SC.15	DI/DII Hinge, DR 1	I8-U6	3	8.0	45.5	30.5	54.0	1.4							0.3	31.3
SC.23	DR 1,3	I2-I8	3												0.3	33.1
SC.1	DR 1 & 3, DI	I2-I8-P4	6	8.0	55.1	40.1	64.5	11.9							1.6	158.2

NanoDSF Analysis																
DENV/ZIKV sE Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
WT	-	-	-	4.0	N/A	-	50.5	-	-	-	-	-	-	-	0.1	-
PM4	DI	G29K, T33V, A35M	3	4.0	N/A	-	60.7	10.1	-	-	-	-	-	-	0.2	1.4
IntFc2	Dimer Region 3	A259W, S262R	2	4.0	N/A	-	52.1	1.6	-	-	-	-	-	-	0.2	1.8
IntFc8	Dimer Region 1	G106D	1	4.0	N/A	-	50.8	0.2	-	-	-	-	-	-	1.9	13.5
UndPk6	DI/DII Hinge	F279W, A280P	2	4.0	N/A	-	50.1	-0.4	-	-	-	-	-	-	0.1	1.0
SC.12	DI, DI/DII Hinge, DR 1 & 3	I2-I8-U6-P4	8	4.0	N/A	-	62.7	12.2	-	-	-	-	-	-	2.2	15.7
UndPk6.1	DI/DII Hinge	A280P	1	4.0	N/A	-	53.3	2.8	-	-	-	-	-	-	0.5	3.5

NanoDSF Analysis																
DENV/ZIKV sE Information				Melting Point Analysis					Dimer Dissociation (T _m ¹) Van't Hoff Analysis					Expression Analysis		
Name	Region	Mutations	# of Mutations	Concentration (μM)	T _m ¹ (°C) (Dimer Dissociation)	ΔT _m ¹ (°C) (Var - WT)	T _m ² (°C) (Protein Unfolding)	ΔT _m ² (°C) (Var - WT)	R ²	Kd (nM) (at 37°C)	ΔH° _{bind} (kcal/mol)	TΔS° _{bind} (kcal/mol*K) (at 37°C)	ΔG° _{bind} (kcal/mol)	ΔΔG° _{bind} (kcal/mol) (Var-WT)	Yield (mg/L)	Yield Fold Change (Var/WT)
HCat3	DR 2	H27P, T48I	2	4.0	N/A	-	55.1	4.6							0.3	2.0
SC.1	DR 1 & 3, DI	I2-I8-P4	6	4.0	N/A	-	61.7	11.2							2.1	15.3
WT	-	-	-	2.0	N/A	-	45.1	-							0.03	-
PM4	DI	S29K, V33, A35M	3	2.0	N/A	-	52.1	7.0							6.8	214.8
IntFc2	Dimer Region 3	A264W, T267R	2	2.0	N/A	-	45.7	0.6							0.3	10.2
IntFc8	Dimer Region 1	G106D	1	2.0	N/A	-	48.7	3.7							0.1	1.8
ZIKV																

Key for Table 1 and Table 2:

N/A: Not applicable; no melting transition observed and no Van't Hoff fit obtained

B.D.: Below detection; insufficient 280nm absorbance to quantify concentration, protein band observed via SDS-PAGE analysis post purification at given scale

N.D.: No detection; unable to observe protein band via SDS-PAGE analysis post purification at given scale

Gray: not tested

DR 1: Dimer Region 1, FL Dimer Interface

DR 2: Dimer Region 2, DI and ij loop Dimer Interface

DR 3: Dimer Region 3, $\alpha\beta$ Helix Central Dimer Interface

Table 3

Amino Acid Residue	Abbreviation	
	Three-Letter Code	One-Letter Code (can be upper or lower case)
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid (Aspartate)	Asp	D
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid (Glutamate)	Glu	E
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

Table 4

Modified Amino Acid Residue	Abbreviation
Amino Acid Residue Derivatives	
2-Aminoadipic acid	Aad
3-Aminoadipic acid	bAad
beta-Alanine, beta-Aminopropionic acid	bAla
2-Aminobutyric acid	Abu
4-Aminobutyric acid, Piperidinic acid	4Abu
6-Aminocaproic acid	Acp
2-Aminoheptanoic acid	Ahe
2-Aminoisobutyric acid	Aib
3-Aminoisobutyric acid	bAib
2-Aminopimelic acid	Apm
t-butylalanine	t-BuA
Citrulline	Cit
Cyclohexylalanine	Cha
2,4-Diaminobutyric acid	Dbu
Desmosine	Des
2,2'-Diaminopimelic acid	Dpm
2,3-Diaminopropionic acid	Dpr
N-Ethylglycine	EtGly
N-Ethylasparagine	EtAsn
Homoarginine	hArg
Homocysteine	hCys
Homoserine	hSer
Hydroxylysine	Hyl
Allo-Hydroxylysine	aHyl
3-Hydroxyproline	3Hyp
4-Hydroxyproline	4Hyp
Isodesmosine	Ide
allo-Isoleucine	alle
Methionine sulfoxide	MSO
N-Methylglycine, sarcosine	MeGly
N-Methylisoleucine	MeIle
6-N-Methyllysine	MeLys
N-Methylvaline	MeVal
2-Naphthylalanine	2-Nal
Norvaline	Nva
Norleucine	Nle
Ornithine	Orn
4-Chlorophenylalanine	Phe(4-Cl)
2-Fluorophenylalanine	Phe(2-F)
3-Fluorophenylalanine	Phe(3-F)
4-Fluorophenylalanine	Phe(4-F)
Phenylglycine	Phg
Beta-2-thienylalanine	Thi

SEQUENCES

Human Serum Albumin Signal Sequence

(SEQ ID NO:1)

ATGAAGTGGGTAAACCTTTATTTCCCTTCTTTTTCTCTTTAGCTCGGCTTATTCC

Glycine-Serine Linker

(SEQ ID NO:2)

GGCAGCAGCGGCGGCAGC

MHC I-alpha Cytoplasmic and Transmembrane Domains

(SEQ ID NO:3)

GTAGGAATCATTGCGGGACTTGTTCTGCTCGGGGCCGTAATAACTGGAGCGGTCGTG
GCGGCTGTGATGTGGCGACGGAAAAGCAGTGATCGGAAGGGTGGTTCATATACCCA
AGCCGCTTCTAGCGATAGCGCACAAAGGATCAGATGTTTCTCTTACCGCATGTAAAGT
A

His Tag

(SEQ ID NO:4)

CATCACCACCATCATCACCATCAT

DENV2 WT sE

SEQ ID NO:5

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAG
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:6

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat1

SEQ ID NO:7

DNA

ATGAGGTGTATCGGCATGTCCAACGTGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGGTGACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCTACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAG
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCATTGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGC
CCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:8

Protein

MRCIGMSNVDFVEGVSGGSWWDIVLEHGSCVVTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVQPENLEYTIVITPYSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIIAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat2

SEQ ID NO:9

DNA

ATGATGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCATGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTG
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:10

Protein

MMCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFMLIKTEAKQPATLR
KYCIEAKLTNTTTESRCPTQGEPSSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIV
TCAMFRCKKNMEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEA
ELTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGS
NWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRL
VLGRLITVNPVTEKDSVNI EAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat3

SEQ ID NO:11

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCCCGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:12

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat4

SEQ ID NO:13

DNA

ATGATGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCCTGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTG
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATCTGACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTATCAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:14

Protein

MMCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFLLIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNLTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAIKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat5

SEQ ID NO:15

DNA

ATGATGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCCCGGAAGCTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCATGCTCATCAAGATCGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATATGACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCAGGCTTACAAGCAGGACGTGGTGGTGCTGGGCAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:16

Protein

MMCIGMSNRDFVEGVSGGSWWDIVLEPGSCVTTMAKNKPTLDFMLIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVQPENLEYTIVITPHSGEEHAVGNMTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPQAYKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat6

SEQ ID NO:17

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACTTCGCCTTTCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCC
TTGGCTGCCTGGCGCCGATACACAGGGCTCCA ACTGGATACAGAAAGAGACCCTC
GTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGCC
AAGAAGGCGCCATGCTGACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTCCACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:18

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENFAFLVHRQWFLDLPLPWLP GADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat7

SEQ ID NO:19

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACTTCGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGTTTCGTGCTGGGCAGC
CAAGAAGGCGCCATGTTACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:20

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENFAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVFLGSQEGAMFTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 HCat8

SEQ ID NO:21

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACTTCGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCTGACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:22

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENFAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc1

SEQ ID NO:23

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCTCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGGGCGAGC
CAAGAAGGCGTGATGCACCACGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCGAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:24

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGVMHHALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc2

SEQ ID NO:25

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:26

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc3

SEQ ID NO:27

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGTGATGCACCGGTGGCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:28

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGVMHRWLTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc4

SEQ ID NO:29

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCTATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCTGGATGCACTACCTCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:30

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHYLLTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc5

SEQ ID NO:31

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACCGGTGGCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:32

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHRWLTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc6

SEQ ID NO:33

DNA

ATGAGGTGTATCGGCATGTCCCTGAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGATACTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCTTCGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:34

Protein

MRCIGMSLRDFVEGVSGGSWWDIVLEHGYCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPFAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc7

SEQ ID NO:35

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:36

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHRALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 IntFc8

SEQ ID NO:37

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:38

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 Mnmer1

SEQ ID NO:39

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCGAA
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:40

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGEQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 Mnmer2

SEQ ID NO:41

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGAGGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:42

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM1

SEQ ID NO:43

DNA

ATGAGGTGTATCGGCCTGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACAATGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCG
ACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGT
GCTGGGCAGGCTCATCACCGTGAACCCATTGTCACAGAGAAAGACTCCCCCGTG
AACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGC
CCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:44

Protein

MRCIGLSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETMHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM2

SEQ ID NO:45

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGATCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCCTGTCCATGTGCACCGGAAAGTTCAAGGTGGTGAA
AGAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:46

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVIPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSLSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM3

SEQ ID NO:47

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGTGGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:48

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
WDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM4

SEQ ID NO:49

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:50

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM4.1

SEQ ID NO:51

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:52

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM4.2

SEQ ID NO:53

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:54

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTVMKKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM4.3

SEQ ID NO:55

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:56

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM5

SEQ ID NO:57

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCTGGGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:58

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTWATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM6

SEQ ID NO:59

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCCTGTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGCAGTGGTTCAAGAAG

SEQ ID NO:60

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFGLSYIIIGVEPGQLKLQWFKK

DENV2 PM7

SEQ ID NO:61

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGCCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:62

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDASPCIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 PM8

SEQ ID NO:63

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCTATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCGTGATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCGGAAG

SEQ ID NO:64

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSVIIIIGVEPGQLKLNWFRK

DENV2 SHP1

SEQ ID NO:65

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGAGAGCGGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCGACGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGAGAAAGAAG

SEQ ID NO:66

Protein

MRCIGMSNRDFVEGESGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPDGD SYIIIIGVEPGQLKLNWRKK

DENV2 SHP2

SEQ ID NO:67

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGAGAGCGGGCGGC
AGCCACGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTG
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCGACGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGCGGAAGAAG

SEQ ID NO:68

Protein

MRCIGMSNRDFVEGESGGSHVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPDGD SYIIIIGVEPGQLKLNWRKK

DENV2 UndPk1

SEQ ID NO:69

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGGTGCAGATGAGC
TCCGGCAACCTGCTGTTTCGCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:70

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEVQMSSGNLLFAGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk2

SEQ ID NO:71

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCTGGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCGAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:72

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVWLQMENKAWLVHRQWFLDLPLPWLPGADTQGS
NWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk3

SEQ ID NO:73

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGATACGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:74

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGYDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk4

SEQ ID NO:75

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGCTGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGAGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAACCTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:76

Protein

MRCIGMSNRDFVFAVSGGSWWDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKY
CIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLKRVH
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk5

SEQ ID NO:77

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTCTACGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:78

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk6

SEQ ID NO:79

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:80

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk6.1

SEQ ID NO:81

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTCCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:82

Protein

SMRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLR
KYCIEAKLTNTTTESRCPTQGEPSSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIV
TCAMFRCKKNMEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEA
ELTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGS
NWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFPGLKLCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSNVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk7

SEQ ID NO:83

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACATGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:84

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNMLFTGHLKCR
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSVNI EAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 UndPk8

SEQ ID NO:85

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCTATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
TACGAAGCCTGGCTGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:86

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSYEAWLHTALTGATEIQMSSGNLLFTGHLKCLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 Cm1

SEQ ID NO:87

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCTGTATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:88

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGCMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 Cm2

SEQ ID NO:89

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGATGTTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCTGTGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCG
ACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGT
GCTGGGCAGGCTCATCACCGTGAACCCATTGTCACAGAGAAAGACTCCCCCGTG
AACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGC
CCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:90

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGCFGKGGIVT
CAMFRCKKNMEGKVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLR
MDKLQLKGMSYSMCTGKFKVVKEICETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.1 (I2-I8-P4)

SEQ ID NO:91

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:92

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.2 (I2-I8-P4-H3)

SEQ ID NO:93

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCCCGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:94

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEPGKCVTVMMKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.3 (I2-I8-U4-U5-U6-P5)

SEQ ID NO:95

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGCTGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCTGGGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:96

Protein

MRCIGMSNRDFVFAVSGGSWWDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKY
CIEAKLTNTTTSRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCR
LRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKR
HVLGRLITVNPVYKDSPPVNEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.4 (I2-I8-U4-U5-U6-P4-P5-H3)

SEQ ID NO:97

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCCCGGAAAGTGCGTGACCGTGCTGATGAAAAA
CAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCACC
CTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGAT
GCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCTGGGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAAG

SEQ ID NO:98

Protein

MRCIGMSNRDFVFAVSGGSWWDIVLEPGKCVTVLMKNKPTLDFELIKIEAKQPATLRKY
CIEAKLTNTTTSRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCR
LRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKR
HVLGRLITVNPVIEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.5 (I2-I8-U4-U6)

SEQ ID NO:99

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGCTGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:100

Protein

MRCIGMSNRDFVFAVSGGSWWDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKY
CIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSVNI EAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.6 (I2-I8-U5-P4)

SEQ ID NO:101

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:102

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.7 (I2-I8-U5-U6)

SEQ ID NO:103

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCTCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCTCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTCTGGGCAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTCTACGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:104

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.8 (I2-I8-U5-U6-P4)

SEQ ID NO:105

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:106

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.9 (I2-I8-U5-U6-P4-S1)

SEQ ID NO:107

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGAGAGCGGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCGACGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGAGAAAGAAG

SEQ ID NO:108

Protein

MRCIGMSNRDFVEGESGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPDGD SYIII GVEPGQLKLNWRKK

DENV2 SC.10 (I2-I8-U6)

SEQ ID NO:109

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGCTGGGCAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:110

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSNVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.11 (I2-I8-U6-H3)

SEQ ID NO:111

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCCCGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:112

MRCIGMSNRDFVEGVSGGSWWDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.12 (I2-I8-U6-P4)

DNA

SEQ ID NO:113

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:114

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.13 (I2-U5-U6-P4)

DNA

SEQ ID NO:115

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:116

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.14 (I2-U6)

SEQ ID NO:117

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

SEQ ID NO:118

Protein

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSVNI EAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.15 (I8-U6)

DNA

SEQ ID NO:119

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:120

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.16 (I2-U6-H3)

DNA

SEQ ID NO:121

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCCCGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGCTGGGCAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:122

MRCIGMSNRDFVEGVSGGSWWDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.17 (I2-U6-P4)

DNA SEQ ID NO:123

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAACCTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:124

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEP SLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVVKIEAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.18 (I2-I8-U4-U6-P4)

DNA

SEQ ID NO:125

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTGCGCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGCTGATGAAAAA
CAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCACC
CTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGAT
GCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:126

MRCIGMSNRDFVFAVSGGSWWDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSVNI EAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.19 (I8-U5-U6-P4)

DNA

SEQ ID NO:127

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:128

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.20 (P4-U4)

DNA

SEQ ID NO:129

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTGCGCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGCTGATGAAAAA
CAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCACC
CTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGAT
GCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAACCTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTTCAACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:130

MRCIGMSNRDFVFAVSGGSWWDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.21 (U4-U5-U6)

DNA

SEQ ID NO:131

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGCTGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:132

MRCIGMSNRDFVFAVSGGSWWDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKY
CIEAKLTNTTTSRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.22 (U4-U5-U6-P5)

DNA

SEQ ID NO:133

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGTTTCGCCGTGAGCGGCGGCA
GCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGCTGGCGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGCCATGCACACAGCCCTGACCTGGGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCATTGTCTACGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:134

MRCIGMSNRDFVFAVSGGSWWDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKY
CIEAKLTNTTTSRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTC
AMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAEL
TGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTWATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVYEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.23 (I2-I8)

DNA

SEQ ID NO:135

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGTGCTGGGCAGC
CAAGAAGGCTGGATGCACCGGGGCCCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTTACCGGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:136

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.24 (M2-H3)

DNA

SEQ ID NO:137

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCCCGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGATCGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGC
CAAGAAGAGGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:138

MRCIGMSNRDFVEGVSGGSWWDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.25 (M2-P4)

SEQ ID NO:139

DNA

CATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGGAGTGAGCGGCGG
CAGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGGCTGGGGCAATGGATGCGGACTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTC AACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGAGGCCATGCACACAGCCCTGACCGGAGCTACCGAGATCCAGATGAGCT
CCGGCAACCTGCTGTTACACCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCT
GCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:140

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCLR
MDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHV
LGRLITVNPVTEKDSPVNIEAEPFPGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.26 (I3-I8-U6)

SEQ ID NO:141

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAGCTGCGTGACCACGATGGCGAAA
AACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCA
CCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAG
ATGCCCTACACAGGGCGAACCAGCCTCAACGAAGAGCAGGACAAGAGGTTTCGT
GTGCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGG
AAAAGGCGGCATCGTGACCTGCGCCATGTTTCAGGTGTAAAAAGAACATGGAAGGC
AAGGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCG
GAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGA
TCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGAC
AATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAG
ATGGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGC
CTTGGCTGCCTGGCGCCGATACACAGGGCTCCAACTGGATACAGAAAGAGACCCT
CGTCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGCTGGGCAGC
CAAGAAGGCGTGATGCACCGGTGGCTGACCGGAGCTACCGAGATCCAGATGAGC
TCCGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGC
TGCAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAA
GAAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGC
GACGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACG
TGCTGGGCAGGCTCATCACCGTGAACCCATTGTACAGAGAAAGACTCCCCCGT
GAACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAG
CCCGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:142

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.27 (I3-I8-U6-P4)

SEQ ID NO:143

DNA

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCGGC
AGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATGAAAA
ACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCCCGCCAC
CCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCGAGTCCAGA
TGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAGAGGTTCTGTGT
GCAAACACAGCATGGTGGACAGGGGCTGGGGCAATGGATGCGACCTCTTCGGAA
AAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAGAACATGGAAGGCAA
GGTGGTGCAGCCCGAAAATCTGGAGTATACCATCGTGATTACCCCCACAGCGGA
GAGGAGCACGCCGTGGGCAATGACACCGGCAAGCACGGCAAAGAGATTAAGATC
ACCCCCAGTCCTCCATTACCGAAGCTGAACTGACAGGCTACGGCACCGTGACAA
TGGAGTGTAGCCCCAGGACCGGACTGGATTTCAACGAGATGGTCCTGCTACAGAT
GGAGAACAAGGCCTGGCTCGTGACAGGCAATGGTTTCTGGATCTGCCTCTGCCT
TGGCTGCCTGGCGCCGATACACAGGGCTCCAAGTGGATACAGAAAGAGACCCTCG
TCACCTTCAAGAATCCCCATGCTAAGAAGCAGGACGTGGTGGTGGTGGGCGAGCCA
AGAAGGCGTGATGCACCGGTGGCTGACCGGAGCTACCGAGATCCAGATGAGCTC
CGGCAACCTGCTGTGGCCCGGCCATCTGAAATGTAGGCTGAGGATGGATAAGCTG
CAACTCAAAGGCATGTCCTACTCCATGTGCACCGGAAAGTTCAAGGTGGTGAAAG
AAATCGCCGAAACACAGCACGGCACCATCGTGATCAGGGTGCAGTATGAGGGCGA
CGGCTCCCCCTGTAAGATCCCCTTCGAAATCATGGACCTGGAAAAGAGGCACGTG
CTGGGCAGGCTCATCACCGTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGA
ACATCGAGGCCGAGCCTCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCC
CGGACAGCTCAAGCTGAACTGGTTCAAGAAG

Protein

SEQ ID NO:144

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRK
YCIEAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVT
CAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAE
LTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSN
WIQKETLVTFKNPHAKKQDVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCRL
RMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRH
VLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFKK

DENV2 SC.28 (P4-UM2)

DNA

SEQ ID NO:145

ATGAGGTGTATCGGCATGTCCAACAGGGACTTTGTGGAGGGAGTGAGCGGCG
GCAGCTGGGTGGACATTGTGCTGGAGCATGGAAAGTGCGTGACCGTGATGATG
AAAAACAAGCCCACCCTGGACTTCGAGCTCATCAAGACAGAGGCTAAACAGCC
CGCCACCCTCAGGAAGTACTGCATCGAGGCCAAGCTGACCAACACAACAACCG
AGTCCAGATGCCCTACACAGGGCGAACCCAGCCTCAACGAAGAGCAGGACAAG
AGGTTCTGTGTGCAAACACAGCATGGTGGACAGGGGGCTGGGGCAATGGATGCG
GATGTTTCGGAAAAGGCGGCATCGTGACCTGCGCCATGTTCAAGGTGTAAAAAG
AACATGGAAGGCAAGGTGGTGCAGCCCCGAAAATCTGGAGTATACCATCGTGAT
TACCCCCCACAGCGGAGAGGAGCACGCCGTGGGCAATGACACCGGCAAGCAC
GGCAAAGAGATTAAGATCACCCCCCAGTCCTCCATTACCGAAGCTGAACTGACA
GGCTACGGCACCGTGACAATGGAGTGTAGCCCCAGGACCGGACTGGATTTCAA
CGAGATGGTCCTGCTACAGATGGAGAACAAGGCCTGGCTCGTGACAGGCAAT
GGTTTCTGGATCTGCCTCTGCCTTGGCTGCCTGGCGCCGATACACAGGGCTCC
AACTGGATACAGAAAGAGACCCTCGTCACCTTCAAGAATCCCCATGCTAAGAAG
CAGGACGTGGTGGTGGTGGGCGAGCCAAGAAGGCGCCATGCACACAGCCCTGA
CCGGAGCTACCGAGATCCAGATGAGCTCCGGCAACCTGCTGTTACACCGGCCAT
CTGAAATGTAGGCTGAGGATGGATAAGCTGCAACTCAAAGGCATGTCCTACTCC
ATGTGCACCGGAAAAGTTCAAGGTGGTGAAGAAATCTGTGAAACACAGCACGG
CACCATCGTGATCAGGGTGCAGTATGAGGGCGACGGCTCCCCCTGTAAGATCC
CCTTCGAAATCATGGACCTGGAAAAGAGGCACGTGCTGGGCAGGCTCATCACC
GTGAACCCCATTTGTCACAGAGAAAGACTCCCCCGTGAACATCGAGGCCGAGCC
TCCCTTTGGCGACTCCTACATCATCATTGGCGTGGAGCCCCGGACAGCTCAAGC
TGAAGTGGTTCAAGAAG

Protein

SEQ ID NO:146

MRCIGMSNRDFVEGVSGGSWWDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATL
RKYCIEAKLTNTTTESRCPTQGEP SLNEEQDKRFVCKHSMVDRGWGNGCGCFGK
GGIVTCAMFRCKKNMEGKVVPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQ
SSITEAELTGYGTVTMECSPTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLP
GADTQGSNWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNL
LFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVKEICETQHGTIVIRVQYEGDGSPC
KIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEPFGDSYIIIGVEPGQLKLNWFK
K

DENV1 sE VV1

SEQ ID NO:147

MRCVGIGNRDFVEGLSGATWWDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKG
SLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTATITPQAP
TSEIQLTDYGALTLDLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAS
TSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAG
HLKCRLKMDKLTLLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPF
SSQDEKGVGTQNGRLITANPIVTDKEKPVNIEAEPFGEYSYIVVGAGEKALKLSWFKK

DENV1 sE PM4

SEQ ID NO:148

MRCVGIGNRDFVEGLSGATWWDVLEHGKCVTVMMKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKG
SLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTATITPQAP
TSEIQLTDYGALTLDLDCSPRTGLDFNEMVLLTMEKKSWLVHKQ
WFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTG
ATEIQTSGTTTIFAGHLKCRLKMDKLTLLKGMSYVMCTGSFKLEKEVAETQHGTVLV
QVKYEGTDAPCKIPFSSQDEKGVGTQNGRLITANPIVTDKEKPVNIEAEPFGEYSYIVV
GAGEKALKLSWFKK

DENV1 sE IntFc2

SEQ ID NO:149

MRCVGIGNRDFVEGLSGATWWDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKG
SLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTATITPQAP
TSEIQLTDYGALTLDLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAS
TSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGWMHRALTGATEIQTSGTTTIFAG
HLKCRLKMDKLTLLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPF
SSQDEKGVGTQNGRLITANPIVTDKEKPVNIEAEPFGEYSYIVVGAGEKALKLSWFKK

