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(54) **CHIMERIC WEST NILE/ZIKA VIRUSES AND METHODS OF USE**

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A61K 39/00 (2006.01)
C07K 14/005 (2006.01)
C12N 7/00 (2006.01)
A61K 39/295 (2006.01)
G01N 33/533 (2006.01)

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CPC **A61K 39/12** (2013.01); **C07K 14/005** (2013.01); **C12N 7/00** (2013.01); **G01N 33/533** (2013.01); **A61K 2039/525** (2013.01); **A61K 2039/5252** (2013.01); **A61K 2039/5254** (2013.01); **A61K 2039/53** (2013.01); **C12N 2770/24122** (2013.01); **C12N 2770/24134** (2013.01); **C12N 2770/24141** (2013.01); **C12N 2770/24144** (2013.01); **Y02A 50/392** (2018.01); **Y02A 50/394** (2018.01)

(58) **Field of Classification Search**
CPC C12N 7/00; C12N 2770/24122; C07K 14/005; Y02A 50/386; Y02A 50/388
See application file for complete search history.

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(57) **ABSTRACT**

Chimeric flaviviruses that include non-coding regions, non-structural proteins, a capsid (C) protein and a portion of a pre-membrane (prM) signal sequence from West Nile virus (WNV), and a portion of a prM signal sequence, a prM protein and an E protein from Zika virus (VIKV) are described. Also described are compositions and methods for eliciting an immune response in a subject, such as an immune response directed against ZIKV. Diagnostic assays that utilize chimeric West Nile/Zika viruses are further described.

39 Claims, 6 Drawing Sheets
Specification includes a Sequence Listing.

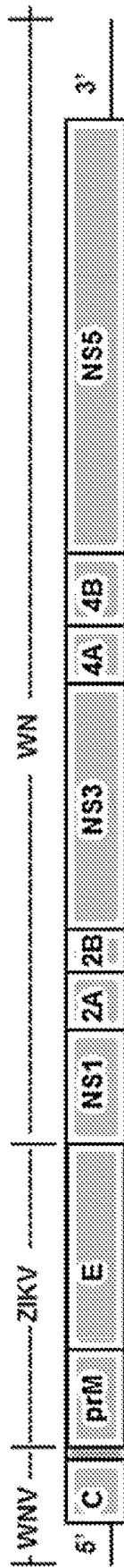


FIG. 1

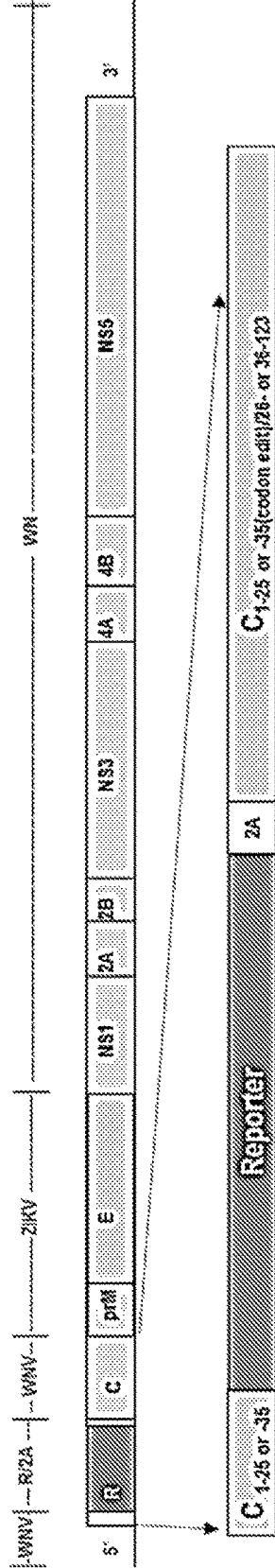
NS2B-3 protease cleavage

	C	PrM Signal Sequence (SS)	Signalase cleavage	PrM
WNV NY99	AAGAAAGA K K R	GGAGGAAGACCGGAATTCAGTCATGATGGCCCTGATGCCCGAGGTAGGAGCA G G K T G I A V M I G L I A S V G A	GTACCCCTCTCTAACYTCCAGGG	V T L S N F Q G
ZIKV R103451	AAGAGACEA K R R	GGCCAGATACTAGTGTGGAAATTTGGCCCTGCTGACACAGCTATGGCA G A D T S V G I V G L L L T T A M A	GCGGAGTCACTAGACGTGGGAGT	A E V T R R G S
Chimeric WN/ZKVs:				
WN/ZKV-23	AAGAAAGA K K R	GGAGGAAGACCGGAATTCAGTCATGATGGCCCTGATGCCCGAGGTATGGCA G G K T G I A V M I G L I A