DENV1 sE IntFc8

SEQ ID NO:150

MRCVGIGNRDFVEGLSGATWWDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCDLFGKG
SLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTATITPQAP
TSEIQLTDYGALTLDLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAS
TSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAG
HLKCRLKMDKLTLLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPF
SSQDEKGVGTQNGRLITANPIVTDKEKPVNIEAEPFGEYSYIVVGAGEKALKLSWFKK

DENV1 sE UndPk6

SEQ ID NO:151

MRCVGIGNRDFVEGLSGATWWDVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKG
SLITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTATITPQAP
TSEIQLTDYGALTLDLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAS
TSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIWPG
HLKCRLKMDKLTLLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPF
SSQDEKGVGTQNGRLITANPIVTDKEKPVNIEAEPFGEYSYIVVGAGEKALKLSWFKK

DENV3 sE WT

SEQ ID NO:152

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE PM4

SEQ ID NO:153

MRCVGVGNRDFVEGLSGATWWDVVLEHGKCVTMMKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE IntFc2

SEQ ID NO:154

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAG
HLKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE IntFc8

SEQ ID NO:155

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE UndPk6

SEQ ID NO:156

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPG
HLKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGHTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE UndPk6 DV2Hingemut

SEQ ID NO:157

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTC AKFQCLESIEGKVVQH ENLKYTVIITVHTGDQH QVGN ETQGVTA EITPQAST
VEAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWLVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGT LIWPG
HLKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHN GR LITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.10 (I2-I8-U6)

SEQ ID NO:158

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTC AKFQCLESIEGKVVQH ENLKYTVIITVHTGDQH QVGN ETQGVTA EITPQAST
VEAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGT SIWPG
HLKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHN GR LITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.14 (I2-U6)

SEQ ID NO:159

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTC AKFQCLESIEGKVVQH ENLKYTVIITVHTGDQH QVGN ETQGVTA EITPQAST
VEAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGT SIWPG
HLKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHN GR LITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE UndPk6.1 (A278P)

SEQ ID NO:160

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTC AKFQCLESIEGKVVQH ENLKYTVIITVHTGDQH QVGN ETQGVTA EITPQAST
VEAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGT SIFPGH
LKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
EDGQGKAHN GR LITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE HCat3

SEQ ID NO:161

MRCVGVGNRDFVEGLSGATWWDVVLEPGGCVT TMAKNKPTLDIELQKIEATQLATL
RKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTC AKFQCLESIEGKVVQH ENLKYTVIITVHTGDQH QVGN ETQGVTA EITPQASTV
EAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGT SIFAGHL
KCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
DGQGKAHN GR LITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.12 (I2-I8-U6-P4)

SEQ ID NO:162

MRCVGVGNRDFVEGLSGATWWDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPG
HLKCRCLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGLRITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.29 (I8-U6-P4)

SEQ ID NO:163

MRCVGVGNRDFVEGLSGATWWDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPG
HLKCRCLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGLRITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.16 (I2-U6-H3)

SEQ ID NO:164

MRCVGVGNRDFVEGLSGATWWDVVLEPGGCVTMTMAKNKPTLDIELQKIEATQLATL
RKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGLRITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.11 (I2-I8-U6-H3)

SEQ ID NO:165

MRCVGVGNRDFVEGLSGATWWDVVLEPGGCVTMTMAKNKPTLDIELQKIEATQLATL
RKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
EDGQGKAHNGLRITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.15 (I8-U6)

SEQ ID NO:166

MRCVGVGNRDFVEGLSGATWWDVVLEHGGCVTMTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPG
HLKCRCLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGLRITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK

DENV3 sE SC.23 (I2-I8)

SEQ ID NO:167

MRCVGVGNRDFVEGLSGATWWDVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTC AKFQCLESIEGKV VQHENLKYTVIITVHTGDQH QVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAG
HLKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGLR LITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK

DENV3 sE SC.1 (I2-I8-P4)

SEQ ID NO:168

MRCVGVGNRDFVEGLSGATWWDVLEHGKCVTVMMKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTC AKFQCLESIEGKV VQHENLKYTVIITVHTGDQH QVGNETQGVTAETPQAST
VEAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATT
ETPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAG
HLKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFS
TEDGQGKAHNGLR LITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK

DENV4 sE WT

SEQ ID NO:169

MRCVGVGNRDFVEGVSGGAWWDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVP HAKRQDVTVLGSQEGAMHSALAGATEVDSGDGN
HMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEGAGA
PCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LH WFRK

DENV4 sE PM4

SEQ ID NO:170

MRCVGVGNRDFVEGVSGGAWWDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVP HAKRQDVTVLGSQEGAMHSALAGATEVDSGDGN
HMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEGAGA
PCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LH WFRK

DENV4 sE IntFc2

SEQ ID NO:171

MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRLAGATEVDSGDG
NHMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEGAG
APCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LHWFRK

DENV4 sE IntFc8

SEQ ID NO:172

MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCDLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGN
HMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEGAGA
PCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LHWFRK

DENV4 sE UndPk6

SEQ ID NO:173

MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGN
HMWPAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEGA
GAPCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LHWFRK

DENV4 sE SC.12 (I2-I8-U6-P4)

SEQ ID NO:174

MRCVGVGNRDFVEGVSGGAWDLVLEHGKCVTMMQKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCDLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWT
GADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRLAGATEVDSGDG
NHMWPAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVYEG
AGAPCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGN SALT
LHWFRK

DENV4 sE UndPk6.1 (A280P)

SEQ ID NO:175

MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTA
GADTSEVHWNYKERMVTFKVPFAKRQDVTVLGSQEGAMHSALAGATEVDSGDGN
HMFPGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKEYEGAGA
PCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLH
WFRK

DENV4 sE HCat3

SEQ ID NO:176

MRCVGVGNRDFVEGVSGGAWDLVLEPGGCVTTMAQGKPTLDFELTKITAKEVAL
LRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTA
ADTSEVHWNYKERMVTFKVPFAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKEYEGAGAP
CKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHW
FRK

DENV4 sE SC.1 (I2-I8-P4)

SEQ ID NO:177

MRCVGVGNRDFVEGVSGGAWDLVLEHGKCVTMMQKPTLDFELTKTTAKEVA
LLRTYCI EASISNITTATRCPTQGEPYLKEEQDQQYICRRDVDRGWGNGCDLFGK
GGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTAMITP
RSPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTA
GADTSEVHWNYKERMVTFKVPFAKRQDVTVLGSQEGWMHRLALAGATEVDSGDG
NHMFAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKEYEGAG
APCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTL
HWFRK

ZIKV sE WT

SEQ ID NO:178

IRCI GVSNRDFVEGMSGGTWWDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEV
RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVD RGWGNGCGLFGK
GSLVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAK
VEITPNSPRAEATLG GFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIP
LPWHAGADTGTPHWNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAE
MDGAKGRLSSGHLKCR LKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQY
AGTDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVI
GVGEKKITHHWHRSG

ZIKV sE PM4

SEQ ID NO:179

IRCIGVSNRDFVEGMSGGTWWDIVLEHGKCVTVMMQDKPTVDIELVTTTTSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCGLFGK
 GSLVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAK
 VEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIP
 LPWHAGADTGTPHWNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAE
 MDGAKGRLSSGHLKCRCLKMDKLRLKGVSYSLSCTAAFTFTKIPAETLHGTVTVEVQY
 AGTDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVI
 GVGEKKITHHWHRSG

ZIKV sE IntFc2

SEQ ID NO:180

IRCIGVSNRDFVEGMSGGTWWDIVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCGLFGK
 GSLVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAK
 VEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIP
 LPWHAGADTGTPHWNKEALVEFKDAHAKRQTVVVLGSQEGWWHRALAGALEAE
 MDGAKGRLSSGHLKCRCLKMDKLRLKGVSYSLSCTAAFTFTKIPAETLHGTVTVEVQY
 AGTDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVI
 GVGEKKITHHWHRSG

ZIKV sE IntFc8

SEQ ID NO:181

IRCIGVSNRDFVEGMSGGTWWDIVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEV
 RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCDLFGK
 GSLVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAK
 VEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIP
 LPWHAGADTGTPHWNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAE
 MDGAKGRLSSGHLKCRCLKMDKLRLKGVSYSLSCTAAFTFTKIPAETLHGTVTVEVQY
 AGTDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVI
 GVGEKKITHHWHRSG

Dengue Virus Serotype 2 (DENV2) Strain 16681

NCBI Reference: NC_001474

(SEQ ID NO:182)

>NP_056776.2:281-775 polyprotein [Dengue virus 2]

MRCIGMSNRDFVEGVSGGSWWDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
 AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
 MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGyGTVTMECS
 PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
 DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVK
 EIAETQHGTVIRVQYEGDGSPCKIPFEIMDLEKRHLVGLRLITVNPVITEKDSPVNIEAEP
 FGDSYIIIGVEPGQLKLNWFKKGSSIGQMFETTMRGAKRMAILGDTAWDFGSLGGVFTSIGK
 ALHQVFGAIYGAAFGSVSWTMKILIGVIITWIGMNSRSTSLSVTLVLVGIVTLYLGVMVQA

Dengue virus Serotype 1 (DENV1) Strain Western Pacific

GenBank Reference: AY145122.1

(SEQ ID NO:183)

>AAN06982.1:281-775 polyprotein precursor [Dengue virus 1]
 MRCVIGIGNRDFVEGLSGATWVDVVEHGGCVTTMAKDKPTLDIELLKTEVTNPVLRKLCIE
 AKISNTTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGSLLITCAKFKCVTK
 LEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLTDYGALTLDSCS
 PRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTSQETWNRQDLLVTFKTAHAKKQ
 EVVVLGSQEGAMHTALTGATEIQTS GTTTIFAGHLKCRLLKMDKLLTKGMSYVMCTGSFKLEK
 EVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTONGRILITANPIVTDKEKPVNIEAEPP
 FGESYIVVGAGEKALKLSWFKKGSSIGKMFEATARGARRMAILGDTAWDFGSIGGVFTSVGK
 LIHQIFGTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGMVTLYLGVMVQA

Dengue virus Serotype 3 (DENV3) Strain CH53489

GenBank Reference: AAB69126

(SEQ ID NO:184)

>AAB69126.2:281-773 polyprotein [Dengue virus 3]
 MRCVGVGNRDFVEGLSGATWVDVVEHGGCVTTMAKNKPTLDIELQKTEATQLATLRKLCIE
 GKITNITTTDSRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSLLVTCAKFQCLES
 IEGKVQHENLKYSVIVTVHTGDQHQVGNETQGVTAETITPQASTVEAILPEYGTGLGLECS
 PR TGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETPTWNRKELLVTFKNAHAKKQEV
 VVLGSQEGAMHTALTGATEIQNSGGTSIFAGHLKCRLLKMDKLELKGMSYAMCLNTFVLKKEV
 SETQHGTVLILIKVEYKGEDAPCKIPFSTEDGQGAHNGRLITANPVVTKKEEPVNIEAEPPFG
 ESNIVIGIGDKALKINWYKKGSSIGKMFEATARGARRMAILGDTAWDFGSVGGVLSLGLKMP
 HQIFGSAYTALFSGVSWIMKIGIGVLLTWIGLNSKNTSMSFSCIAIGIITLYLGAVVQA

Dengue virus Serotype 4 (DENV4) Strain TVP-376

GenBank Reference: AGS14893.1

(SEQ ID NO:185)

>AGS14893.1 polyprotein, partial [Dengue virus 4]
 MAYMIGQTGIQRTVFFVLMMLVAPSYGMRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMA
 QGKPTLDFELTKTTAKEVALLRTYICIEASISNITTATRCPTQGEPYLKKEEQDQYICRRD
 VV DRGWGNGCGLFGKGGVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHG
 VTAMITPRSPSVEVKLPDYGELTLDCEPRSGIDFNEMI LMKMKKTWLVHKQWFLDLPLPWT
 AGADTSEVHWNKYKERMVTFKVPFAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHL
 KCKVRMEKLRIKMSYTMCSGKFSIDKEMAETQHGTTVVVKVYEGAGAPCKVPIEIRDVNKE
 KVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNLSALT LHWFRKGSSIGKMFESTYR
 GAKRMAILGETAWDFGSVGGGLFTSLGKAVHQVFGSVYTTMFGGVSWMIRILIGFLVLWIGTN
 SRNTSMAMTCIAVGGITLFLGFTVQADMGCVVSWSGKELKCGSGIFVVDNVHTWTEQYKFQP

Zika Virus (ZIKV) Strain PF13/251013-18

(SEQ ID NO:186)

>ANN44857.1:291-795 polyprotein [Zika virus]
 IRCIGVSNRDFVEGMSGGTWVDVVEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMAS
 DSRCPQTQGEAYLDKQSDTQYVCKRTLVDRGWNGCGLFGKGSLLVTCAKFACSKKMTGKSIQ
 PENLEYRIM LSVHGSQHSGMIVNDTGHETDENRAKVEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNKH
 WLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDGA
 KGRLLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKI PAETLHGTVTVEVQYAGTDGPCKVPAQMAVDMQ
 TLTPVGRILITANPVITESTENSKMMLELDPPFGDSYIVIGVGEKKITHHWRSGSTIGKA
 FEATVRGAKR MAVLGDTAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLA
 LGGVLIIFLSTAVSAD

Yellow Fever Virus. Strain 17D

GenBank: X03700.1

(SEQ ID NO:187)

>AAR87742.1 protein E, partial [Yellow fever virus]
HGGTWVSATLEQDKCVTVMAPDKPSLDISLETVAIDRPAEVRKVCYNAVLTHVKINDKCPSTGEAHLAEE
NEGDNACKRTYSDRGWNGCGLFGKGSIVACAKFTCAKSMSLFEVDQTKIQYVIRAQLHVGAKQENWTTD
IKTLKFDALSGSQEVEFIGYGKATLECQVQTAVDFGNSYIAEMETESWIVDRQWAQDLTLPLWQSGSGGVW
REMHHLVEFEPHAATIRVLALGNQEGSLKTALTGAMRVTKDTNDNNLYKLHGHHVSCRVKLSALTCLKGT
SYKICTDKMFFVKNPTDTGHGTVVMQVKVSKGAPCRIPVIVADDLTAAINKGILVTNPIASTNDDEVL
EVNPPFGDSYIIIVGRGDSRLTYQWHKEGSSIGKLFQTQTMKGVRLAVMGDTAWDFSSAGGFFTSVGKGIH
TVFGSAFQGLFGGLNWITKVIMGAVLIWVGINTRNMTSMMSMILVGVIMMFLSLGVGADQGCAINFGKRE
LKCGDGIFIF

Japanese Encephalitis virus. Strain SA14-14-2

GenBank: QCZ42158.1

(SEQ ID NO:188)

>QCZ42158.1 polyprotein [Japanese encephalitis virus]
FNCLGMGNRDFIEGASGATWVDLVLEGDSCLTIMANNKPTLDVRMINIEASQLAEV
RSYCYHASVTDISTVARCPTTGEAHNEKRADSSYVCKQGFTDRGWNGCGFFGKGSIDTCAKFSCTSKAI
GRTIQPENIKYKVGIFVHGTTTSENHGNYSAQVVGASQAQAKFTVTPNAPSVALKLGDYGEVTLDCPRSG
NTEAFYVMTVGSKSFLVHREWFHDLALPWTSPSSATAWRNRELLMEFEGAHATKQSVVALGSQEGGLHHAL
AGAIVVEYSSSVMLTSGHLKCRCLKMDKLALKGTTYGMCTEKFSFAKNPVDTGHTVVIELSYSGSDGPCK
IPIVSVASLNDMTPVGRLVTNPFVATSSANSKVLVEMEPPFGDSYIVVGRGAKQINHHWHKAGSTLGKA
FSTTLKGAQRLAALGDTAWDFSGISGGVFNSIGRAVHQVFGGAFRTLFGGMSWITQGLMGALLLWMGVNAR
DRSIALAFLATGGVLVFLATNVHA

West Nile virus. Strain NY99

NCBI Reference: YP_001527880.1

(SEQ ID NO:189)

>YP_001527880.1 envelope protein [West Nile virus]
FNCLGMSNRDFLEGVSGATWVDLVLEGDSVCVTIMSKDKPTIDVKMMNMEANLAEVRSYCYLATVSDLS
KAACPTMGAEHNDKRAPAFVCRQGVVDRGWNGCGLFGKGSIDTCAKFACSTKAIGRTILKENIKYEVA
IFVHGPTTVESHGNYSTQVGATQAGRLSITPAAPSYTLKLGEYGEVTVDCPRSGIDTNAYYVMTVGTKT
FLVHREWFMDLNLPSWSSAGSTVWRNRETLMEFEEPHATKQSVIALGSQEGALHQAAGAI PVEFSSNTVK
LTSGHLKCRVKMEKLQKLGTTYGVCSKAFKFLGTPADTGHTVVLLELQYTGTDGPCKVPISSVASLNDLT
PVGRLVTNPNFVSVATANAKVLIELEPPFGDSYIVVGRGEQQINHHWHKSGSSIGKAFTTTLKGAQRLAA
LGDTAWDFGSVGGVFTSVGKAVHQVFGGAFRSLFGGMSWITQGLLGALLLWMGINARDRSIALTFLAVGG
VLLFLSVNVHA

Tick-borne encephalitis virus. Strain: Moscow B-4

NCBI Reference: 2022145A

(SEQ ID NO:189)

>prf||2022145A protein E
SRCTHLENRDFVTGTQGTTRVTLVLELGGCVTIIAEGKTSMDVWLDAIYQENPAKTREYCLHAKLSDTKV
AARCPTMGPATLAEHQQGTVCVRDQSDRGWNGCGLFGKGSIVACVKAACEAKKATGHVYDANKIVYT
VKVEPHTGDYVAANETHSGRKTASFTISSEKTIILTMGEYGDVSLLCRVASGVDLAQTVILELDKTVEHLP
TAWQVHRDWFNDLALPWKHEGAQNWNNAERLVEFGAPHAVKMDVYNLGDQTGVLLKALAGVPVAHIEGTK
YHLKSGHVTCEVGLEKLKMKGLTYTMCDDTKFTWKRAPTDSGHDTVVMVETFSGTKPCRI PVRVAHGSP
DVNVAMLITPNPTIENNGGGFIEMQLPPGDNI IYVGELSHQWFQKGSSIGRVFQKTKKGIERLTVIGEHA
WDFGSAGGFLSSIGKAVHTVLGGAFNSIFGGVVFLPKLLLGVALLAWLGLNMRNPTMSMSFLLAGGLVLAM
TLGVGA

Usutu virus. Strain: MB119/06

European Nucleotide Archive Reference: APT69982.1

(SEQ ID NO:190)

```
>APT69982.1 polyprotein [Usutu virus]
FNCLGMSNRDFLEGVSGATWVDVVLEGDSCITIMAKDKPTIDIKMMETEATNLAEVR
SYCYLATVSDVSTVSNCPPTTGEAHNPKRAEDTYVCKSGVTDRGWNGCGLFGKGSIDTCANFTCSLKAVG
RMIQPENVKYEVGIFIHGSTSSDTHGNYSSQLGASQAGRFTITPNSPAITVKMGDYGEISVECEPRNGLN
TEAYYIMSVGTKHFLVHREWFNDLALPWTSPASSNWRNREILLEFEEPHATKQSVVALGSQEGALHQALA
GAIPVSFSGSVKLTSGHLKCRVKMEKLTCLKGTTYSMCTEKFSFAKNPADTGHGTVVLELQYTGSDGPCKI
PISIVASLSDLTPIGRMVTANPYVASSEANAKVLVEMEPPFGDSYIVVGRGDKQINHHWHKAGSSIGKAF
ITTIKGAQRLAALGDTAWDFGSGGIFNSVGKAVHQVFGGAFRTLFGGMSWITQGLMGALLLWMGVNARD
RSIALVMLATGGVLLFLATNVHA
```

Powassan virus. Strain: Lineage I

Genbank Reference: AAL32154

(SEQ ID NO:191)

```
>AAL32154.1 polyprotein, partial [Powassan virus]
TRCTHLENRDFVTGVQGTTRVSLVLELGGCVTITAEGKPSIDVWLEDIFQESPAETREYCLHAKLSNTKV
EARCPTTGPATLPEEHQADMVCKRDQSDRGWNGHCGFFGKGSIVACAKFECEEEAKKAVGHVYDSTKITYV
VKAEPHTGDYQAANETNENRKTQFTVASEKVI LN LGDYGDVSLTCKVASGIDVAQTVMVSLGSSKDHL P
SAWQVHRDWFEDLALPWKHKDNQDWNIVEKLVEFGPPHAVKMDIFNLGDQTAVLLKSLAGVPLASVDNQK
YHLKSGHVTCDVGLEKLKLKGTTYSMCDKTKFKWKRVPVDSGHDTVMEVSYTGSDKPCRI PVRAVAHGV
PTTNVAMLITPNPTIETSGGGFIEMQLPLGDNI IYVGDL SQQWFQKGSTIGRMFEKTRKGLERLSVVEH
AWDFGSGGILSSVGKAIHTVLGGAFNTLFGGVGFIPKMLLGVALVWLGLNARNPTMSMTFLAVGALTLM
MTMGVGA
```

What is claimed is:

1. A stabilized recombinant flavivirus E glycoprotein, comprising a flavivirus E glycoprotein backbone; and one or more amino acid substitution selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any combination thereof, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**.
2. The stabilized recombinant flavivirus virus E glycoprotein of claim 1, wherein the flavivirus E glycoprotein backbone comprises a backbone of a dengue virus (DENV), Zika virus (ZIKV), yellow fever virus (YFV), Japanese encephalitis virus (JEV), West Nile virus (WNV), Tick-borne Encephalitis virus (TBEV), Powassan virus, Usutu virus, or any combination thereof.
3. The stabilized recombinant flavivirus virus E glycoprotein of claim 2, wherein the flavivirus E glycoprotein backbone comprises a dengue virus backbone.
4. The stabilized recombinant flavivirus virus E glycoprotein of claim 2, wherein the flavivirus E glycoprotein backbone comprises a Zika virus (ZIKV) backbone.
5. The stabilized recombinant flavivirus E glycoprotein of any one of claims 1-4, wherein the E glycoprotein backbone comprises a soluble E glycoprotein ectodomain of domains DI, DII, and DIII.
6. The stabilized recombinant flavivirus E glycoprotein of any one of claims 1-5, wherein the E glycoprotein comprises at least one quaternary epitope.
7. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: R2M and E44M.

8. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3 or 5-7, comprising the amino acid sequence:

MMCI GMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFMLIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:10)

9. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H27P and T48I.

10. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 9, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:12)

11. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: R2M, E44L, D154L, and K246Y.

12. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 11, comprising the amino acid sequence:

MMCI GMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFLLIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNLTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAIKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:14)

13. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: K204F and H261L.

14. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 13, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENFAWLVRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHLVLRGLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:22)

15. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A259V and T262H.

16. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 15, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGVMHHALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHLVLRGLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:24)

17. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A259W and T262R.

18. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 17, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:26)

19. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A259W, T262Y, and A263L.

20. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 19, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:28)

21. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T262R and A263W .

22. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 21, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHRWLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:32)

23. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: N8L, S29Y, and H244F.

24. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 23, comprising the amino acid sequence:

MRCIGMSLRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPFAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:34)

25. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T262R.

26. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 25, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:36)

27. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D.

28. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 27, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:38)

29. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: M6L and Q316M.

30. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 29, comprising the amino acid sequence:

MRCIGLSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETMHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:44)

31. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: Q131I and Y299L.

32. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 31, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVIPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSLSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:46)

33. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A35M and M289W.

34. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 33, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRWDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:48)

35. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, and A35M.

36. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 34, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:50)

37. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A35M.

38. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 37, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:52)

39. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T33V and A35M.

40. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 39, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:54)

41. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K.

42. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 41, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:56)

43. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H209D and G266W.

44. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 43, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTWATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:58)

45. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: V15E, F373D, and F392R.

46. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 45, comprising the amino acid sequence:

MRCIGMSNRDFVEGESGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
DGDSYIIIGVEPGQLKLNWRKK (SEQ ID NO:66)

47. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, and M34L.

48. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 47, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:76)

49. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T359Y.

50. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 49, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:78)

51. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: F279W and T280P.

52. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 51, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:80)

53. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T280P.

54. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 53, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:82)

55. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: T48I and L277M.

56. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 54, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNMLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:84)

57. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: Q256Y, G258A, A259W, and M260L.

58. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 57, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSYEAWLHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:86)

59. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, A259W, and T262R.

60. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 59, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:92)

61. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H27P, S29K, T33V, A35M, T48I, G106D, A259W, and T262R.

62. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 61, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGKCVTVMMKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:94)

63. The stabilized recombinant flavivirus E glycoprotein any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, H209D, A259W, T262R, G266W, F279W, F280P, and T359Y.

64. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 63, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:96)

65. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, H27P, S29K, T33V, M34L, A35M, T48I, A259W, T262R, F279W, T280P, and T359Y.

66. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 65, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEPGKCVTVLMKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:98)

67. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, M34L, G106D, A259W, T262R, F279W, T280P.

68. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 67, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:100)

69. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, A259W, T262R, and T359Y.

70. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 69, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRVHLGRLITVNPPIVYEKDSPPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:102)

71. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D, A259W, T262R, F279W, T280P, and T359Y .

72. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 71, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:104)

73. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, A259W, T262R, F279W, T280P, and T359Y.

74. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 73, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:106)

75. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: V15E, S29K, T33V, A35M, G106D, A259W, T262R, F279W, T280P, T359Y, F373D, and F392R.

76. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 75, comprising the amino acid sequence:

MRCIGMSNRDFVEGESGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDSPVNIEAEP
DGDSYIIIGVEPGQLKLNWRKK (SEQ ID NO:108)

77. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D, A259W, T262R, F279W, and T280P.

78. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 75, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:110)

79. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H27P, T48I, G106D, A259W, T262R, F279W, and T280P.

80. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 79, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:112)

81. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, A259W, T262R, F279W, and T280P.

82. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 81, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:114)

83. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, A259W, T262R, F279W, T280P, and T359Y.

84. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 83, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:116)

85. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A259W, T262R, F279W, and T280P.

86. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 85, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:118)

87. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D, F279W, and T280P.

88. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 87, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:120)

89. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H27P, T48I, A259W, T262R, F279W, and T280P.

90. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 89, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:122)

91. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, A259W, T262R, F279W, and T280P.

92. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 91, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:124)

93. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, S29K, T33V, M34L, A35M, G106D, A259W, T262R, F279W, and T280P.

94. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 93, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:126)

95. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, F279W, T280P, and T359Y.

96. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 95, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP IIVYEKDSPPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:128)

97. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, S29K, T33V, M34L, and A35M.

98. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 97, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGKCVTVLMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:130)

99. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence (**SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, M34L, F279W, T280P, and T359Y).

100. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 99, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VYEKDS PVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:132)

101. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: E13F, G14A, M34L, H209D, G266W, F279W, T280P, and T359Y.

102. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 101, comprising the amino acid sequence:

MRCIGMSNRDFVFAVSGGSWVDIVLEHGSCVTTLAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTWATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVYEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:134)

103. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D, A259W, and T262R .

104. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 103, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHRALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:136)

105. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: H27P, T48I, and G258E.

106. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 105, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFELIKIEAKQPATLRKYCIE
AKLTNTTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:138)

107. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, and G258E.

108. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 107, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:140)

109. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G106D, A259V, T262R, A263W, F279W, and T280P.

110. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 109, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEPF
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:142)

111. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, G106D, A259V, T262R, A263W, F279W, and T280P.

112. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 111, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCDLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGVMHRWLTGATEIQMSSGNLLWPGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:144)

113. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S29K, T33V, A35M, L107C, and A313C.

114. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 113, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGKCVTVMMKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGCFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EICETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:146)

115. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: R9V, T32V, H144Y, and E368I.

116. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 115, comprising the amino acid sequence:

MRCIGMSNVDFVEGVSGGSWVDIVLEHGSCVVTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPYSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:8)

117. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: R2M, H27P, E44M, T48I, D154M, H244Q, and K246Y.

118. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 117, comprising the amino acid sequence:

MMCI GMSNRDFVEGVSGGSWVDIVLEPGSCVTTMAKNKPTLDFMLIKIEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNMTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPQAYKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:16)

119. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: K204F, W206F, and H261L.

120. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 119, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENFAFLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEGAMLTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNP I VTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:18)

121. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: K204F, W251F, and H261F.

122. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 121, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENFAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVFVLGSQEGAMFTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:20)

123. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: A259W, T262Y, and A263L.

124. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 123, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGWMHYLLTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:30)

125. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: D375L and N390Q.

126. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 125, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGLSYIIIGVEPGQLKLQWFKK (SEQ ID NO:60)

127. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G330A.

128. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 127, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDASPCIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:62)

129. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: Y377V and K393R.

130. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 129, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSVIIIGVEPGQLKLNWFRK (SEQ ID NO:64)

131. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: I270V and T280A.

132. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 131, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEVQMSSGNLLFAGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:70)

133. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: L198W.

134. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 133, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVWLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:72)

135. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: L191Y and H209D.

136. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 135, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGYDFNEMVLLQMENKAWLVDRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:74)

137. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: V15E, W20H, F373D, and F392R.

138. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 137, comprising the amino acid sequence:

MRCIGMSNRDFVEGESGGSHVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVT FKNPHAKKQ
DVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCLRLMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
DGDSYIIIGVEPGQLKLNWRKK (SEQ ID NO:68)

139. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:147**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 1 (DENV1) identified as **SEQ ID NO:147**: S29K, T33V, and A35M.

140. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 139, comprising the amino acid sequence:

MRCVGIGNRDFVEGLSGATWVDVVLEHGKCVTVMMKDKPTLDIELLKTEVTNPAV
LRKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGS
LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPT
SEIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGAST
SQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGH
LKCRCLKMDKLTCLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFS
SQDEKGVQTQNGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
(SEQ ID NO:148)

141. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:147**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 1 (DENV1) identified as **SEQ ID NO:147**: A259W and S262R.

142. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 141, comprising the amino acid sequence:

MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
RKLCIEAKISNTTDSRCPTQGEATLVEEQDTNFVCRRTFVDRGWGNGCGLFGKGS
LITCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTS
QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGWMHRALTGATEIQTSGTTTIFAGHL
KCRLKMDKLTCLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
QDEKGVQTQNGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
(SEQ ID NO:149)

143. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:147**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 1 (DENV1) identified as **SEQ ID NO:147**: G106D.

144. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 143, comprising the amino acid sequence:

MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
 RKLCIEAKISNTTTDSRCPTQGEATLVEEQDTNFCRRRTFVDRGWGNGCDLFGKGSLI
 TCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
 EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTS
 QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIFAGHL
 KCRLKMDKLTLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
 QDEKGVTONGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 (SEQ ID NO:150)

145. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:147**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 1 (DENV1) identified as **SEQ ID NO:147**: F279W and A280P.

146. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 145, comprising the amino acid sequence:

MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIELLKTEVTNPAVL
 RKLCIEAKISNTTTDSRCPTQGEATLVEEQDTNFCRRRTFVDRGWGNGCGLFGKGSLI
 TCAKFKCVTKLEGKIVQYENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTS
 EIQLTDYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPWTSGASTS
 QETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTALTGATEIQTSGTTTIWPGHL
 KCRLKMDKLTLKGMSYVMCTGSFKLEKEVAETQHGTVLVQVKYEGTDAPCKIPFSS
 QDEKGVTONGRLITANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKK
 (SEQ ID NO:151)

147. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 1 (DENV1) identified as **SEQ ID NO:152**: G29K, T33V, and A35M.

148. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 147, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKG
SLVTCAKFQCLESIEGKV VQHENLK YTVIITVHTGDQH QVGNETQGVTA EITPQASTV
EAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHG TILIKVEYKGEDAPCKIPFSTE
DGQGKAHN GRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
(SEQ ID NO:153)

149. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: A257W and T260R.

150. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 149, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTCAKFQCLESIEGKV VQHENLK YTVIITVHTGDQH QVGNETQGVTA EITPQASTV
EAILPEYGT LGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHG TILIKVEYKGEDAPCKIPFSTE
DGQGKAHN GRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
(SEQ ID NO:154)

151. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G106D.

152. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 151, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWNGCDLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
DGQGKAHNGLRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:155)

153. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: F277W and A278P.

154. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 153, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWNGCGLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
DGQGKAHNGLRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:156)

155. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: F277W, A278P, S275L, and M205L.

156. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 155, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWLVHRQWFFDLPLPWTSGATTET
PTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTLIWPGLK
CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTED
GQGKAHNGLRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:157)

157. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G106D, A257W, T260R, F277W, and A278P.

158. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 157, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
LKCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFST
EDGQGKAHNGLRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:158)

159. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: A257W, T260R, F277W, and A278P.

160. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 159, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
LKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHG TILIKVEYKGEDAPCKIPFST
EDGQGKAHNGLR LITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:159)

161. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: A278P.

162. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 161, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFPGHL
KCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHG TILIKVEYKGEDAPCKIPFSTE
DGQGKAHNGLR LITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:160)

163. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: H27P and T48I.

164. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 163, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTMAKNKPTLDIELQKIEATQLATL
 RKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSL
 VTCAKFQCLESIEGKV VQHENLKYTVIITVHTGDQHVGNETQGVTAETPQASTVE
 AILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
 TWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIFAGHLKC
 RLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTEDG
 QGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 (SEQ ID NO:161)

165. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G29K, T33V, A35M, G106D, A257W, T260R, F277W, and A278P.

166. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 165, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
 TLRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
 SLVTCAKFQCLESIEGKV VQHENLKYTVIITVHTGDQHVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGH
 LKCR LKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFST
 EDGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
 (SEQ ID NO:162)

167. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G29K, T33V, A35M, G106D, F277W, and A278P.

168. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 167, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCIEGKITNITDSRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
DQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:163)

169. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: H27P, T48I, A257W, T260R, F277W, and A278P.

170. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 169, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTMAKNKPTLDIELQKIEATQLATL
RKLCIEGKITNITDSRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCGLFGKGSL
VTCAKFQCLESIEGKVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTVE
AILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
TWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRAALTGATEIQNSGGTSIWPGHLK
CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTED
GQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
(SEQ ID NO:164)

171. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: H27P, T48I, G106D, A257W, T260R, F277W, and A278P.

172. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 171, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEPGGCVTMAKNKPTLDIELQKIEATQLATL
 RKLCLIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
 VTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTVE
 AILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTETP
 TWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIWPGHLK
 CRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTED
 GQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 (SEQ ID NO:165)

173. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G106D, F277W, and A278P.

174. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 173, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTMAKNKPTLDIELQKTEATQLAT
 LRKLCLIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
 LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
 EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
 TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGAMHTALTGATEIQNSGGTSIWPGHL
 KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTILIKVEYKGEDAPCKIPFSTE
 DGQGKAHNGRLITANPVVTKKEEPVNIEAEPPFGESNIVIGIGDKALKINWYKK
 (SEQ ID NO:166)

175. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G106D, A257W, and T260R.

176. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 175, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGGCVTTMAKNKPTLDIELQKTEATQLAT
LRKLCIEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKGS
LVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
DGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
(SEQ ID NO:167)

177. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:152**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 3 (DENV3) identified as **SEQ ID NO:152**: G29K, T33V, A35M, G106D, A257W, and T260R.

178. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 177, comprising the amino acid sequence:

MRCVGVGNRDFVEGLSGATWVDVVLEHGKCVTVMMKNKPTLDIELQKTEATQLA
TLRKLCEGKITNITTD SRCPTQGEAILPEEQDQNYVCKHTYVDRGWGNGCDLFGKG
SLVTCAKFQCLESIEGKVVQHENLKYTVIITVHTGDQHQVGNETQGVTAETPQASTV
EAILPEYGTGLGLECSPRTGLDFNEMILLTMKNKAWMVHRQWFFDLPLPWTSGATTE
TPTWNRKELLVTFKNAHAKKQEVVVLGSQEGWMHRALTGATEIQNSGGTSIFAGHL
KCRLKMDKLELKGMSYAMCLNTFVLKKEVSETQHGTLIKVEYKGEDAPCKIPFSTE
DGQGKAHNGRLITANPVVTKKEEPVNIEAEPFPGESNIVIGIGDKALKINWYKK
(SEQ ID NO:168)

179. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: G29K, T33V, and A35M.

180. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 179, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVALLR
TYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
CKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
RK (SEQ ID NO:170)

181. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: A259W and S262R.

182. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 181, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVALLR
TYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRALAGATEVDSGDGN
HMFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGA
PCKVPIEIRDVNKEKVVGRISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHW
FRK (SEQ ID NO:171)

183. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: G106D.

184. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 183, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVALLR
TYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCDLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
CKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
RK (SEQ ID NO:172)

185. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: F279W and A280P.

186. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 185, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVALLR
TYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MWPAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAG
APCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLH
WFRK (SEQ ID NO:173)

187. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: G29K, T33V, A35M, G106D, A259W, S262R, F279W, and A280P.

188. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 187, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVAL
LLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCDLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGWMHRALAGATEVDSGDGN
HMWPAGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGA
GAPCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTL
HWFRK (SEQ ID NO:174)

189. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: A280P.

190. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 189, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGGCVTTMAQGKPTLDFELTKTTAKEVAL
LLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNH
MFPGHLKCKVRMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAP
CKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWF
RK (SEQ ID NO:175)

191. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: H27P and T48I.

192. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 191, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEPGGCVTTMAQGKPTLDFELTKITAKEVAL
LRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCGLFGKGG
VVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPRSP
SVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAGA
DTSEVHWNYKERMVTFKVPFAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHM
FAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAPC
KVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFR
K (SEQ ID NO:176)

193. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, comprising the amino acid sequence **SEQ ID NO:169**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 4 (DENV4) identified as **SEQ ID NO:169**: G29K, T33V, A35M, G106D, A257W, and S262R.

194. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 193, comprising the amino acid sequence:

MRCVGVGNRDFVEGVSGGAWVDLVLEHGKCVTVMMQGKPTLDFELTKTTAKEVA
LLRTYCIEASISNITTATRCPTQGEPYLKEEQDQQYICRRDVVDRGWGNGCDLFGKG
GVVTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMITPR
SPSVEVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAG
ADTSEVHWNYKERMVTFKVPFAKRQDVTVLGSQEGWMHRLAGATEVDSGDGN
HMFAGHLKCKVRMEKLRKIGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGA
PCKVPIEIRDVNKEKVVGRIISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHW
FRK (SEQ ID NO:177)

195. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6, comprising the amino acid sequence **SEQ ID NO:178**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of Zika virus (ZIKV) identified as **SEQ ID NO:178**: S29K, V33, and A35M.

196. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6 or 195, comprising the amino acid sequence:

IRCI GVS NRDF VEGMSG GTWVDIV LEHGK CVTVMMQDKPTVDIELVTTTVSNMAEV
RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTL VDRGWGNGCGLFGKGS
LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEI
TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPW
HAGADTGTPHWNNEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDG
AKGRLSSGHLKCRLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGT
DGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVIGV
EKKITHHWHRSG (SEQ ID NO:179)

197. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6, comprising the amino acid sequence **SEQ ID NO:178**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of Zika virus (ZIKV) identified as **SEQ ID NO:178**: A264W and T267R.

198. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6 or 197, comprising the amino acid sequence:

IRCI GVS NRDF VEGMSG GTWVDIV LEHG GCVTVMAQDKPTVDIELVTTTVSNMAEV
RSYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTL VDRGWGNGCGLFGKGS
LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEI
TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPW
HAGADTGTPHWNNEALVEFKDAHAKRQTVVVLGSQEGWVHRALAGALEAEMD
GAKGRLSSGHLKCRLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAG
TDGPCKVPAQMAVDMQTLTPVGRLITANPVITESTENSKMMLELDPPFGDSYIVIGV
GEKKITHHWHRSG (SEQ ID NO:180)

199. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6, comprising the amino acid sequence **SEQ ID NO:178**, wherein said amino acid sequence comprises the following amino acid substitutions, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of Zika virus (ZIKV) identified as **SEQ ID NO:178**: G106D.

200. The stabilized recombinant flavivirus E glycoprotein of any one of claims 4-6 or 199, comprising the amino acid sequence:

IRCI GVS NRDFVEGMSGGTWVDIVLEHG GCVTVMAQDKPTVDIELVTTTVSNMAEV
RSYCYEASISDMA SD SRCPTQGEAYLDKQSDTQYVCKRTL VDRGWGNGCDLFGKGS
LVTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEI
TPNSPRAEATLG GFGSLGLDCEPRTGLDFSDLYYLT MNNKHWLVHKEWFHDIPLPW
HAGADTGTPHWNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDG
AKGRLSSGHLKCRLKMDKLRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGT
DGPCKVPAQMAVDMQTLTPVGR LITANPVITESTENSKMMLELDPPFGDSYIVIGVG
EKKITHHWHRSG (SEQ ID NO:181)

201. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: S255E.

202. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 201, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLN EEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQ MENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGEQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:40)

203. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, or 6, comprising the amino acid sequence **SEQ ID NO:6**, wherein said amino acid sequence comprises the following amino acid substitutions: G258E.

204. The stabilized recombinant flavivirus E glycoprotein of any one of claims 3, 5, 6, or 203, comprising the amino acid sequence:

MRCIGMSNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPATLRKYCIE
AKLTNTTTESRCPTQGEPSLN EEQDKRFVCKHSMVDRGWGNGCGLFGKGGIVTCAMFRCKKN
MEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSITEAELTGYGTVTMECS
PRTGLDFNEMVLLQ MENKAWLVHRQWFLDLPLPWLPGADTQGSNWIQKETLVTFKNPHAKKQ
DVVVLGSQEEAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVK
EIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEP
FGDSYIIIGVEPGQLKLNWFKK (SEQ ID NO:42)

205. A stabilized recombinant flavivirus E glycoprotein dimer comprising two flavivirus E glycoproteins of any one of claims 1-200.

206. The stabilized recombinant flavivirus E glycoprotein dimer of claim 205, wherein the dimer T_m^1 melting point of about 0.5 °C to about 45 °C higher than the T_m^1 melting point of a wildtype flavivirus E glycoprotein of the corresponding backbone.
207. The stabilized recombinant flavivirus E glycoprotein dimer of claim 205 or 206, wherein the dimer has a dimer affinity (K_d) of about 18 μ M or lower as measured at 37 °C.
208. A flavivirus particle or virus like particle (VLP) comprising the E glycoprotein of any of claims 1-204.
209. An isolated nucleic acid molecule encoding the E glycoprotein of any of claims 1-204.
210. An isolated nucleic acid molecule encoding the flavivirus particle or VLP of claim 208.
211. A population of flavivirus particles comprising the flavivirus particle of claim 208.
212. A composition comprising the E glycoprotein of any of claims 1-204, the E glycoprotein dimer of any one of claims 205-207, the flavivirus particle or VLP of claim 208, the nucleic acid molecule of claim 209 or 210, and/or the population of claim 211, in a pharmaceutically acceptable carrier.
213. A method of producing a virus like particle (VLP) comprising the E glycoprotein of any of claims 1-204, wherein the method does not comprise co-expression of pr.
214. A method of producing an immune response to a flavivirus in a subject, comprising administering to the subject an effective amount of the E glycoprotein of any of claims 1-204, the E glycoprotein dimer of any one of claims 205-207, the flavivirus particle or VLP of claim 208, the nucleic acid molecule of claim 209 or 210, the population of claim 211, the composition of claim 212 and any combination thereof.

215. A method of treating a flavivirus infection in a subject, comprising administering to the subject an effective amount of the E glycoprotein of any of claims 1-204, the E glycoprotein dimer of any one of claims 205-207, the flavivirus particle or VLP of claim 208, the nucleic acid molecule of claim 209 or 210, the population of claim 211, the composition of claim 212 and any combination thereof.

216. A method of preventing a disorder associated with a flavivirus infection in a subject, comprising administering to the subject an effective amount of the E glycoprotein of any of claims 1-204, the E glycoprotein dimer of any one of claims 205-207, the flavivirus particle or VLP of claim 208, the nucleic acid molecule of claims 209 or 210, the population of claim 211, and/or the composition of claim 212 and any combination thereof.

217. A method of protecting a subject from the effects of a flavivirus infection, comprising administering to the subject an effective amount of the E glycoprotein of any of claims 1-204, the E glycoprotein dimer of any one of claims 205-207, the flavivirus particle or VLP of claim 208, the nucleic acid molecule of claim 209 or 210, the population of claim 211, the composition of claim 212 and any combination thereof.

218. A method of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising:

a) administering a composition comprising the E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 to the subject in an amount effective to induce an antibody response to the E glycoprotein;

b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of step (a) above under conditions whereby neutralization of the flavivirus particles can be detected; and

c) detecting neutralization in step (b), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

219. A method of identifying the presence of a neutralizing antibody to a flavivirus in a biological sample from a subject, comprising:

a) contacting a biological sample from a subject that has been administered a E glycoprotein of any of claims 1-204 or a E glycoprotein dimer of any one of claims 205-207

with flavivirus particles comprising the E glycoprotein under conditions whereby neutralization of the flavivirus particles can be detected; and

b) detecting neutralization in step (a), thereby identifying the presence of a neutralizing antibody to the flavivirus in the biological sample from the subject.

220. A method of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising:

a) administering an immunogenic composition comprising the E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 to a subject in an amount effective to induce an antibody response to the E glycoprotein;

b) contacting a biological sample from the subject with flavivirus particles comprising the E glycoprotein of step (a) under conditions whereby neutralization of the flavivirus particles can be detected;

c) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and

d) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of (a).

221. A method of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, the method comprising:

a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising the E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 with flavivirus particles comprising the E glycoprotein under conditions whereby neutralization of the flavivirus particles can be detected;

b) determining if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of step (a); and

c) identifying the immunogenic composition as inducing a neutralizing antibody to the flavivirus in the subject if the biological sample comprises an antibody that neutralizes flavivirus particles comprising the E glycoprotein of (a).

222. A method of detecting an antibody to a flavivirus in a sample, comprising:
- a) contacting the sample with E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 under conditions whereby an antigen/antibody complex can form; and
 - b) detecting formation of an antigen/antibody complex, thereby detecting an antibody to the flavivirus in the sample.
223. A method of identifying an antibody to a flavivirus in a biological sample from a subject, comprising:
- a) administering a composition comprising E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 to the subject in an amount effective to induce an antibody response to the E glycoprotein;
 - b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and
 - c) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.
224. A method of identifying an antibody to a flavivirus in a biological sample from a subject, comprising:
- a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and
 - b) detecting formation of an antigen/antibody complex, thereby identifying an antibody to the flavivirus in the biological sample from the subject.
225. A method of identifying an immunogenic composition that induces an antibody to a flavivirus in a subject, the method comprising:
- a) contacting a biological sample from a subject that has been administered an immunogenic composition comprising the E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 with the E glycoprotein under conditions whereby an antigen/antibody complex can form; and
 - b) detecting formation of an antigen/antibody complex, thereby identifying an immunogenic composition that induces an antibody to the flavivirus in the subject.

226. A method of identifying an immunogenic composition that induces a neutralizing antibody to a flavivirus in a subject, comprising:

- a) administering an immunogenic composition comprising the E glycoprotein of any of claims 1-204 or the E glycoprotein dimer of any one of claims 205-207 to a subject in an amount effective to induce an antibody response to the E glycoprotein;
- b) contacting a biological sample from the subject with the E glycoprotein of (a) under conditions whereby an antigen/antibody complex can form; and
- c) detecting formation an antigen/antibody complex, thereby identifying an immunogenic composition that induces a neutralizing antibody to the flavivirus in the subject.

227. A method of producing a stabilized recombinant E glycoprotein of any one of claims 1-200, comprising:

introducing one or more amino acid substitution into a flavivirus E glycoprotein backbone, wherein the one or more amino acid substitution are selected from the group consisting of 2M, 6L, 8L, 9V, 13F, 14A, 15E, 27P, 29Y, 29K, 32V, 33V, 34L, 35M, 44M, 44L, 48I, 106D, 107C, 131I, 144Y, 154L, 154M, 191Y, 198W, 204F, 205L, 206F, 209D, 244Q, 244F, 246I, 246Y, 251F, 255E, 256Y, 258A, 258E, 259V, 259W, 259C, 260L, 261L, 261F, 262H, 262R, 262Y, 263W, 263L, 266W, 270V, 277M, 279W, 280A, 280P, 289W, 299L, 313C, 316M, 330A, 359Y, 373D, 375L, 377V, 386I, 390Q, 392R, 393R, and/or any combination thereof, wherein the numbering is based on the reference amino acid sequence of an E glycoprotein of dengue virus serotype 2 (DENV2) identified as **SEQ ID NO:6**, thereby stabilizing the flavivirus E glycoprotein into dimer conformation.

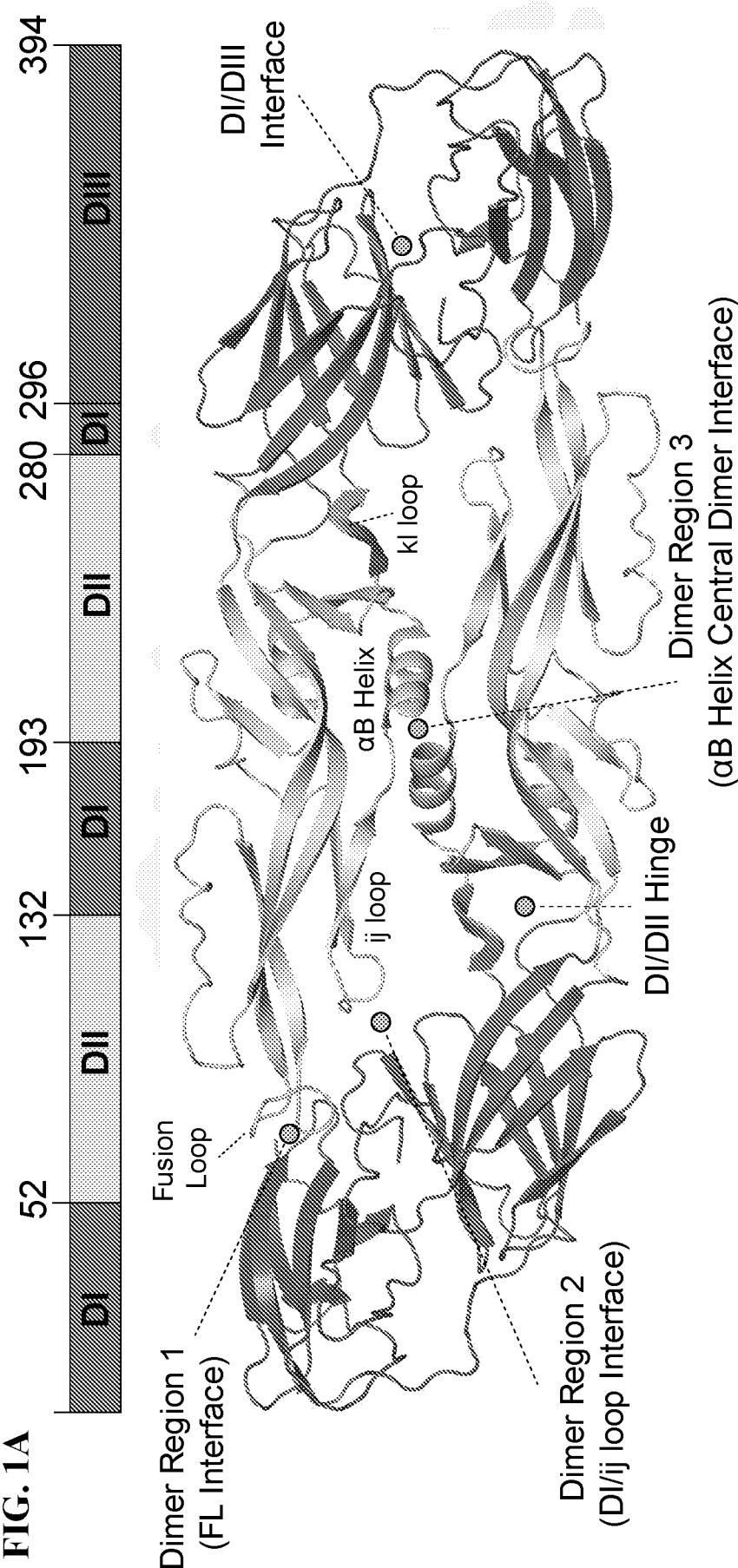


FIG 1B

DENV2 sE Stability Design Pipeline

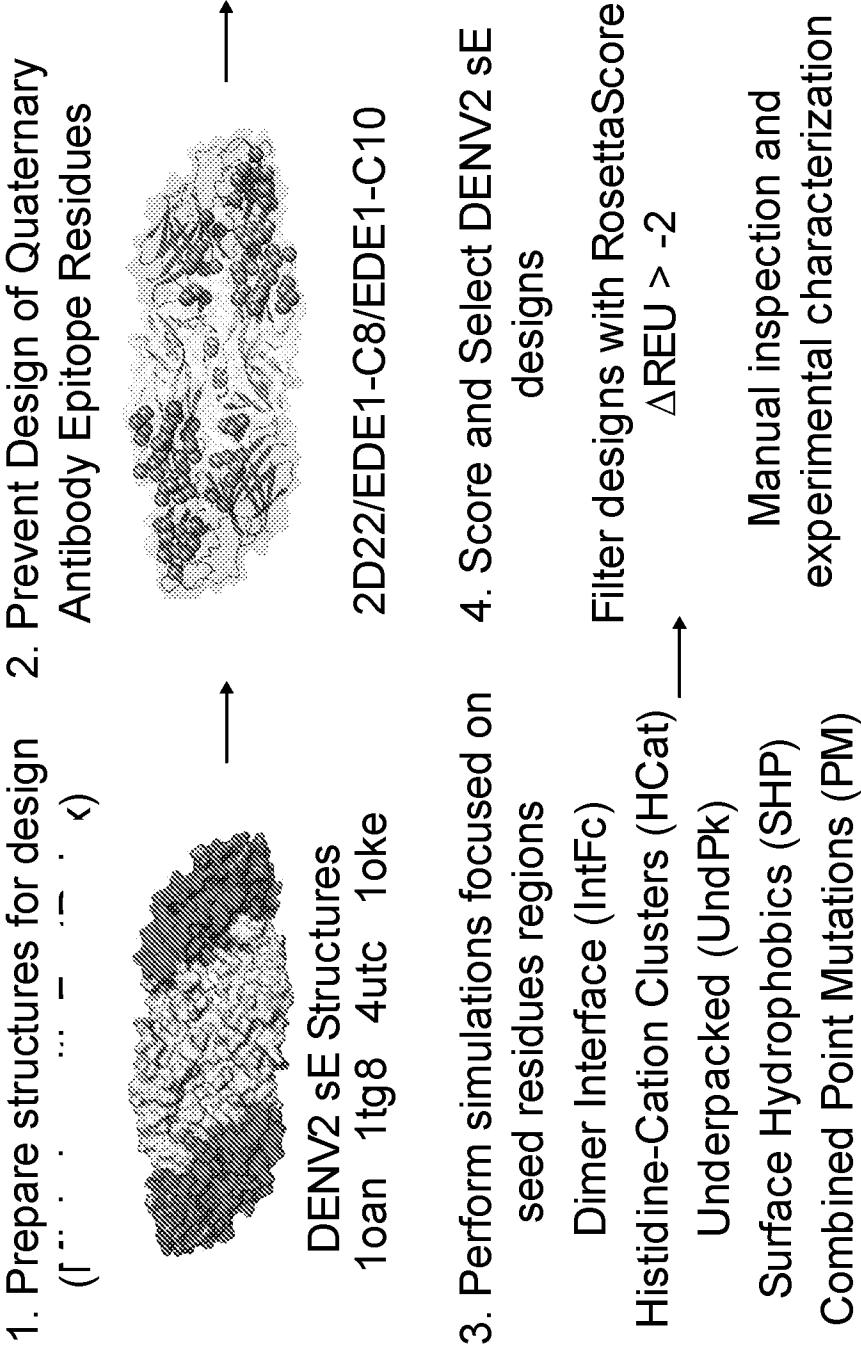


FIG. 1C

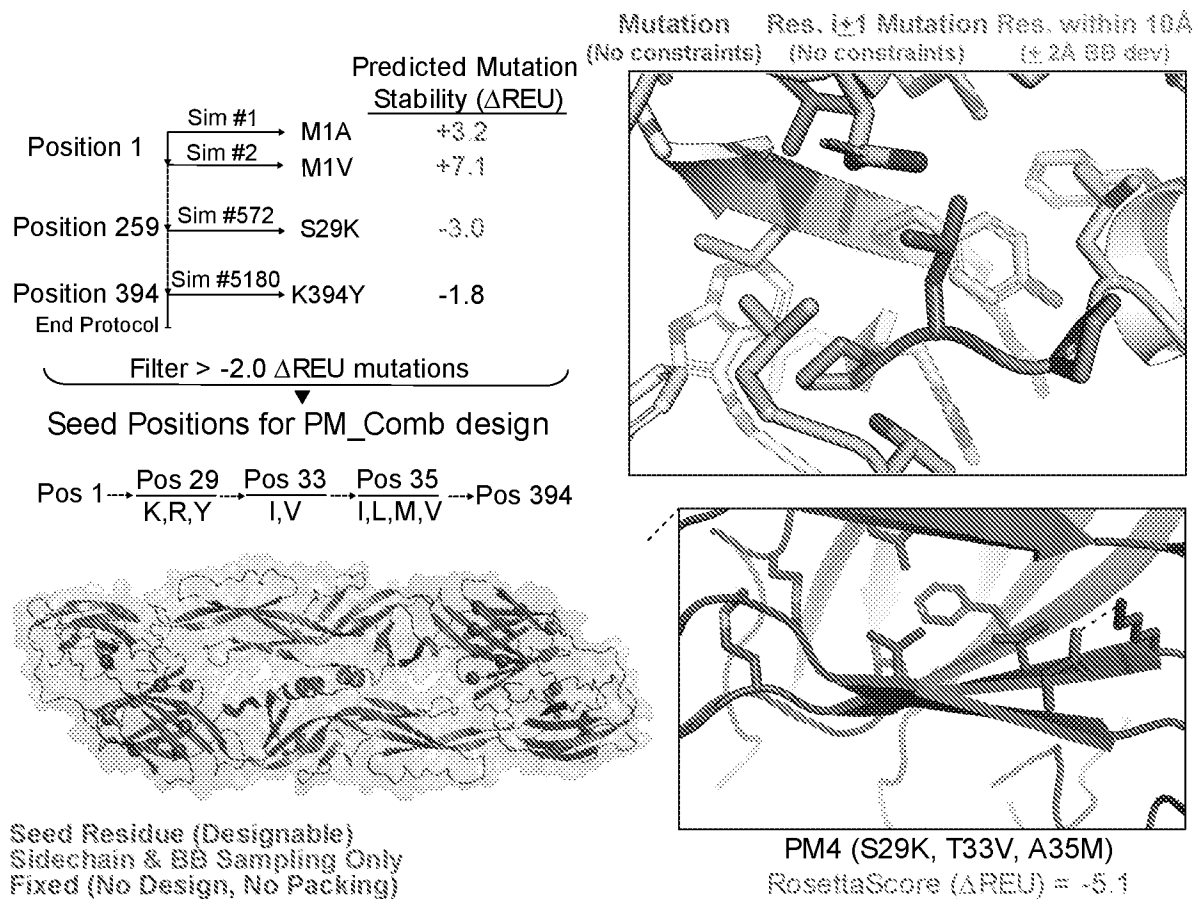
Site Saturation Mutagenesis and Combination
(PM_ssm and PM_Comb)

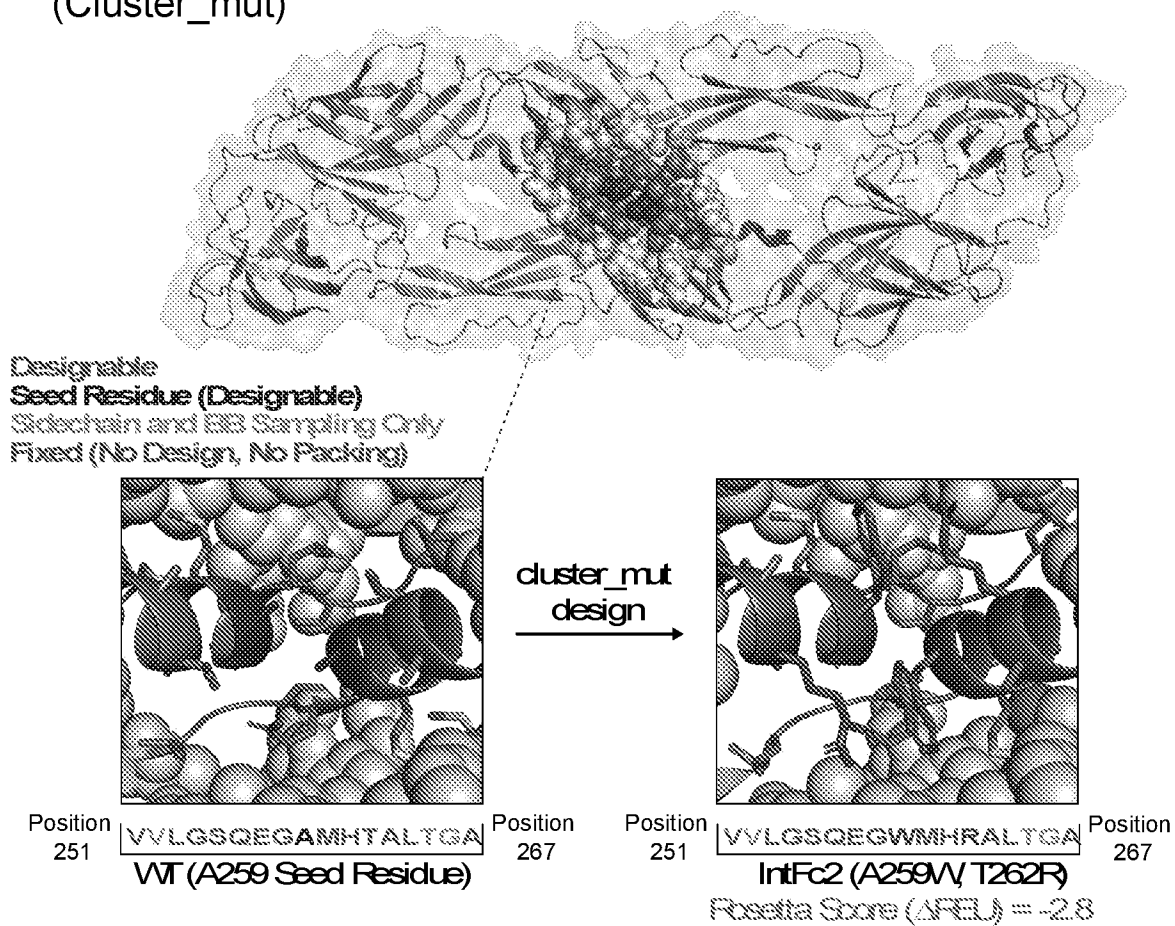
FIG. 1D**Clustered Mutations
(Cluster_mut)**

FIG. 1E

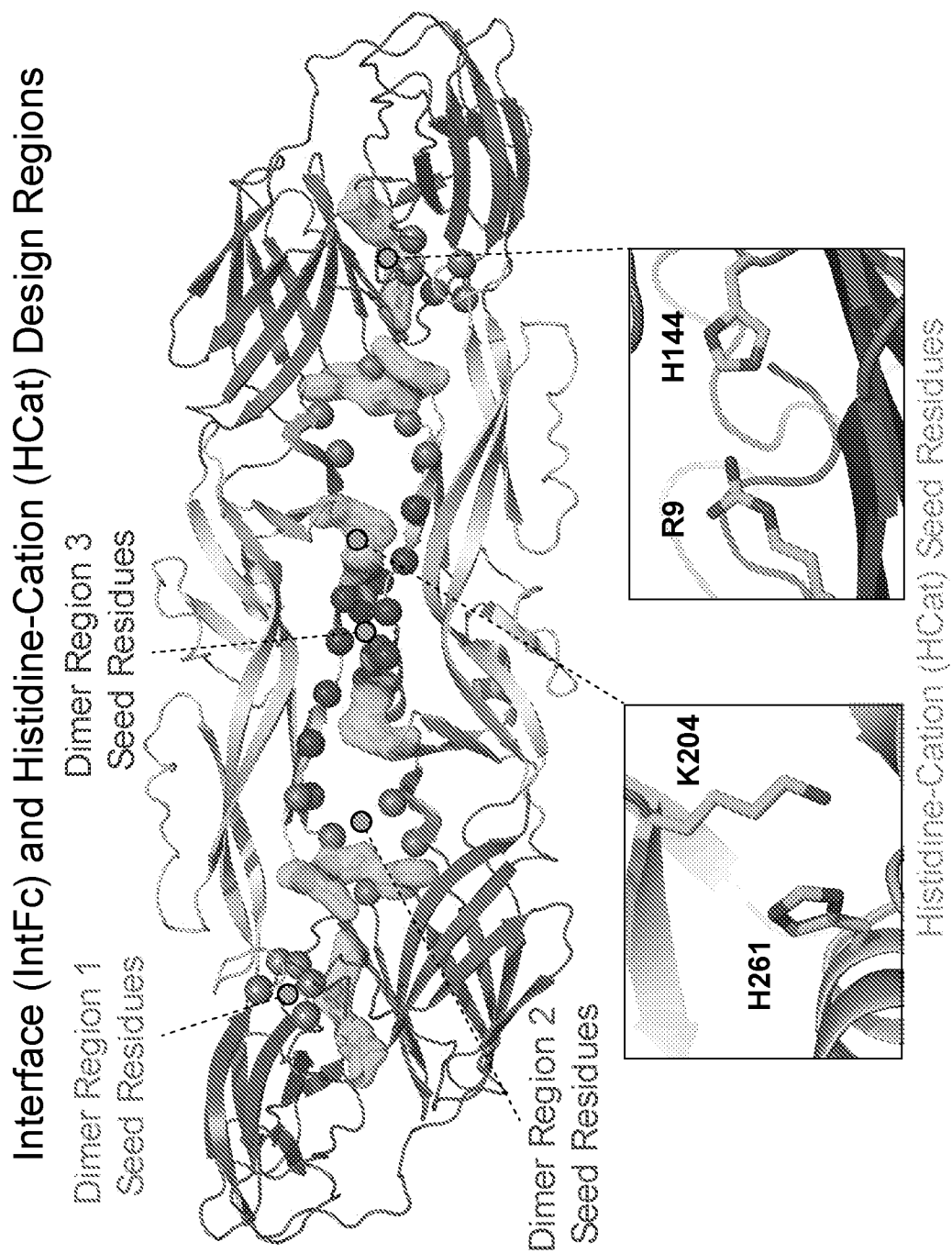


FIG. 1E cont.

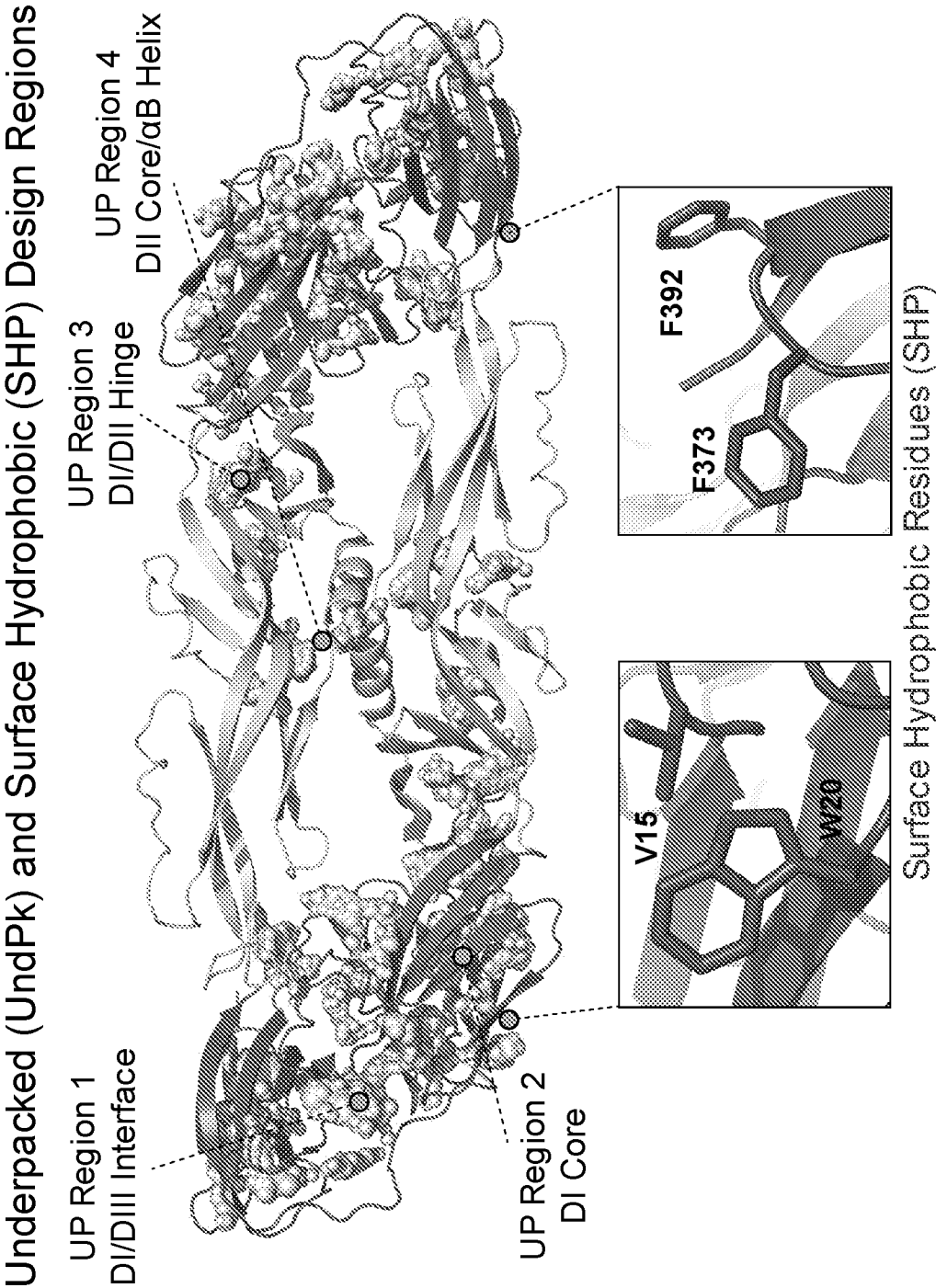
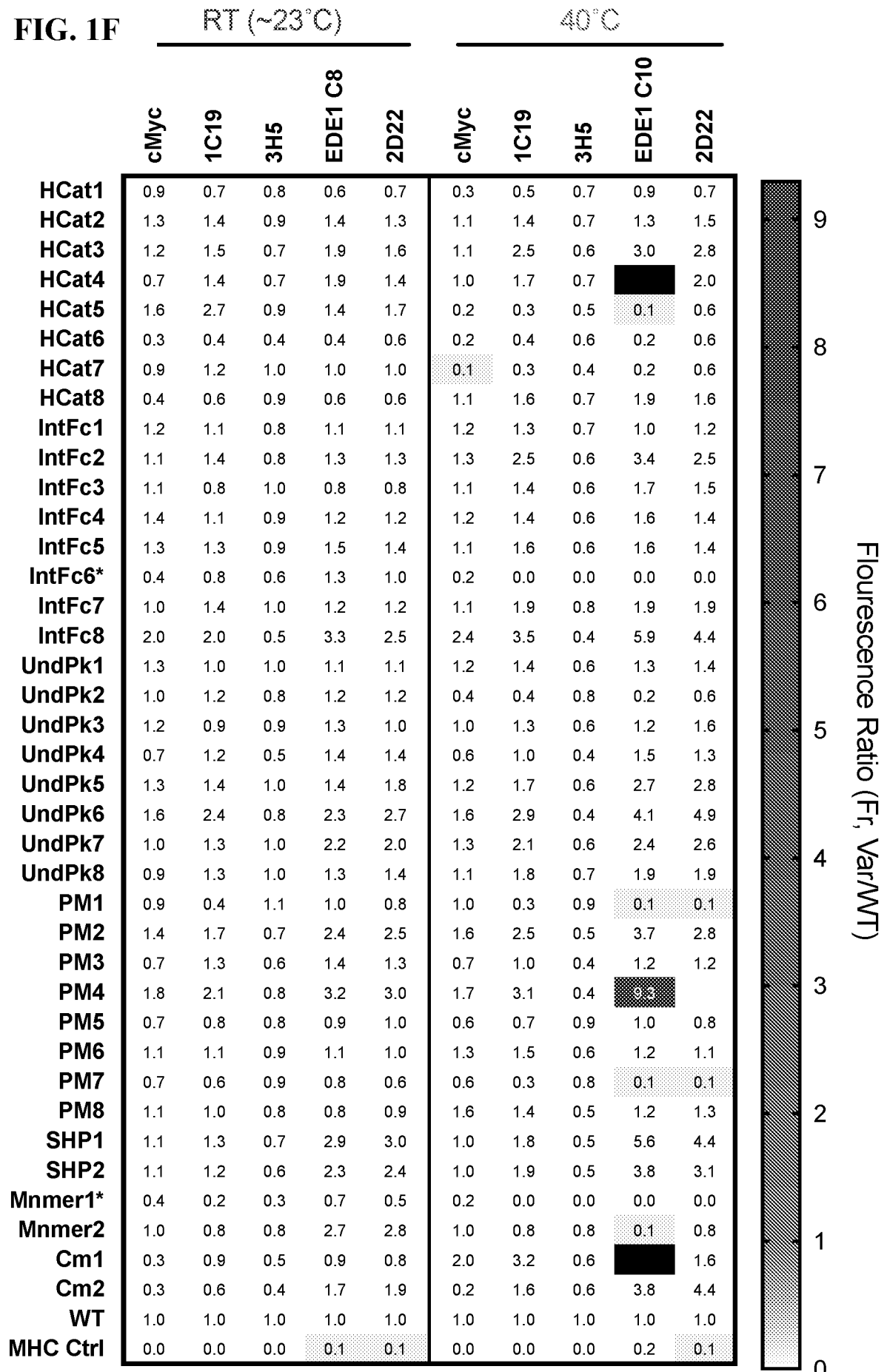


FIG. 1F



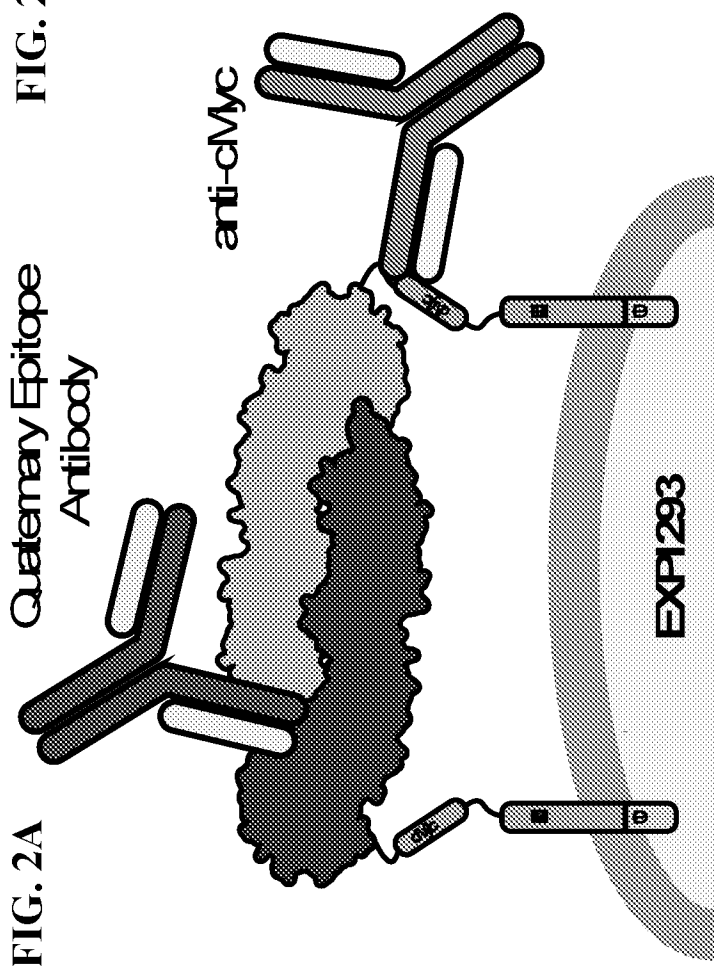
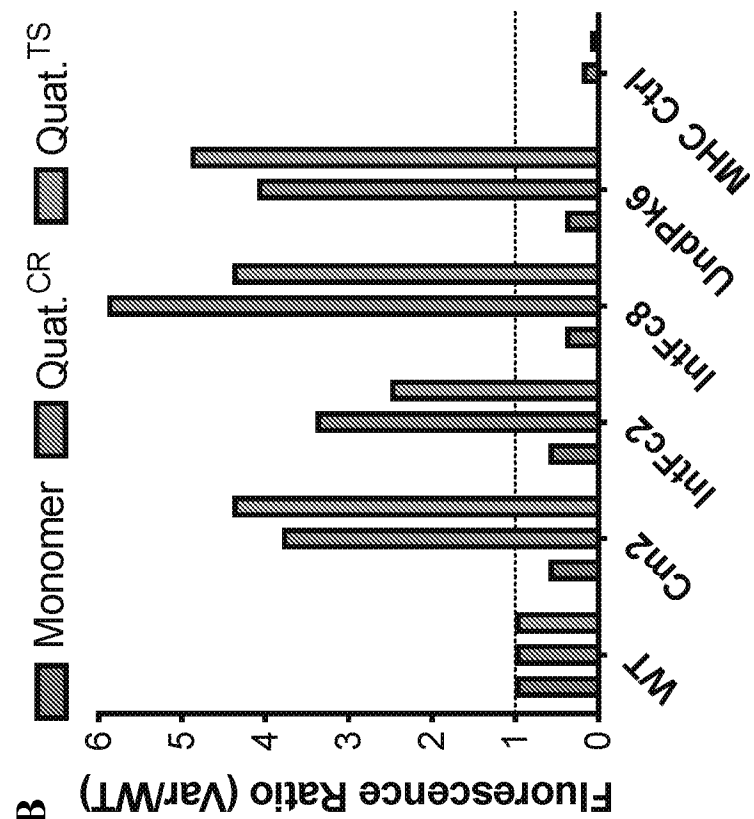


FIG. 2D

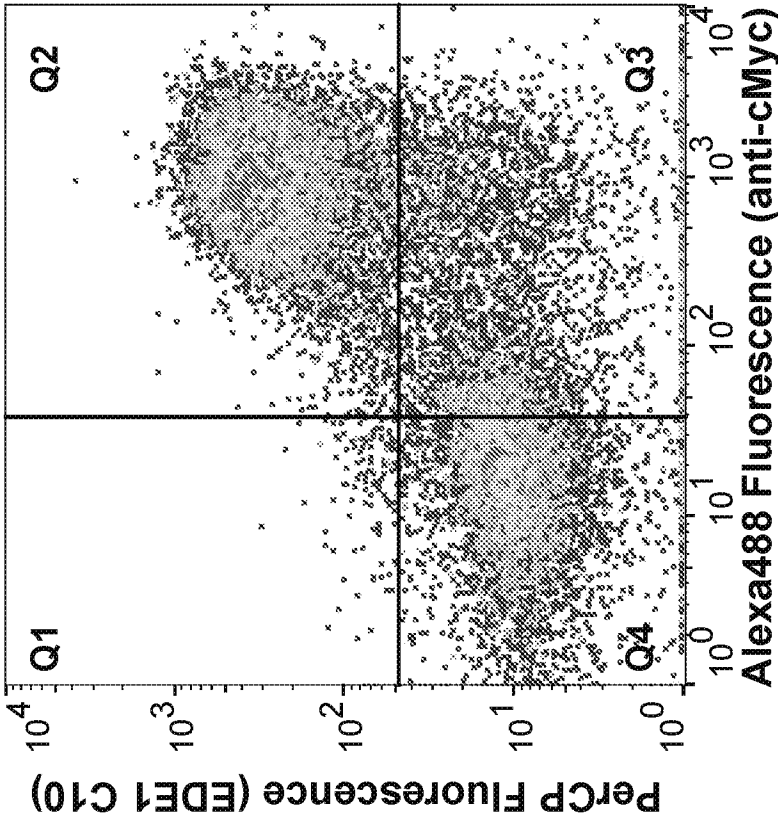


FIG. 2C

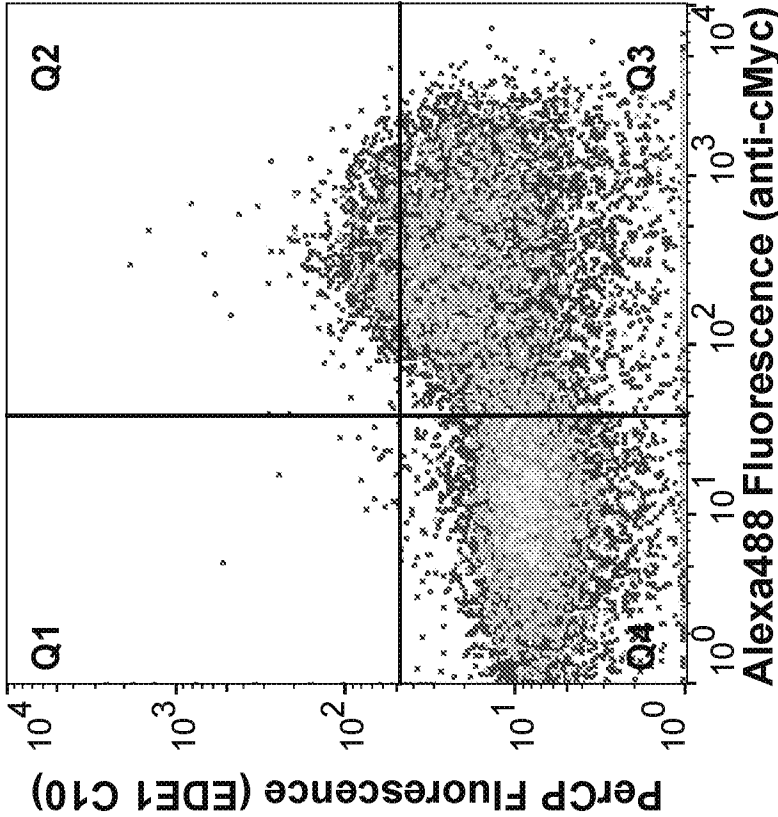


FIG. 3A

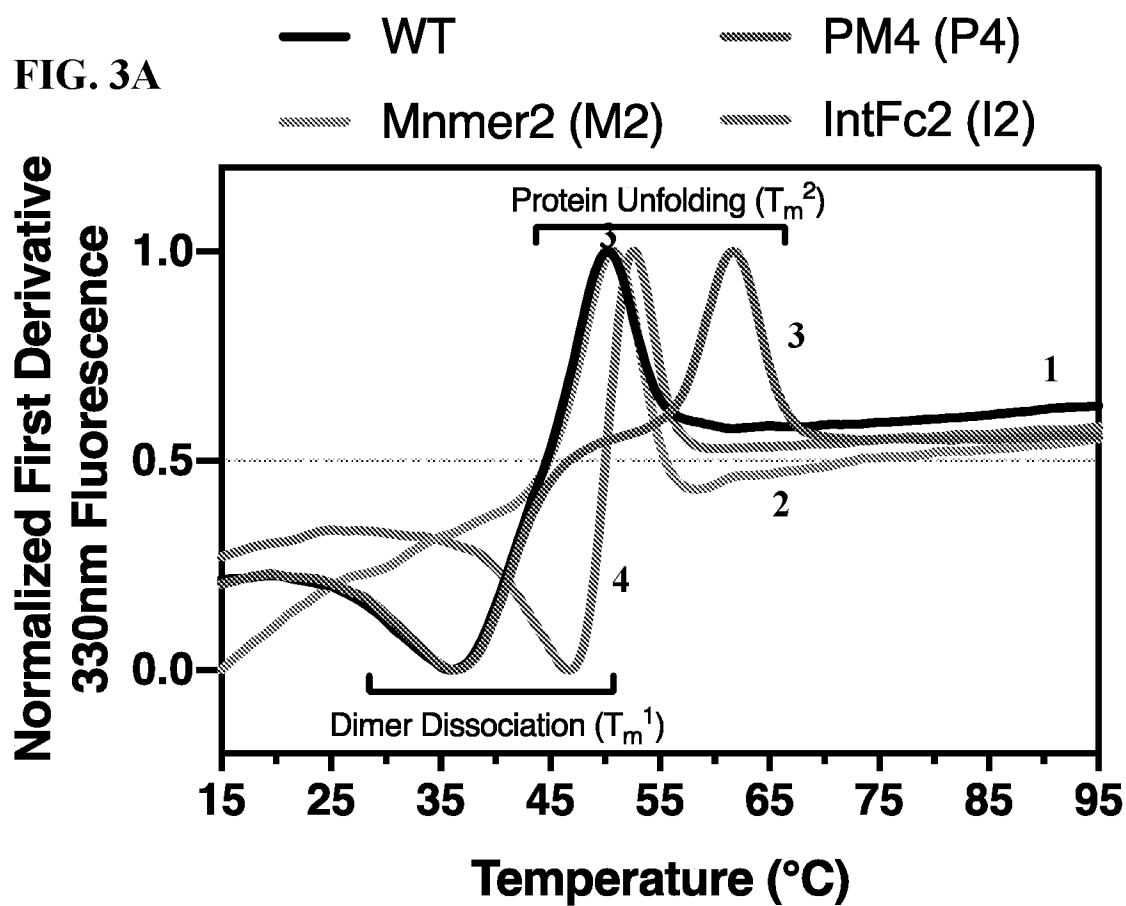


FIG. 3B

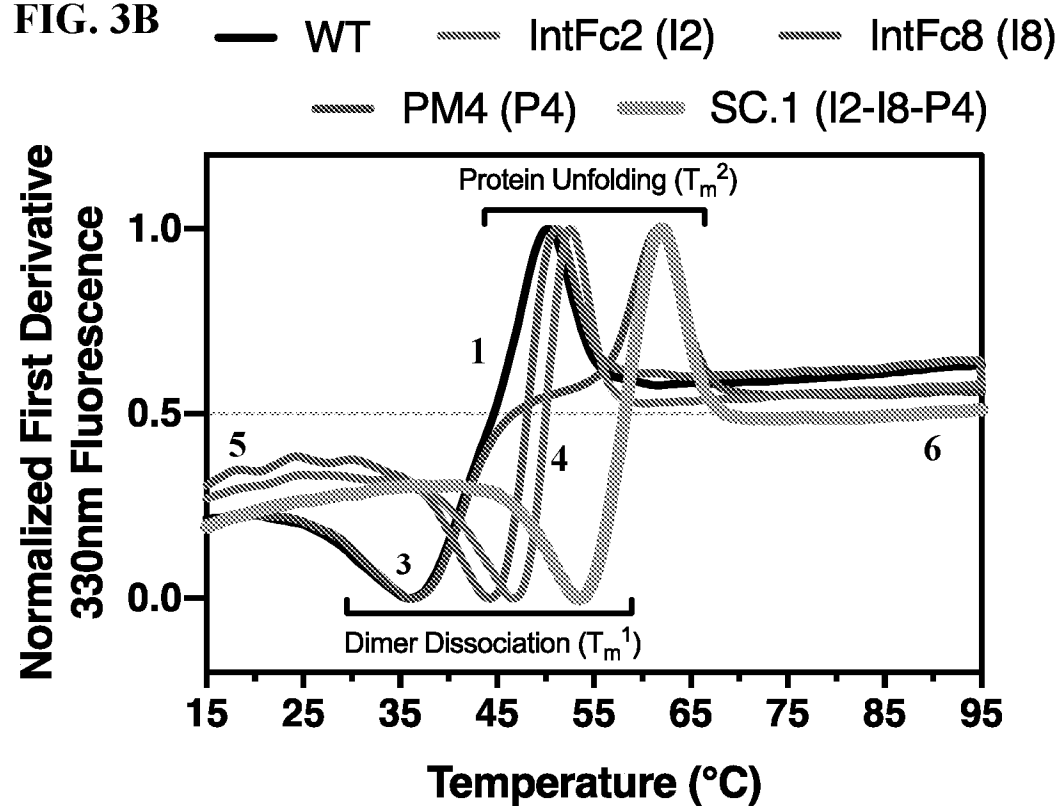


FIG. 3C

		T_m^1	ΔT_m^1	T_m^2	ΔT_m^2
1	WT	35.9		50.3	
2	Mnmer2	N.D	N.D	50.6	+0.4
3	PM4	36.2	+0.3	61.6	+11.4
4	IntFc2	46.4	+10.5	52.8	+2.5
5	IntFc8	44.0	+8.1	51.3	+1.1
6	SC.1 (I2-I8-P4)	53.3	+17.4	62.0	+11.7

FIG. 3D

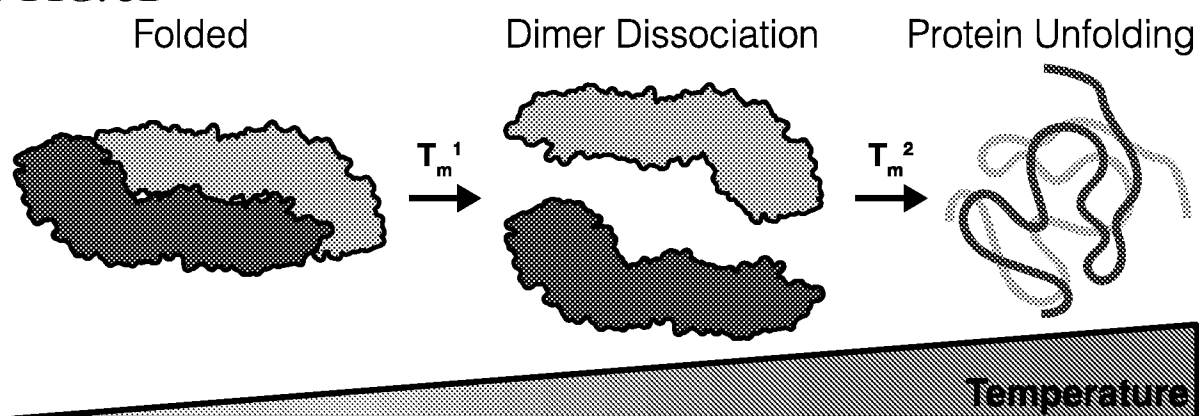


FIG. 4A

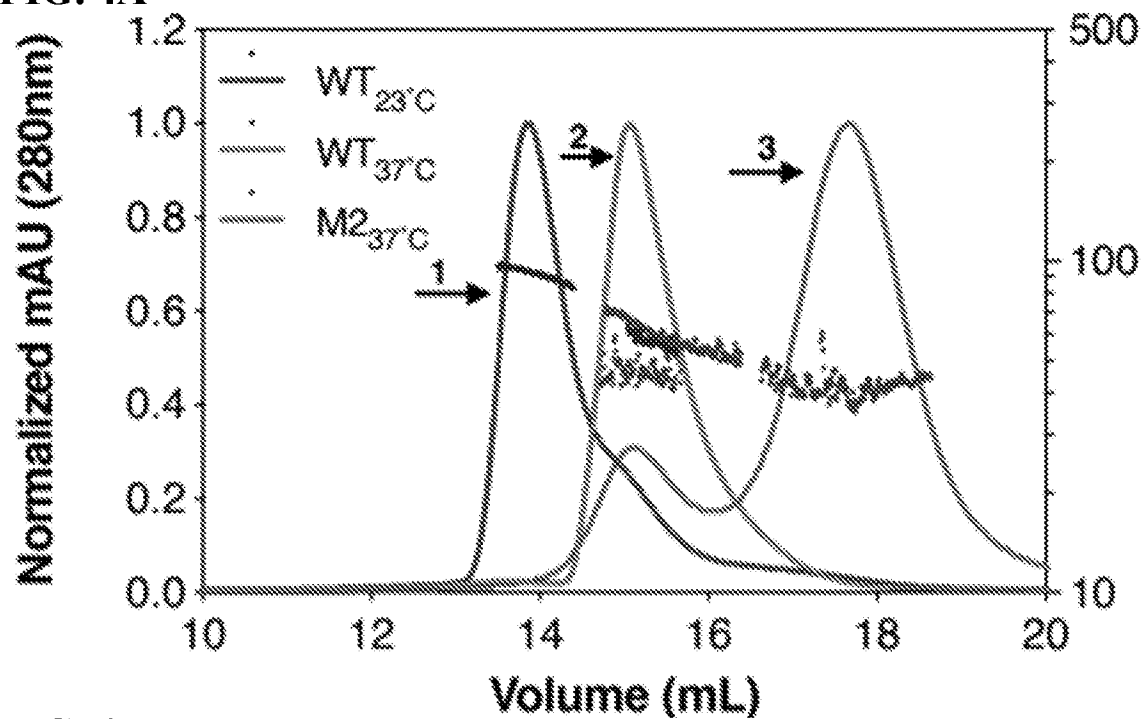


FIG. 4B

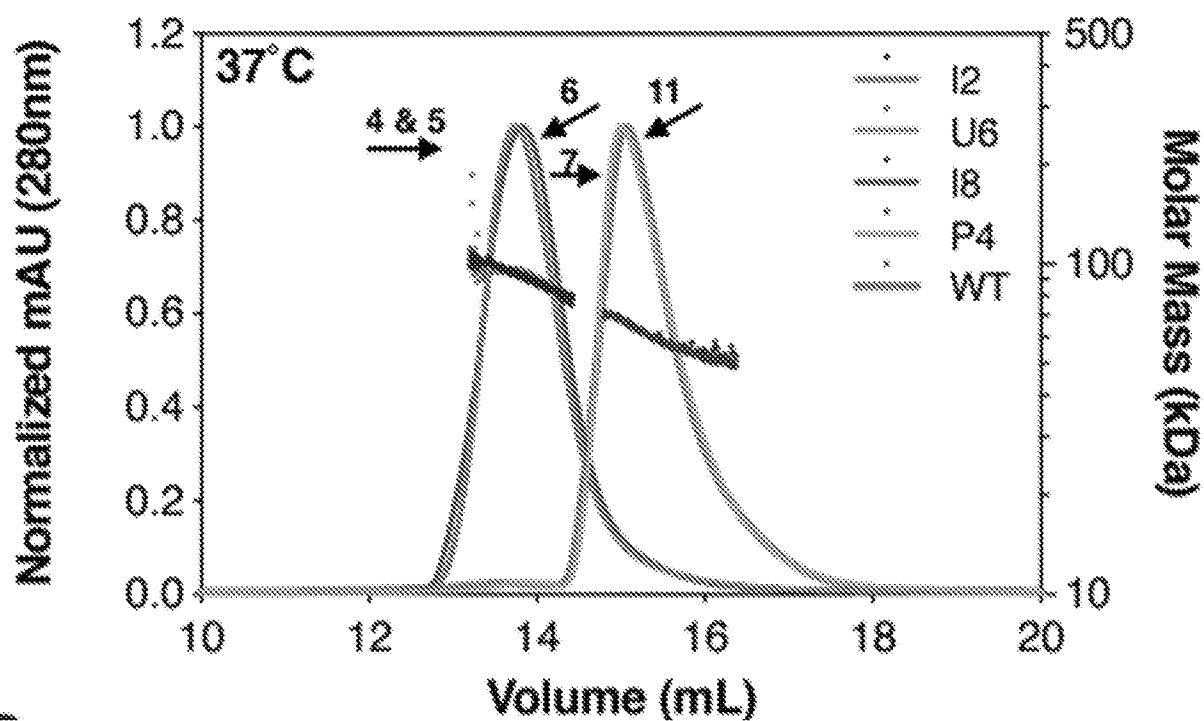


FIG. 4C

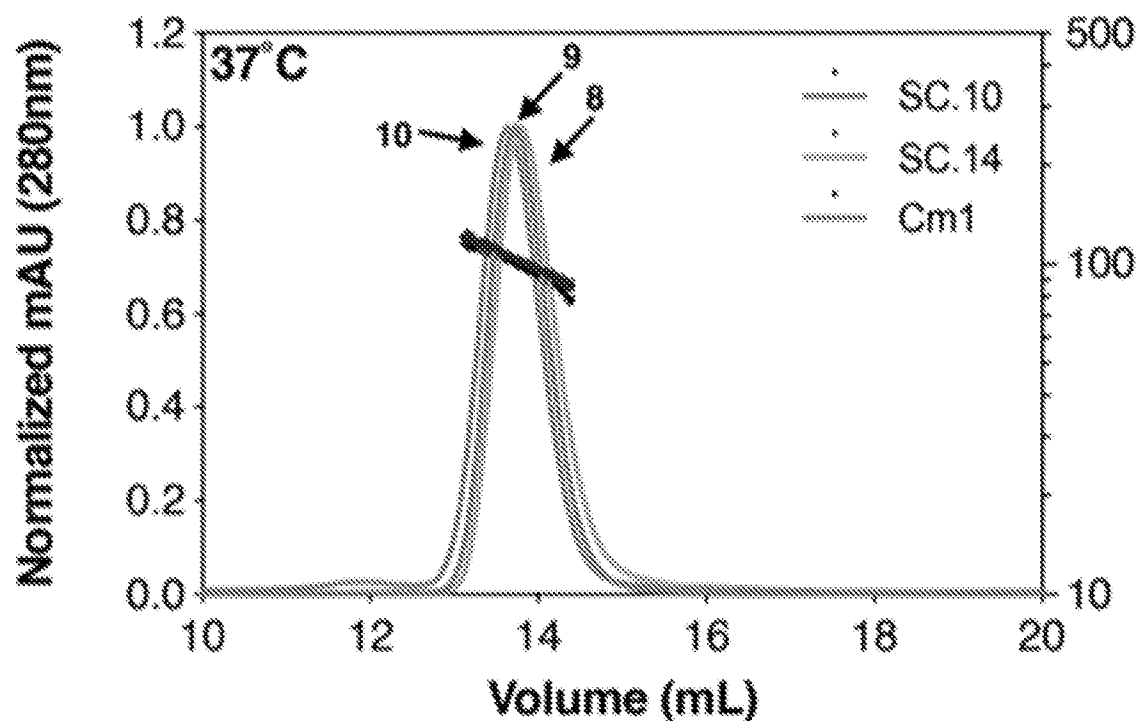


FIG. 4D

		Expected Molar Mass (kDa)		Measured Molar Mass (kDa)	
		Dimer	Monomer	Peak 1	Peak 2
Panel A	1 → WT _{src}	90.2	45.1	91.0 ± 0.7	57.5 ± 3.7
	2 → WT _{src}	90.2	45.1	61.6 ± 1.6	
	3 → Mnmer2 (M2) _{src}	90.8	45.4	45.4 ± 5.9	44.1 ± 2.6
Panel B	4 → IntFc2 (I2) _{src}	91.0	45.5	92.4 ± 1.6	
	5 → IntFc8 (I8) _{src}	90.8	45.4	88.4 ± 1.6	
	6 → UndPk6 (U6) _{src}	90.8	45.4	87.2 ± 1.5	
	7 → PM4 (P4) _{src}	91.0	45.5	60.1 ± 2.6	
Panel C	8 → SC.14 _{src}	91.2	45.6	99.5 ± 0.9	
	9 → SC.10 _{src}	91.6	45.8	102.2 ± 1.3	
	10 → Cm1 _{src}	90.2	45.1	100.7 ± 1.9	

FIG. 5A

DENV2 sE SC.10

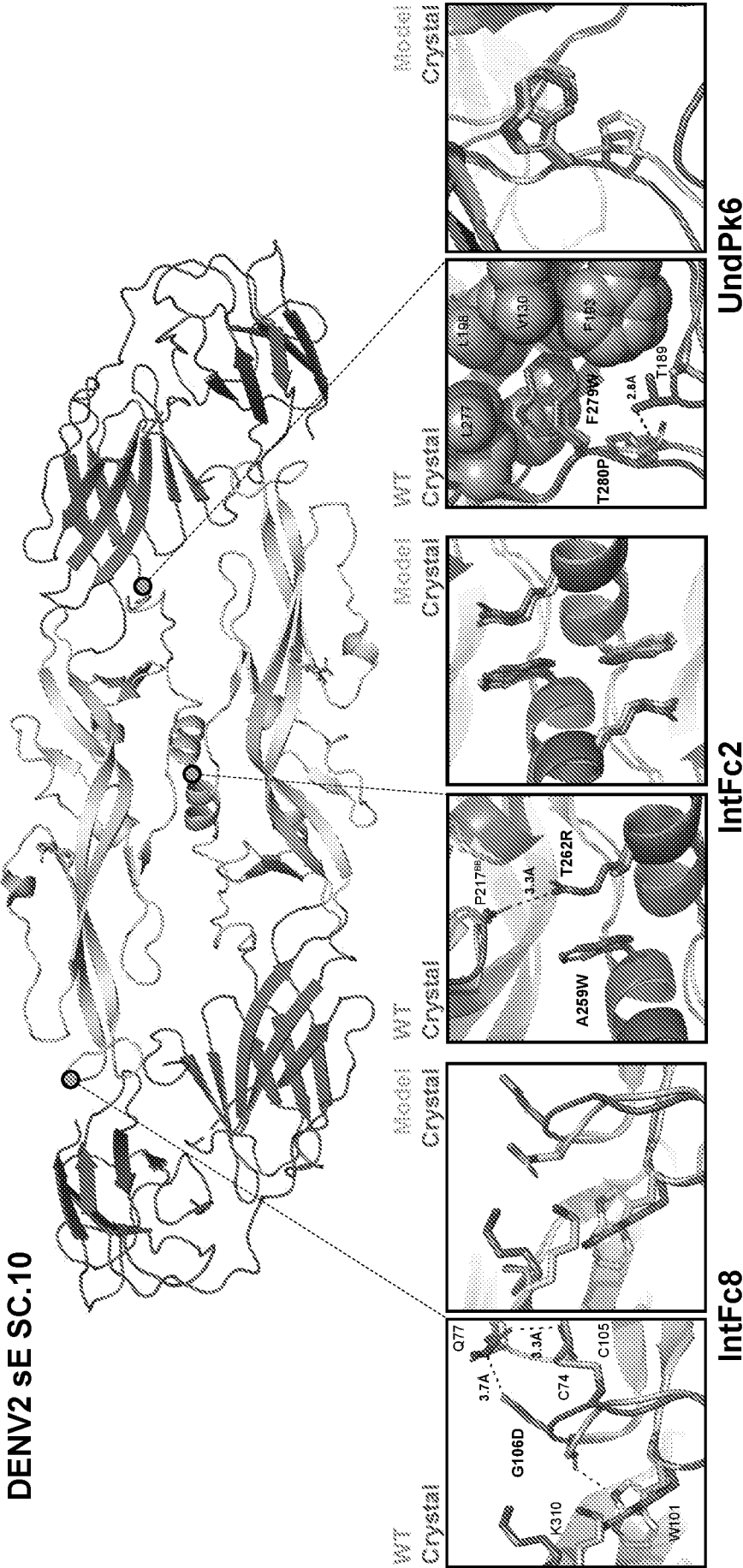


FIG. 5B

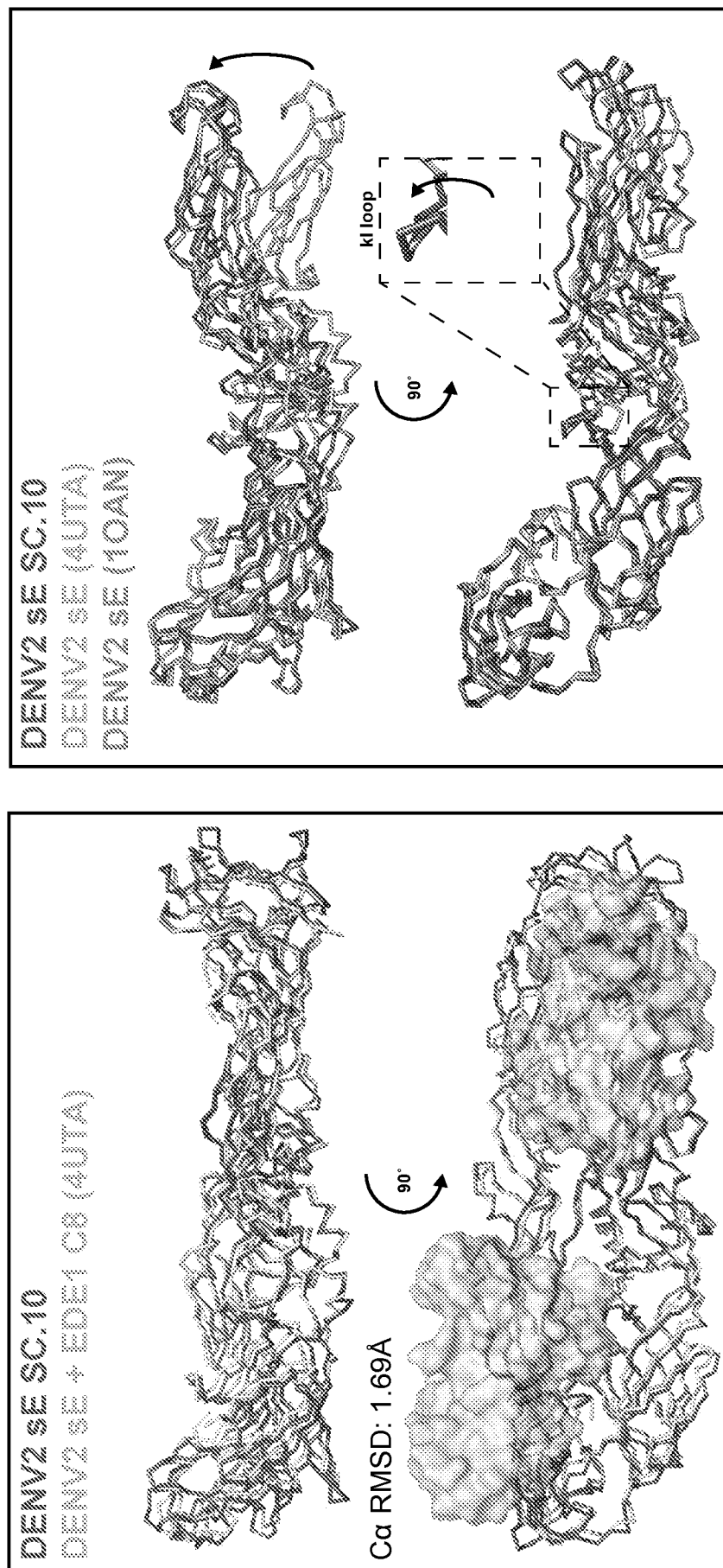


FIG. 6A

Antibody	Species	TS/CR	Epitope
3F9	Human	DV2 TS	EDI
4G2	Mouse	CR	EDII FL
1M7	Human	CR	EDII FL
1C19	Human	CR	EDII BC loop
3H5	Mouse	DV2 TS	EDIII Lateral Ridge
2D22	Human	DV2 TS	Quaternary/Dimer
C8	Human	CR	Quaternary/Dimer
A11	Human	CR	Quaternary/Dimer
1F4 (control)	Human	DV1 TS	ED/II hinge

FIG. 6B

DENV2 sE Mnmer2

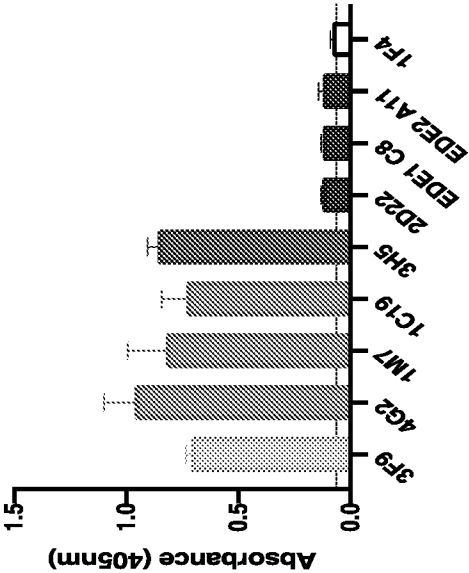


FIG. 6C

DENV2 sE WT

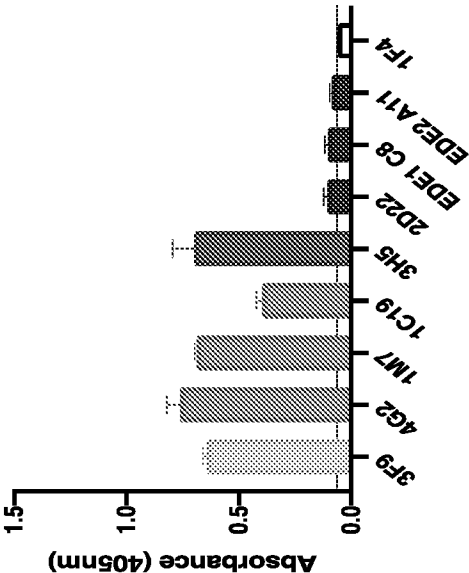


FIG. 6D

DENV2 sE Cm1

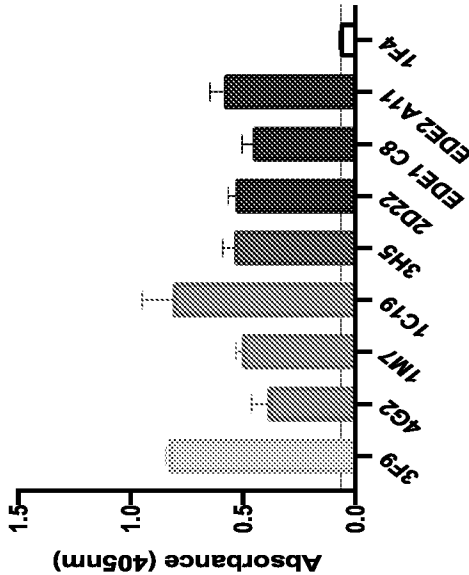


FIG. 6E

DENV2 sE SC.14

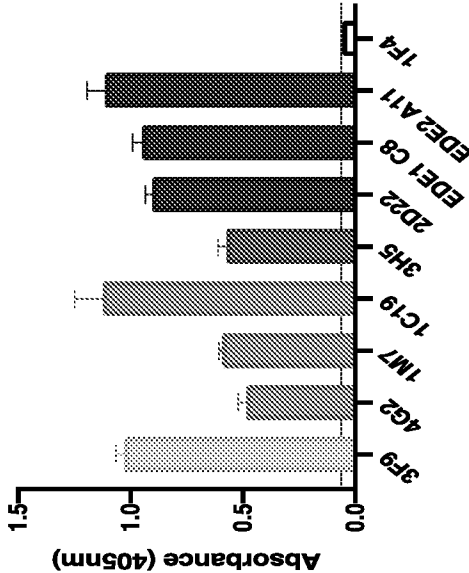


FIG. 6F

DENV2 sE SC.10

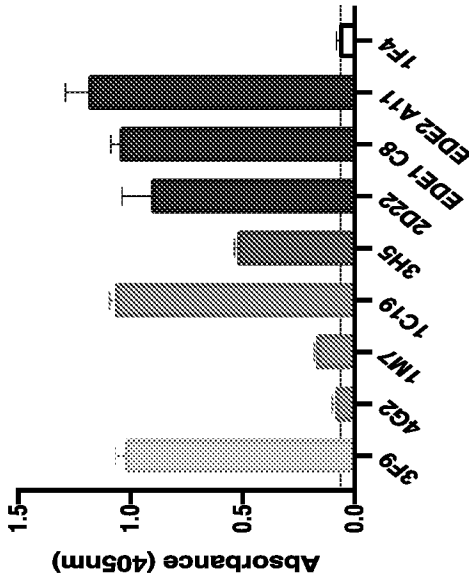


FIG. 7A

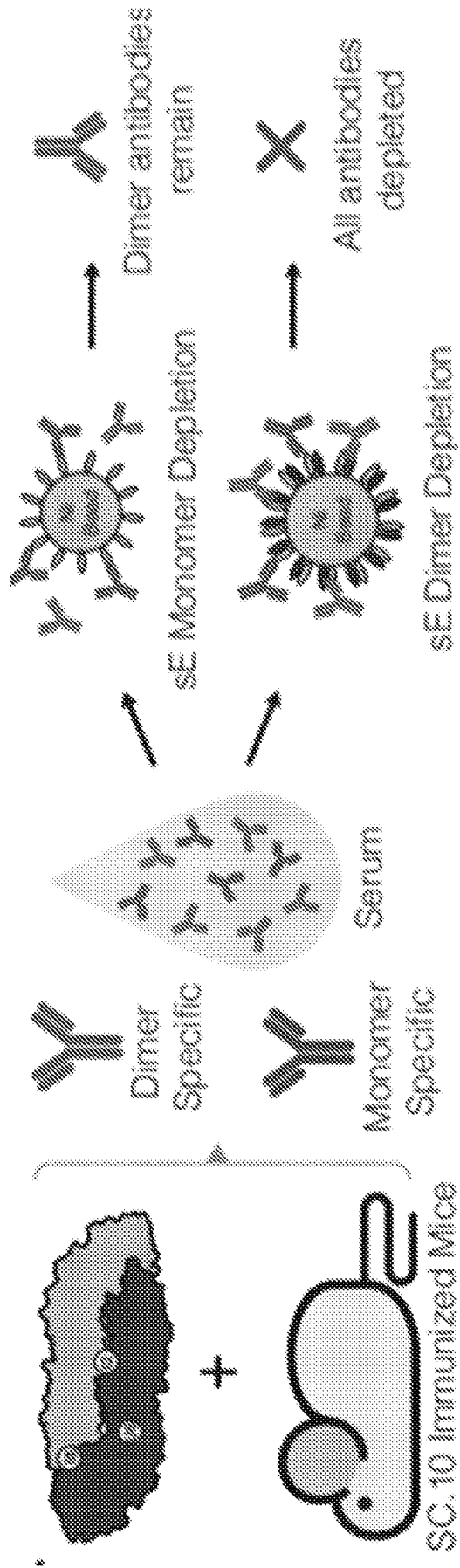


FIG. 7B

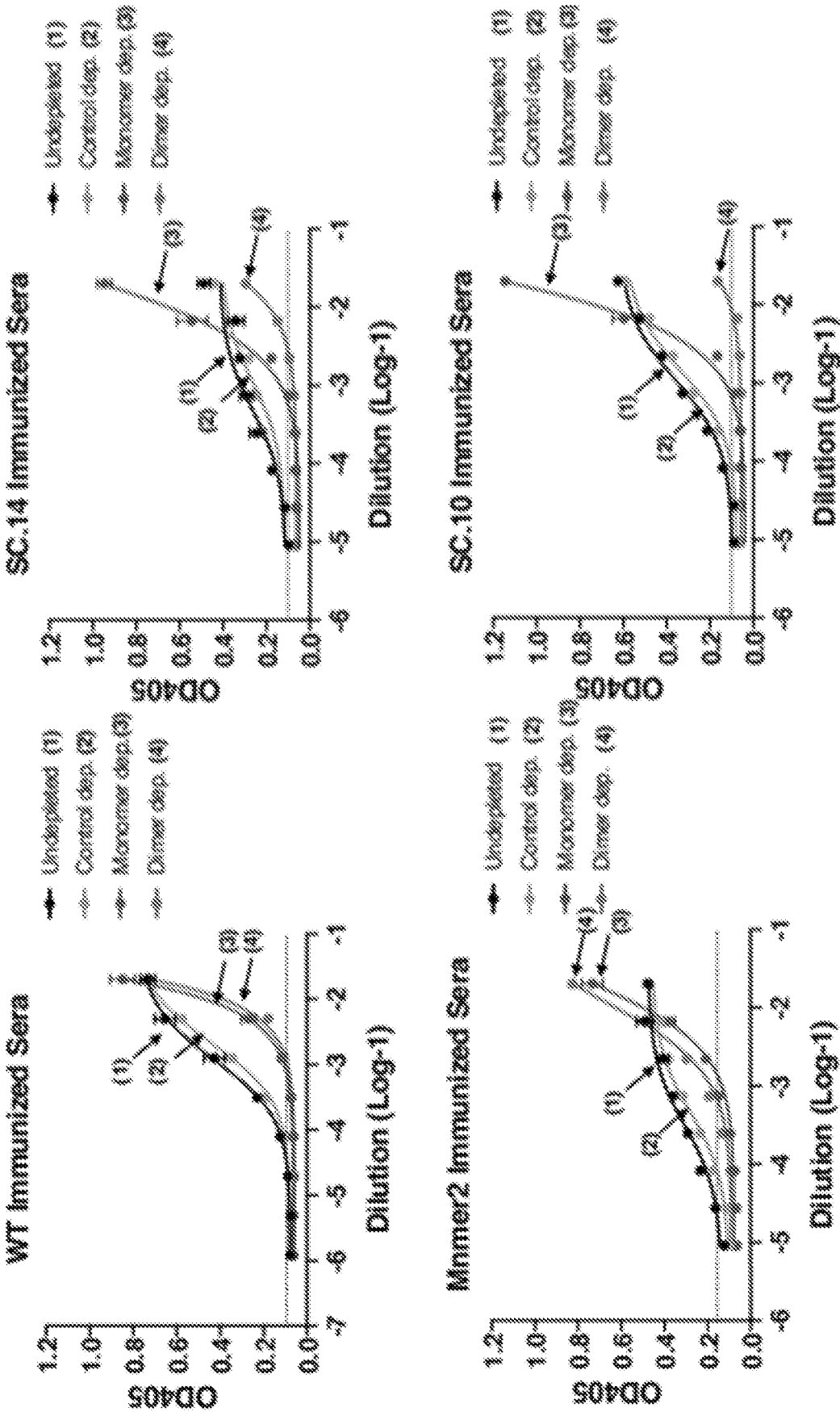


FIG. 7C

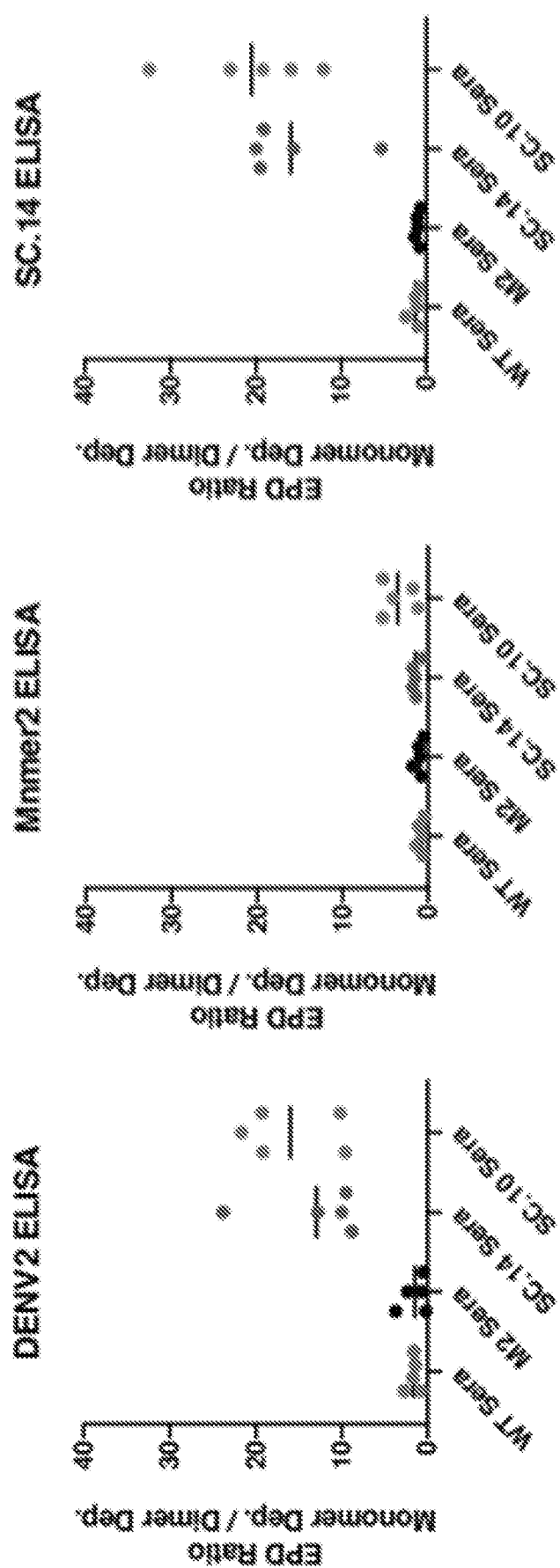


FIG. 8

Problem: sRecE Dimer Stability is Concentration & Temperature
Dependent

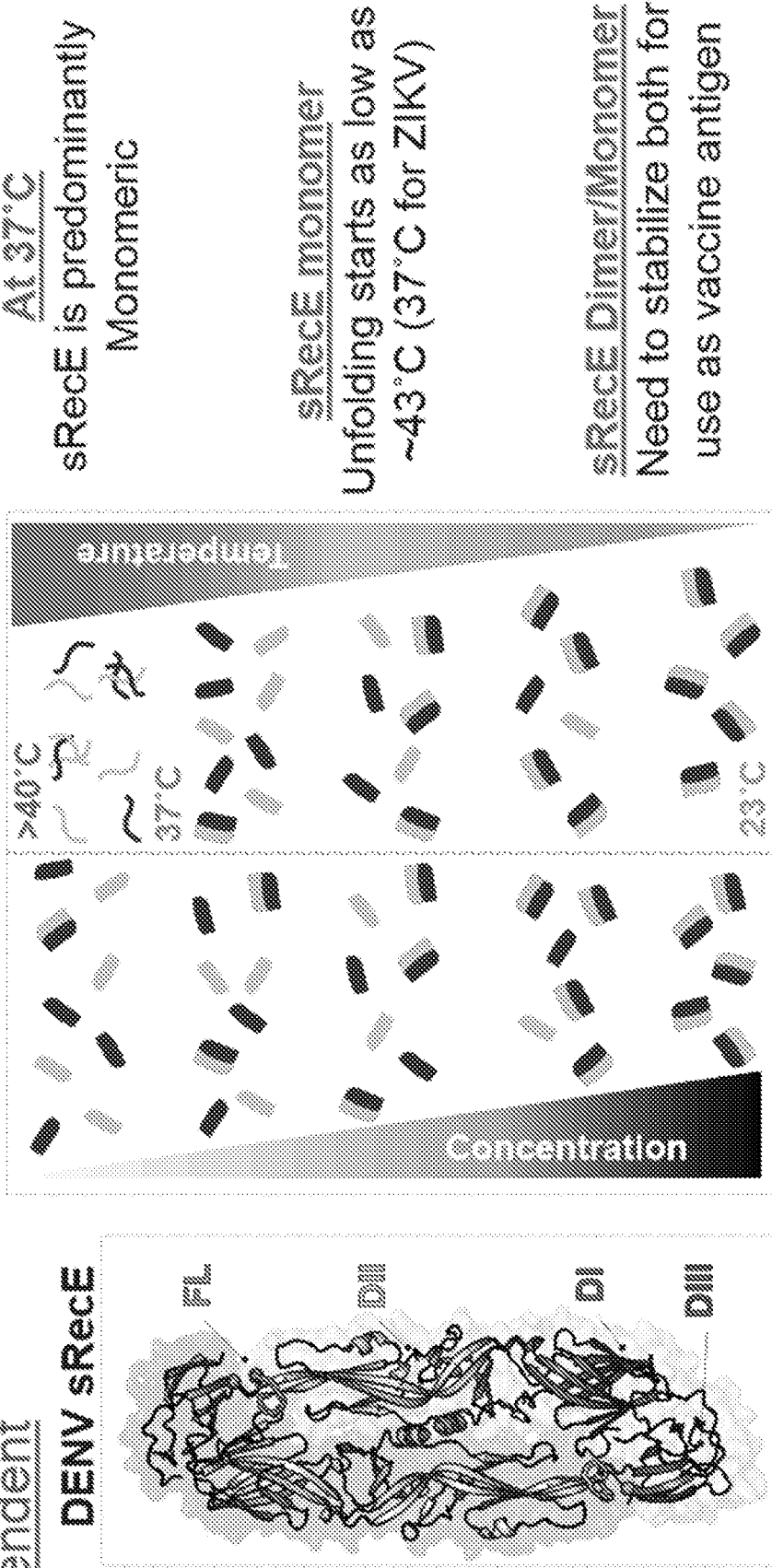


FIG. 9A

Modeling Strategy: Target Regions of Instability at sRecE

Dimer Interface

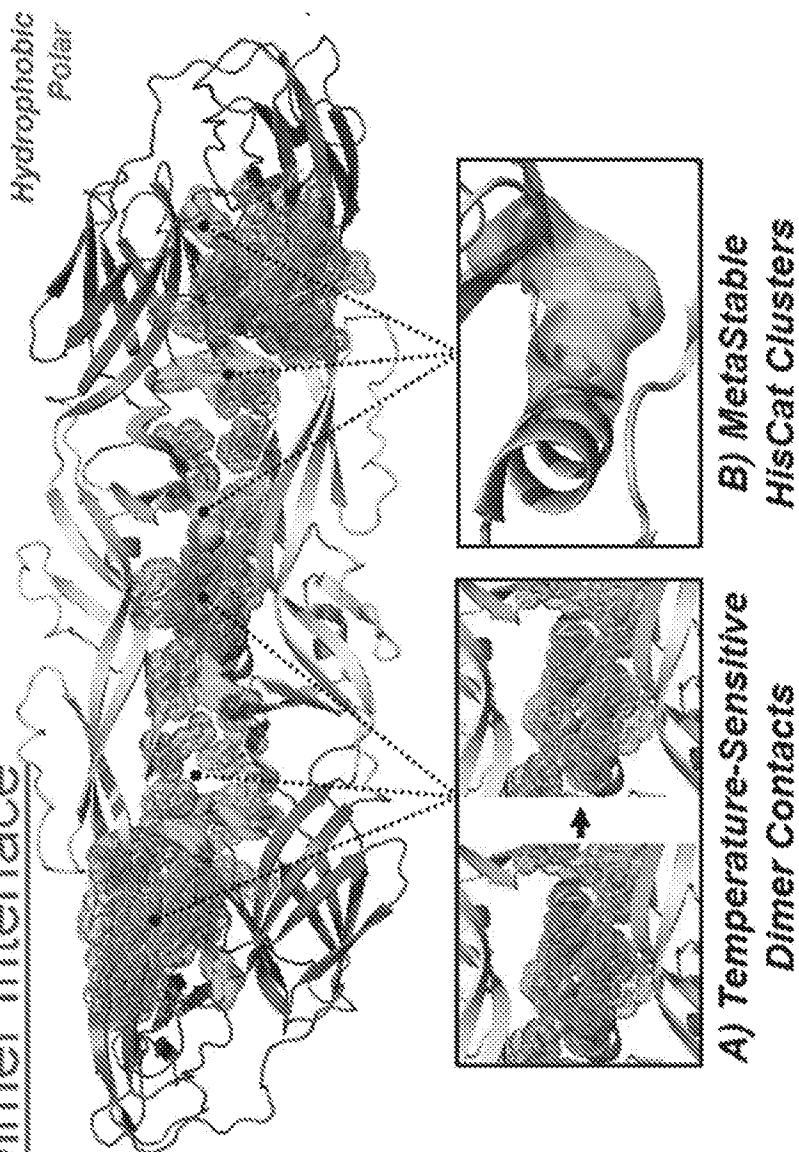


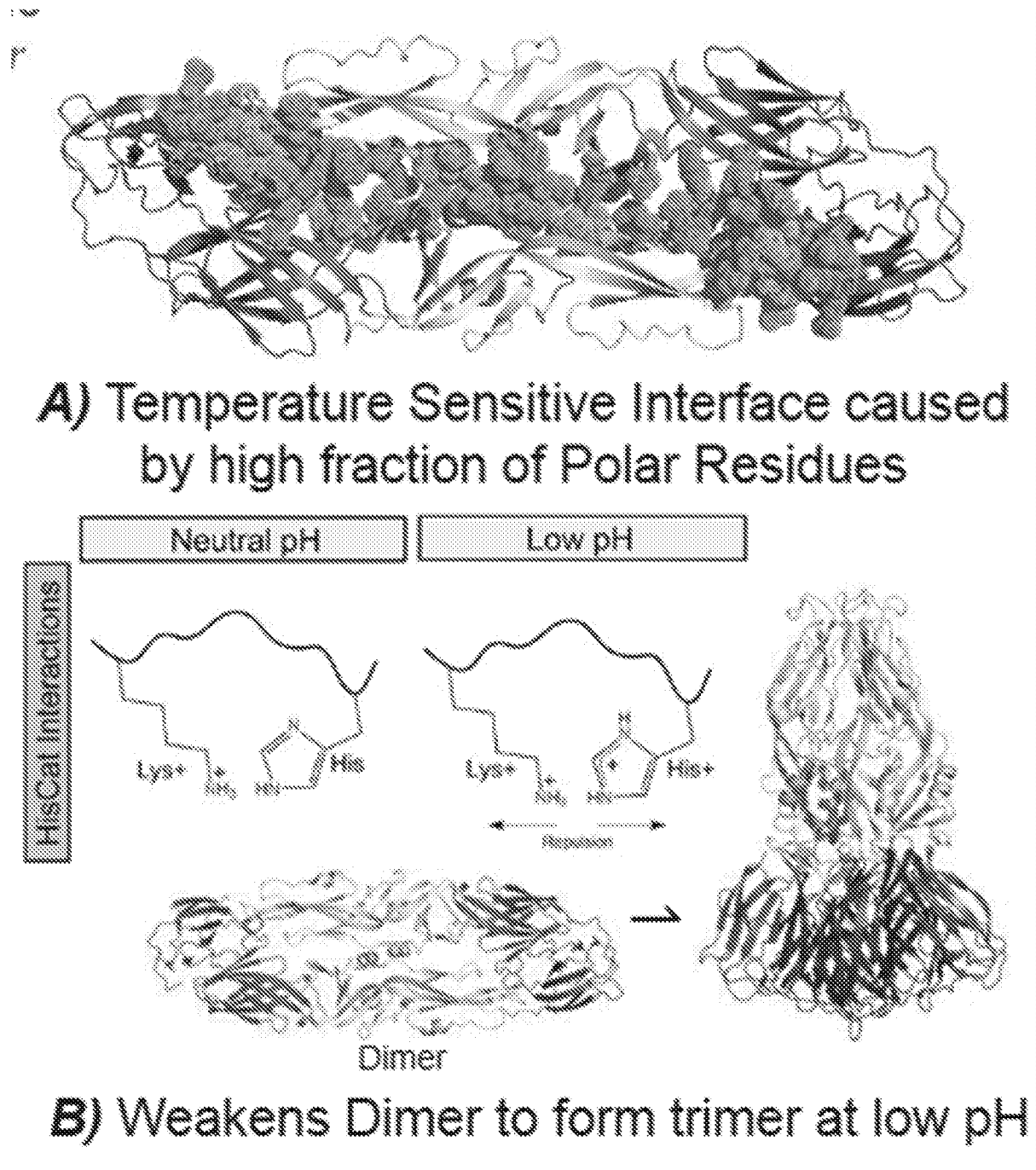
FIG. 9A cont.

FIG. 9B

Modeling Strategy : Target Regions of Instability within sRecE Monomer

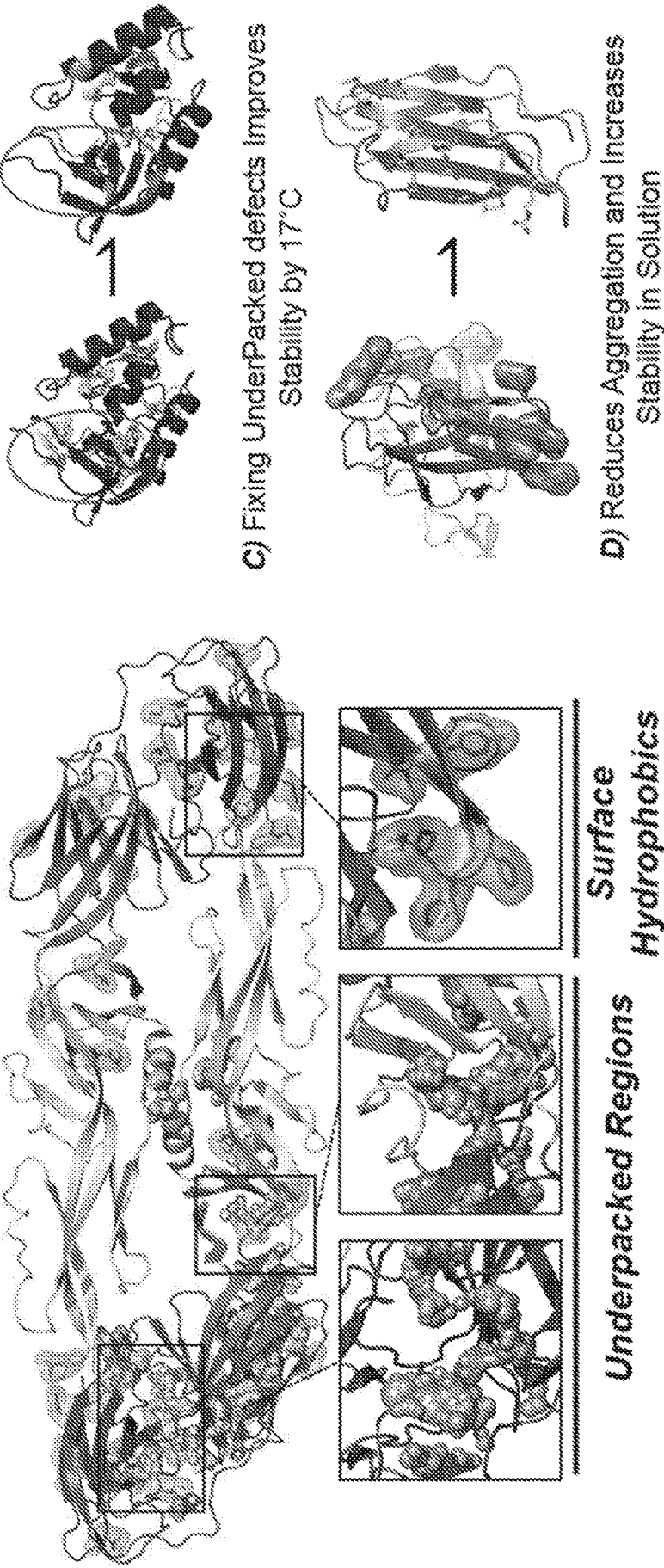


FIG. 9C

Rosetta Modeling: Predicts Stabilizing Mutations

1) Select Region and Design New Interactions

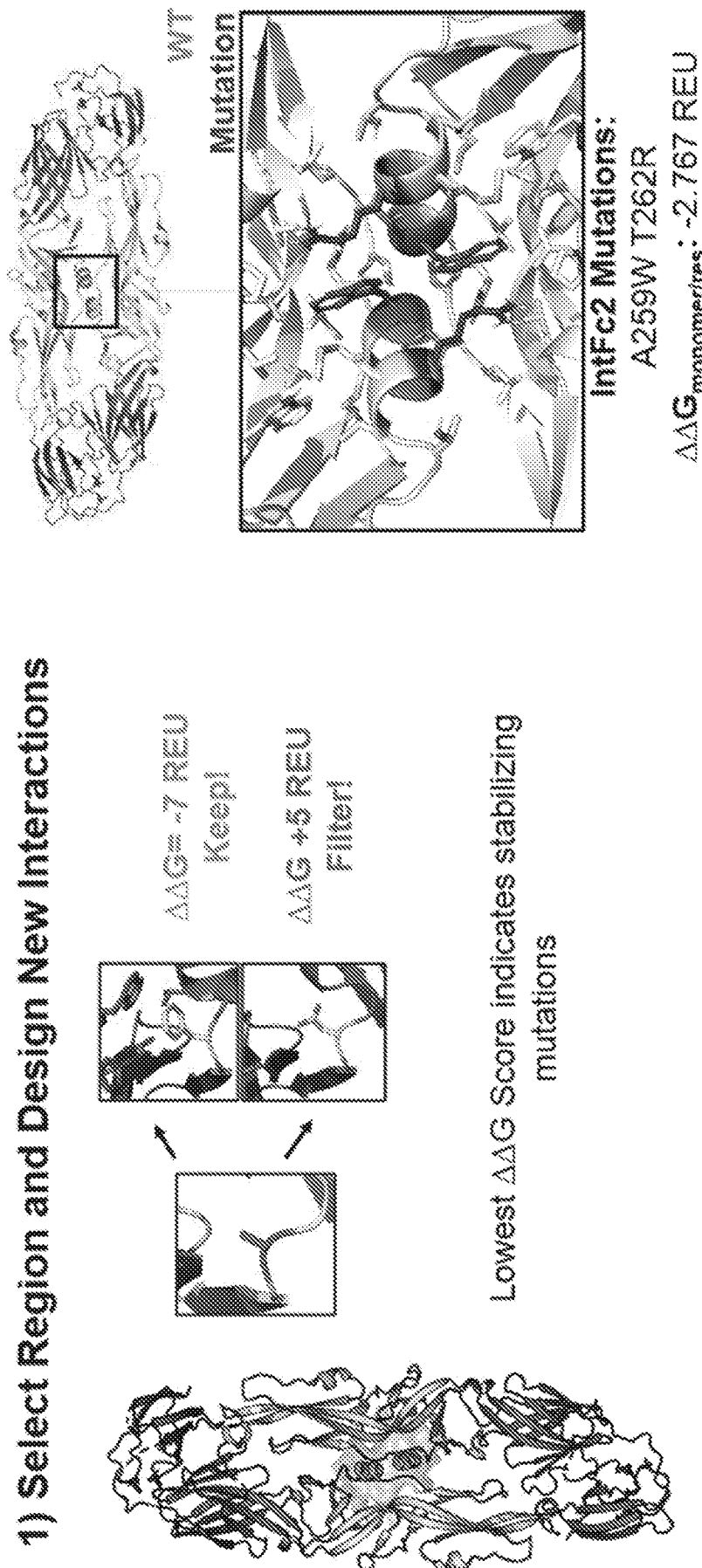


FIG. 10

Location of Stabilizing Mutations



FIG. 11 cont.

on Positions are Conserved

- DENV2 sRecE stabilizing mutations are in conserved positions and should also stabilize with DENV1-4 and ZIKV, as well as other flavivirus envelope proteins monomers and dimers

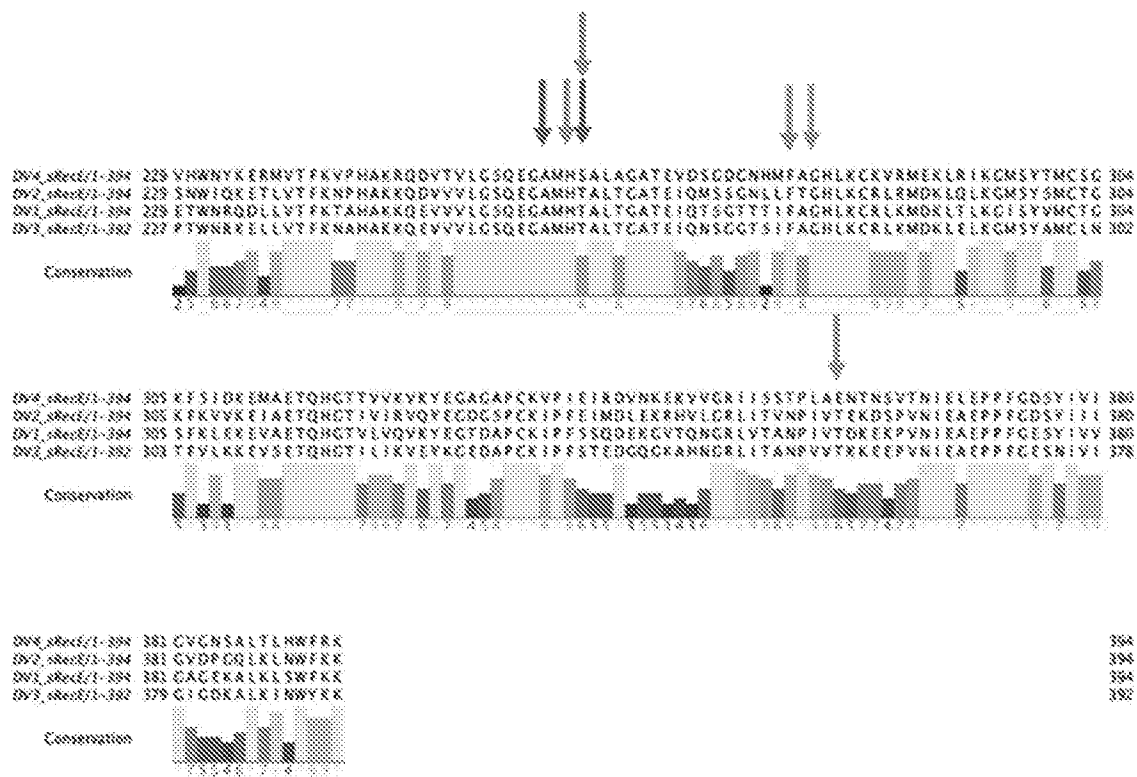


FIG. 12A

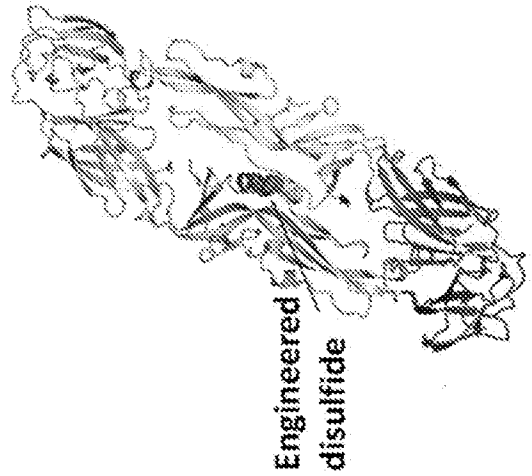


FIG. 12B

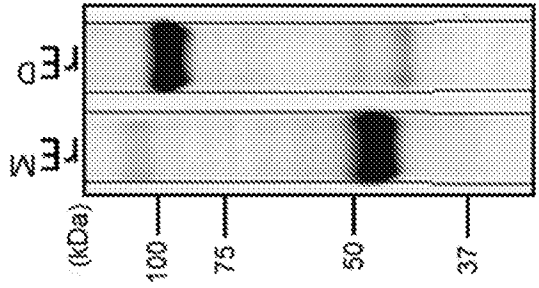


FIG. 12C

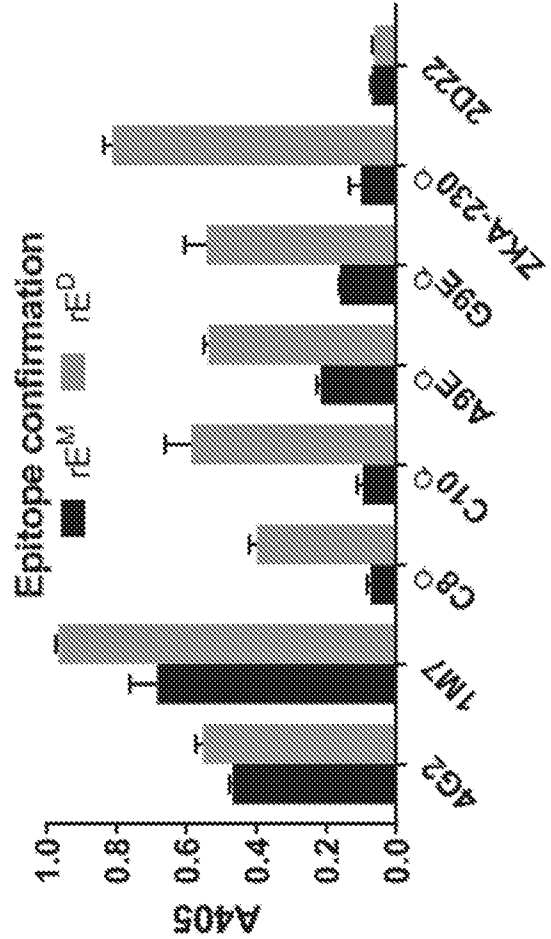


FIG. 13B

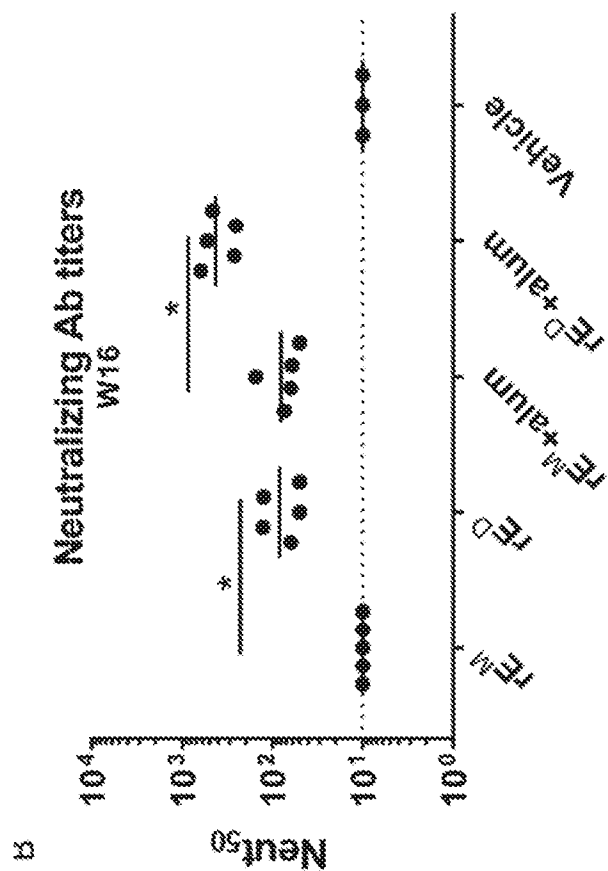


FIG. 13A

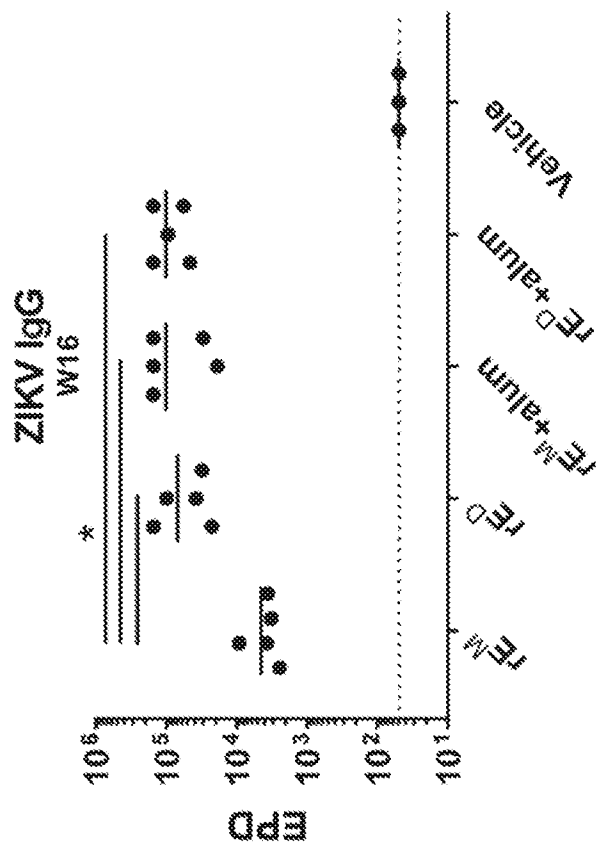


FIG. 14A

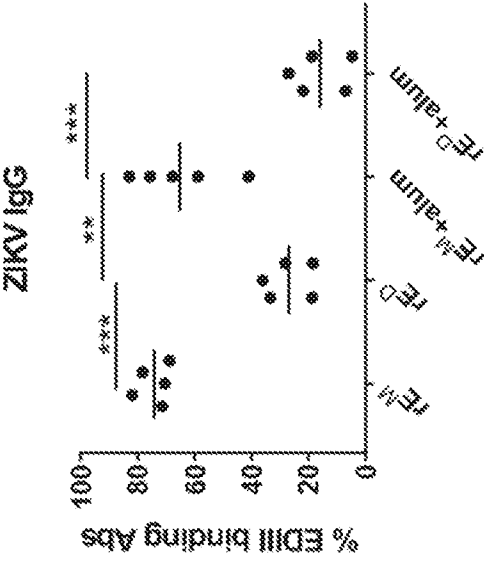


FIG. 14B

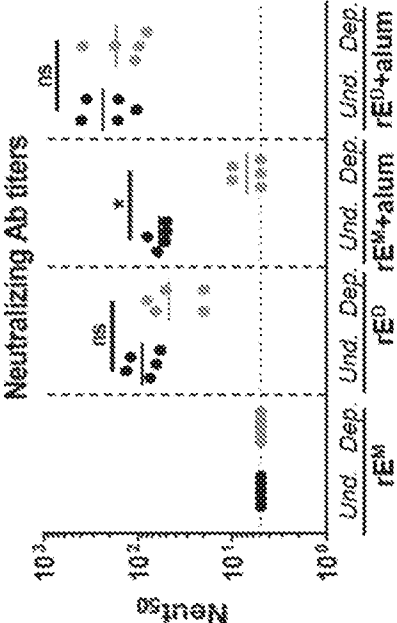


FIG. 14C

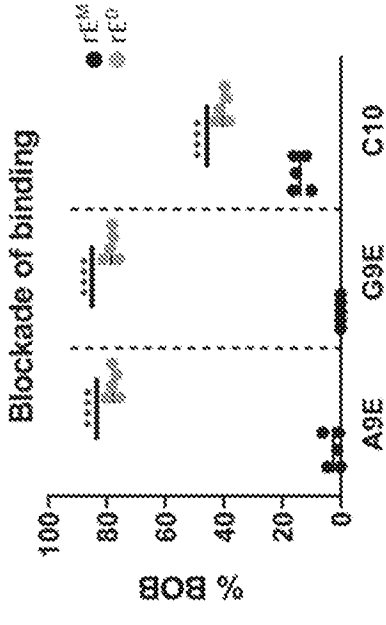


FIG. 15A

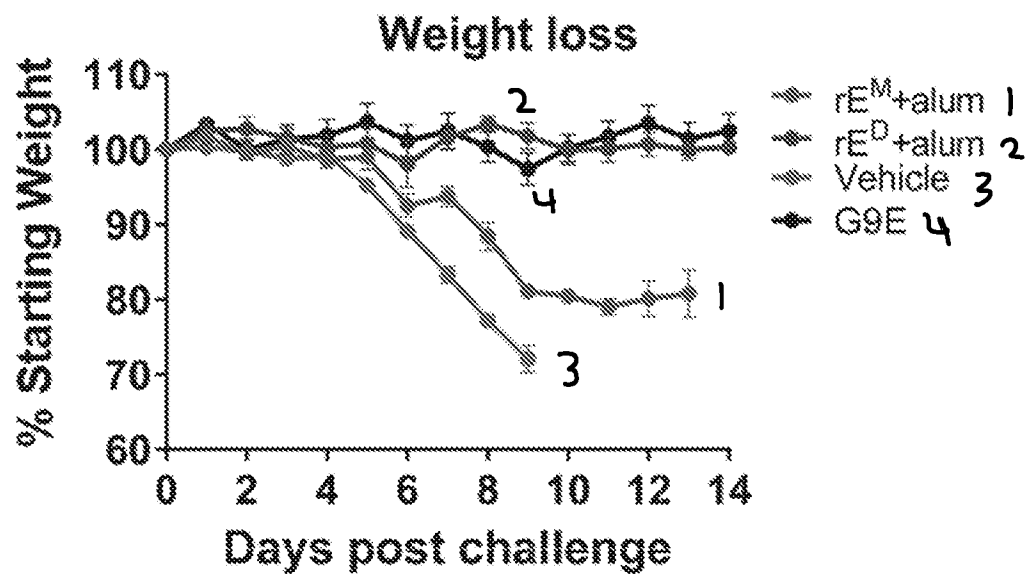


FIG. 15B

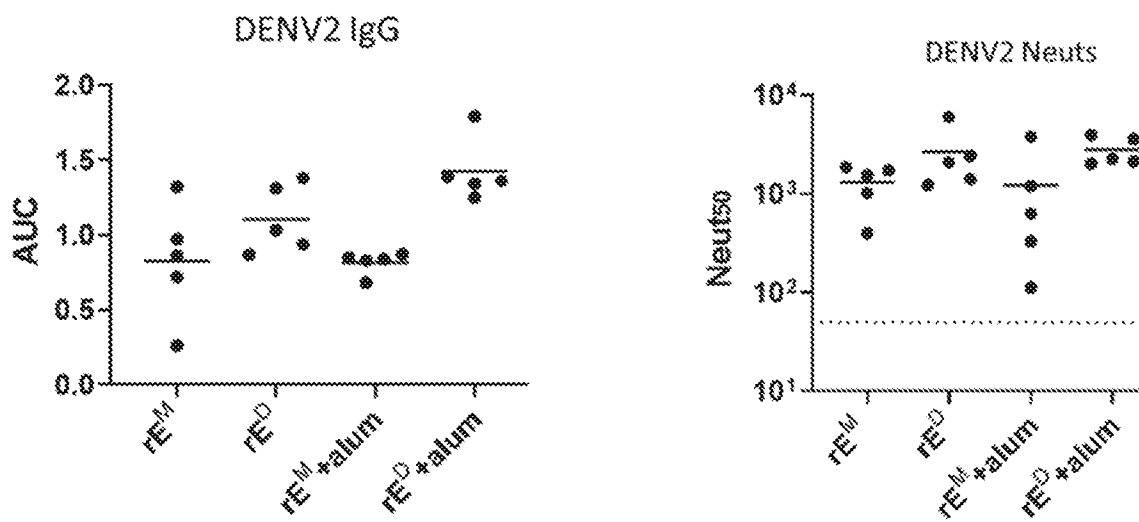


FIG. 16A

expression constructs

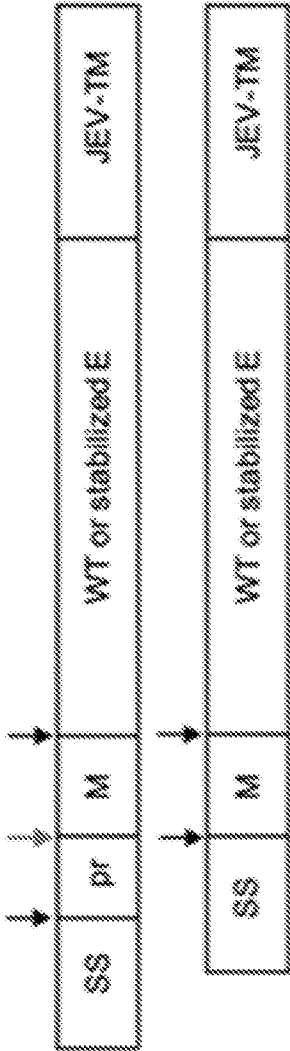


FIG. 16B

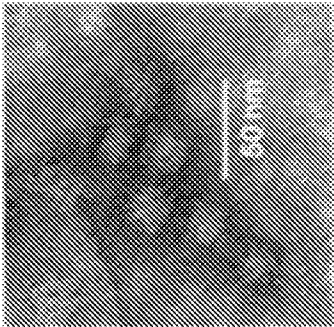
expression yields during VLP production

E protein	yield (mg/L)
WT E, no pr	undetected
WT E, with pr	0.1
Stabilized E, no pr	3.1
Stabilized E, with pr	1.5

FIG. 16C

negative stain EM

commercial VLP: WT E, with pr



in house VLP: stabilized E, no pr

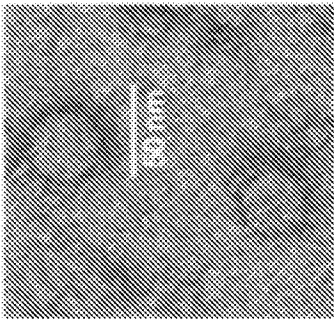


FIG. 17A

CLUSTAL O(1.2.4) multiple sequence alignment

ZIKV_FF13/251013-18	IRCIQVSNRDFVEGMSGGTWDVVLHSGGCVTMAGQKPTVDIELVTTTVGNMAEVRASYC	60
DENV4_TVP-376	MRCVGVGNRDFVEGMSGGANVDVLHSGGCVTMAGQKPTLDPELTTTAKVALLRTYC	60
DENV2_16681	MRCIGMSNRDFVEGMSGGSVVDIVLHSGGCVTMANNKPTLDPELINTKAKQFATLRKTC	60
DENV1_WestPac	MRCVIGGNRDFVEGLSGATWVDVVLHSGGCVTMAGQKPTLDIELLLKTEVTNPAYLAKLC	60
DENV3_CH53489	MRCVGVGNRDFVEGLSGATWVDVVLHSGGCVTMANNKPTLDIELQKTEATQLATLAKLC	60
* ** * : : * * * * * : * * : *		
ZIKV_FF13/251013-18	YEASISDMASDSRCPTQGEAYLDRKQSDTQYVCKNTLVDRGWGNGCGLPFGGSLVTCARFA	120
DENV4_TVP-376	IEASISNITTATRCPTQGEFPYLKEEQDQYICARDVVDKMGNGCGLPFGGCVVTCARFS	120
DENV2_16681	IEAKLTNTTTESSCPTQGEFSLNEEQDKRFVCHSMVDKMGNGCGLPFGGCVVTCAMFR	120
DENV1_WestPac	IEAKISNTTDSRCPTQGEATLVESQDTNFVCKRTFVDRGWGNGCGLPFGGSLVTCARFK	120
DENV3_CH53489	IEGKITNITTSRCPTQGEAILPEEQDQNTYVCKNTYVDRGWGNGCGLPFGGSLVTCARFQ	120
* . . . : : : : * * * * * * : : * * : : * * * * * * * * * * * * * * * *		
ZIKV_FF13/251013-18	CSEKMTGKSIQFENLEYSINLSVHGSQHSQSMIVNDTGHETDENKARVEITPNSPRAEATL	180
DENV4_TVP-376	CSEKITGKSLVQIENLETTVTVTHNGDTH-----AVGNDTSNRCVTAHITPNSPVEVEL	175
DENV2_16681	CRKNMEGKVVQFENLETTIVITPHSGEEH-----AVGNDTGKSGKRIKITPQSSITEAEL	175
DENV1_WestPac	CVTKLEGKIVQYENLKYSVIVTVHTGDQH-----QVGMETTEHGTATITPQAPTSEIQQL	175
DENV3_CH53489	CLESIEGKVVQHENLKYTVITVHTGDQH-----QVGMET---QCVTAETPQASTVEAIL	173
* . . : : * : * * * * * : : : : * : : * * : : * * * * * * * * * * * *		
ZIKV_FF13/251013-18	GGPGSLGLDCEPRTGLDFSDLYLLTHNNKHVLVHKEWPHDIFLPWHAGADTGTTPHWNKEE	240
DENV4_TVP-376	PDYGLTLDCPEKSGIDFENMIIMKMKAKTTLVHKKQWFLDLPLPWTAGADTSEVHWNYKE	235
DENV2_16681	TGYGTVTNRCSPRTGLDFENMVLQENKAWLVHKKQWFLDLPLPWLPGADTQGENWIKQE	235
DENV1_WestPac	TOYGALTLDCEPRTGLDFENMVLITMEKKSWLVHKKQWFLDLPLPWTSGASTSQETPWRQD	235
DENV3_CH53489	PEYGTGLGLECSPRTGLDFENMILLTHNNKAWVHRCWFFDLPLPWTSGATTETPTWNRKE	233
* * : : : * * * * * : : : : * : * * * * * * * * * * * * * * * * *		
ZIKV_FF13/251013-18	ALVEFKDAHAKRQTVVVLGSGEGAVRTALAGALEAENDGAKGRISSEGLKCRILKMDKRLRL	300
DENV4_TVP-376	RMVTFKVPFAKRDQTVVLGSGEGAMHEALAGATEVDSGGD--NMFAGHLCEVVRHEHLRI	294
DENV2_16681	TLVTFKNPRANKQDVVVLGSGEGAMHTALTGATEIQMSSG--NLLFTGHLKCRILKMDKQLQL	294
DENV1_WestPac	LLVTFETAHAKRQTVVVLGSGEGAMHTALTGATEIQTSQT--TFIFAGHLKCRILKMDKLTLL	294
DENV3_CH53489	LLVTFKNNAHAKRQTVVVLGSGEGAMHTALTGATEIQNSGG--TSIFAGHLKCRILKMDKRLRL	292
* * * * * * * * * * * : *		
ZIKV_FF13/251013-18	KGVSYSLCTAAPTFTKIPASTLHGTVTVVEVQYAGTDGPKCVPAQMAVDMQTLTPVGRLLIT	360
DENV4_TVP-376	KGMSYTNCSCKFSDIKEMASTQHGTTVVVKYKYGAGAPCKVPIEI--RDVNRKRVVGRHIS	353
DENV2_16681	KGMSYMCCTGKFKVVKELIAETQHGTFIVINQYEGDGGSPCKIPFEI--MDLEKRRVVLGRLLIT	353
DENV1_WestPac	KGMSYVMCTGSGFLEKEVAETQHGTVLVQVRYEGTDAPCKIPFSS--QDEKGVTVGRLLIT	353
DENV3_CH53489	KGMSYAMCLNTFVLKKEVSETQHGTFILKVEYKGEDAPCKIPFST--EDGQGAHNGRLLIT	351
* *		
ZIKV_FF13/251013-18	ANFVITESTENSEMMLELDPFFGDSYIVIGVGEKKITHNWHRSCTIGKAFETVAGARR	420
DENV4_TVP-376	STPLAENTN---SVTNIELEPFFGDSYIVIGVGNLSALTILHWFRAGSSIGKMFESTYAGARR	411
DENV2_16681	VNPIVTEKD---SPVNIEAEFFFGDSYIIIGVEPGLKLNWFKKSSSIGKMFETMRGARR	411
DENV1_WestPac	ANPIVTDKE---KPVNIEAEFFFGESYIVVGAGEKALKLSWFRKSSSIGKMFETATARGARR	411
DENV3_CH53489	ANFVVTKKE---EPVNIEAEFFFGESNIVIGIGDKALKINWYKSSSIGKMFETATARGARR	409
* * : . . . : *		
ZIKV_FF13/251013-18	MAVLGDTANDFGSGVGLNSLGRGQINQIFGAAPKSLFGGMSWFSQILIGTLLMWLGLNTE	480
DENV4_TVP-376	MAILGETANDFGSGVGLFTSLGKAVNQVFGSVYTTMFGGVSWHRIILIGFLVLWIGTNSK	471
DENV2_16681	MAILGDTANDFGSLGGVFTSIGKALQVFGAIYGAAPSGVSWTKILIGVITWIGMNSK	471
DENV1_WestPac	MAILGDTANDFGSIGGVFTSVGKLINQIFGTAYGVLFSGVSWTKIGIGILLTWIGLNSK	471
DENV3_CH53489	MAILGDTANDFGSGVGLNSLGRKNSQIFGSAYTALFSGVSWIMKIGIGVLLTWIGLNSK	469
* *		
ZIKV_FF13/251013-18	NGSISIMCLALGGVLIPLSTAVSAD	505
DENV4_TVP-376	NTSMANTCIAVGGITLFLGPTVQA--	495
DENV2_16681	STSLVTLVLVGIIVTLVLGVNVQA--	495
DENV1_WestPac	STSLSMTCIAVGMYTLVLGVNVQA--	495
DENV3_CH53489	NTSMSPSCIAIGIITLYLGAVVQA--	493

FIG. 17B

CLUSTAL O(1.2.4) multiple sequence alignment

```

Tick-borne encephalitis_virus_Strain_Moscow
Powassan_virus_Strain_Lineage_I
Yellow_Fever_virus_Strain_17D
DENV2_16681
West_Nile_Virus_Strain_NY99
Japanese_Encephalitis_Virus_Strain_SA14-14-2
Usutu_virus_Strain_MB119/06

Tick-borne encephalitis_virus_Strain_Moscow
Powassan_virus_Strain_Lineage_I
Yellow_Fever_virus_Strain_17D
DENV2_16681
West_Nile_Virus_Strain_NY99
Japanese_Encephalitis_Virus_Strain_SA14-14-2
Usutu_virus_Strain_MB119/06

Tick-borne encephalitis_virus_Strain_Moscow
Powassan_virus_Strain_Lineage_I
Yellow_Fever_virus_Strain_17D
DENV2_16681
West_Nile_Virus_Strain_NY99
Japanese_Encephalitis_Virus_Strain_SA14-14-2
Usutu_virus_Strain_MB119/06

SRCTHLENRDFVTGCTGTTNVTVLVLELGGCVTTIABGKTSMDVWLDALYQENPAKTRREYC 60
TRCTHLENRDFVTGVTGCTTTRVSLVLELGGCVTTIABGKPSIDVWLEDFQESPAETREYC 60
AHCIGITDRDFIEGVHGGCTWVSATLEQDKCVTVMAHPKPSLDLSLETVAIDRPAEVRKVC 60
MRCIGMSNRDFVECVSGGSWVDIVLEHSGCVTTMAKNKPTILDELIKTEAKQPATLRKYC 60
FNCIGMSNRDFLEGVSGATWVDIVLEGDSCTTMSDKKPTIDVKNMMEZAAALAEVRSYC 60
FNCIGMSNRDFIEGASGATWVDIVLEGDSCTTMANNNKPTIDVEMINTEASQLAEVRSYC 60
FNCIGMSNRDFLEGVSGATWVDIVLEGDSCTTMAKDKPTIDIKNMETEAATNLAEVRSYC 60
* : :***: * . * : * .** . * : * : * : * : * : * : * : * : * : *
LHAKLSDTKVAARCPITMGPAITLAEHQGGCTVCKRDQSDRGWGNHCGLFCKGSIIVACVKA 120
LHAKLSNTXVEARCPITGPAITLPEHQADWCKRDQSDRGWGNHCGFFCKGSIIVACAKFE 120
YNAVLTHTVKINDKCPSTGEAHLAEENEGDNACKRTYSDRGWNGCGGLFCGKSIIVACAKFT 120
IEAKLTNTTTSRCPTQGEPSLNEEQKRFVCKHSMVDRGWNGCGGLFCGKSGIVTCAMFR 120
YLATVSDLSTKAACPTMGCAHNDKRAPAFVCRGVVDRGWNGCGGLFCGKSIDTCAKFA 120
YHASVTDISTVARCPITGCAHNEKRAESSYVCKGFTDRGWNGCGFFCKGSIIDTCAKFS 120
YLATVSDVSTVSNCPITGCAHNPKRAEDTYVCKSGVTDRGWNGCGGLFCGKSIDTCAKFT 120
* : : . . ** : * : * : * : * : * : * : * : * : * : * : * : * : *
CEAKKATGHVYDANKIVTVKVEPHGTGDYVAANETHS-----GKRTASPTISSEKTL 174
CEEAKKAVGHVYOSTKITVYVKAEPHTGDYQANETNE-----NRKTAQFTVASEKVIL 174
CA---KSMSLFEVDQTKIQVVIRACLHVGAQENWFT-----DITKLPFDALSGSQEV 170
CK---KNNEGRVVQOPENLETTIVITPHSGEEHA--VGNDT-----GKHGKEIKITPQESITEA 173
CS---TKAIGRTILKENIKYEAIFVHGPTTVESHGNYSTQVGATQAGKLSITPAAPSYTL 178
CT---SKAIGRTIOPENIKYKVGIFVHGTTTSENHGNYSQVGAAGAAKFTVTFNAPSVAL 178
CS---LKAVGRMIQOPENVKYEVGIFINGSTSSDTHGNYSSQLGASQAGKFTTTFNSPAITY 178
* * * * * : : * : * : * : * : * : * : * : * : * : * : * : * : *

```

FIG. 17B cont.

Tick-borne encephalitis virus Strain_Moscow	231
Powassan virus Strain_Lineage_1	231
Yellow Fever Virus Strain_17D	221
DENV2_16681	227
West Nile Virus Strain_NY99	229
Japanese Encephalitis Virus Strain_SA14-14-2	229
Usutu virus Strain_MB119/06	229
Tick-borne encephalitis virus Strain_Moscow	288
Powassan virus Strain_Lineage_1	288
Yellow Fever Virus Strain_17D	281
DENV2_16681	283
West Nile Virus Strain_NY99	286
Japanese Encephalitis Virus Strain_SA14-14-2	285
Usutu virus Strain_MB119/06	285
Tick-borne encephalitis virus Strain_Moscow	347
Powassan virus Strain_Lineage_1	348
Yellow Fever Virus Strain_17D	339
DENV2_16681	341
West Nile Virus Strain_NY99	345
Japanese Encephalitis Virus Strain_SA14-14-2	344
Usutu virus Strain_MB119/06	344

Strain	Lineage	Position	Sequence
Tick-borne encephalitis virus	Strain_Moscow		CSPOVNVAMLITPNPTIEN---NGCGFIEMQLPPGDNLIYVC-----ELSHQWFOKSSSIG
Powassan virus	Strain_Lineage_1		CVPTTNVAMLITPNPTIET---SCGGFIEMQLPLGDNLIYVC-----DLSDQWFOKSGTIG
Yellow Fever Virus	Strain_17D		LTAAINKGILVTNPIAST---NDEEVLIENVNPPFGDSYIIVGSGDSRLTYQNHKEGSSIG
DENV2_16681			LEKHHVLGRLITVNPPIVTE---KDSPVNIEAEPFPFGDSYIIGVEPQQLNWEKKGSSIG
West Nile Virus	Strain_NY99		LNDLTPVGRITVNPFPVSATANAKVLIELEPPFGDSYIIVGGEQQIHHWHKSGSSIG
Japanese Encephalitis Virus	Strain_SA14-14-2		LNDMTPVGRITVNPFPVATSSANSKVLVEMEPFPFGDSYIIVGREGAKQIHHWHKAGSTLG
Usutu virus	Strain_MB119/06		LSDLTPIGRMTANPYVASSEANAKVLVEMEPFPFGDSYIIVGRCGRQIHHWHKAGSSIG
Tick-borne encephalitis virus	Strain_Moscow		RVQKTKKGIERTLVIGEHANDFGSAGGFLSSIGKAVHTVLGGAFNLSIFGCVVFLPKLL
Powassan virus	Strain_Lineage_1		RNFERTKGLERLSVVGHEANDFGSVGGILSSVSKAIHTVLGGAFNTLFGGVGFIPKMLL
Yellow Fever Virus	Strain_17D		KLFTQTMKGVERLAVMGDTAMDPFSSNGGPFTSVKGIGIHTVFGSAFQGLFGGLNWLITVIM
DENV2_16681			QMFETTMGAKRMALIGDTAMDPGSLGCGVFTSIGKALHQVFQAIYCAAFSGVSWTKILI
West Nile Virus	Strain_NY99		KAPFTTLKGAORLAALGDTAMDPGSVGCGVFTSVGKAVHQVFGGAFRSLFGGMSWITQGLL
Japanese Encephalitis Virus	Strain_SA14-14-2		KAPSTTLKGAORLAALGDTAMDPGSIGGVFNLSIGKAVHQVFGGAFRTLFGGMSWITQGLM
Usutu virus	Strain_MB119/06		KAPITTLKGAORLAALGDTAMDPGSVGGIFNLSVSKAVHQVFGGAFRTLFGGMSWITQGLM
Tick-borne encephalitis virus	Strain_Moscow		GVALAWLGLNMRNPTMSNLFLLAGGIVLAMITLGVGA-----
Powassan virus	Strain_Lineage_1		GVALVWLGLNARNPTMSNLTFLAVGALTNMTMGVGA-----
Yellow Fever Virus	Strain_17D		CAVLIVVGINTRNPTMSNMLVGVIMFSLGVCADQGCAGNFCNRELKCGDGFIF
DENV2_16681			GVITITWIMNSRSTLSVTLVLGVITVLYLGVNVQA-----
West Nile Virus	Strain_NY99		GALLMMGNINARDSIALTLFVAVGGVLLFLSVNVHA-----
Japanese Encephalitis Virus	Strain_SA14-14-2		GALLMMGNINARDSIALATLATGGVLLVFLATNVHA-----
Usutu virus	Strain_MB119/06		GALLMMGNINARDSIALVMLATGGVLLFLATNVHA-----

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2020/045241**Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 206,210,211
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
As claims 206, 210 and 211 each refer to an unsearchable claim which does not comply with PCT Rule 6.4(a), claims 206, 210 and 211 are unclear (PCT Article 6).
3. ☒ Claims Nos.: 6-205,207-209,212-227
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of any additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2020/045241**A. CLASSIFICATION OF SUBJECT MATTER****C07K 14/005(2006.01)i, A61K 39/12(2006.01)i, A61P 31/14(2006.01)i, G01N 33/68(2006.01)i, G01N 33/569(2006.01)i**

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K 14/005; A61K 39/12; G01N 33/569; G01N 33/68; A61P 31/14

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Korean utility models and applications for utility models

Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

eKOMPASS(KIPO internal) & Keywords: flavivirus, dengue virus, serotype, E glycoprotein, amino acid substitution

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2018-0280494 A1 (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL) 04 October 2018 paragraphs [0018]–[0140]; and figure 1	1–5
Y	NCBI Reference Sequence: ANG57777.1 polyprotein [Dengue virus 2] 28 May 2016 definition; and fasta	1–5
A	US 2015-0328303 A1 (THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL et al.) 19 November 2015 claims 1–42	1–5
A	WO 2015-019253 A2 (INTERNATIONAL CENTRE FOR GENETIC ENGINEERING AND BIOTECHNOLOGY – ICGEB) 12 February 2015 claims 1–25	1–5
A	US 2016-0367658 A1 (THE GOVERNMENT OF THE USA, AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES et al.) 22 December 2016 claims 1–20	1–5



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"D" document cited by the applicant in the international application

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

19 November 2020 (19.11.2020)

Date of mailing of the international search report

19 November 2020 (19.11.2020)

Name and mailing address of the ISA/KR

International Application Division

Korean Intellectual Property Office

189 Cheongsa-ro, Seo-gu, Daejeon, 35208, Republic of Korea



Facsimile No. +82-42-481-8578

Authorized officer

HEO, Joo Hyung

Telephone No. +82-42-481-5373



INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2020/045241

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2018-0280494 A1	04/10/2018	AU 2016-335120 A1 AU 2016-335120 A1 CA 3004422 A1 EP 3359652 A1 JP 2018-531256 A PH 12018500986 A1 SG 11201803787 A US 10772948 B2 WO 2017-062174 A1	24/05/2018 13/04/2017 13/04/2017 15/08/2018 25/10/2018 17/12/2018 28/06/2018 15/09/2020 13/04/2017
US 2015-0328303 A1	19/11/2015	CN 104428312 A CN 108912215 A EP 2834265 A1 US 10117924 B2 US 2018-125964 A1 US 2019-255168 A1 US 9821050 B2 WO 2013-151764 A1	18/03/2015 30/11/2018 11/02/2015 06/11/2018 10/05/2018 22/08/2019 21/11/2017 10/10/2013
WO 2015-019253 A2	12/02/2015	IT RM20130458 A1 WO 2015-019253 A3	06/02/2015 28/05/2015
US 2016-0367658 A1	22/12/2016	AT 526411 T AU 2001-238441 B2 AU 2001-38441 A1 AU 2007-200319 A1 AU 2007-200319 B2 AU 2007-200319 B8 AU 2009-212794 A1 AU 2009-212794 B2 AU 2012-202659 A1 AU 2012-202659 A8 AU 2012-202659 B2 AU 2015-213355 A1 AU 2015-213355 B2 AU 2018-200081 A1 AU 2018-200081 B2 AU 3844101 A CA 2398872 A1 CA 2398872 C CA 2941182 A1 CY 1116971 T1 DK 2278012 T3 EP 1263965 A2 EP 1263965 B1 EP 2278012 A2 EP 2278012 A3 EP 2278012 B1 EP 3000477 A1	15/10/2011 26/10/2006 27/08/2001 15/02/2007 28/05/2009 07/01/2010 17/09/2009 09/02/2012 31/05/2012 10/12/2015 14/05/2015 03/09/2015 05/10/2017 25/01/2018 21/11/2019 27/08/2001 23/08/2001 20/03/2018 23/08/2001 05/04/2017 07/12/2015 11/12/2002 28/09/2011 26/01/2011 09/03/2011 26/08/2015 30/03/2016

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2020/045241

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
		ES 2374131 T3	14/02/2012
		ES 2554254 T3	17/12/2015
		JP 2003-523189 A	05/08/2003
		JP 4656794 B2	23/03/2011
		PT 2278012 E	30/11/2015
		US 10335478 B2	02/07/2019
		US 2006-0062803 A1	23/03/2006
		US 2009-0010961 A1	08/01/2009
		US 2010-0255030 A1	07/10/2010
		US 2012-0014981 A1	19/01/2012
		US 2014-0141040 A1	22/05/2014
		US 7094411 B2	22/08/2006
		US 7641909 B2	05/01/2010
		US 8025887 B2	27/09/2011
		US 8673316 B2	18/03/2014
		US 9463233 B2	11/10/2016
		WO 01-60847 A2	23/08/2001
		WO 01-60847 A3	16/02/2000
		WO 01-60847 A3	25/04/2002
		WO 01-60847 A9	17/10/2002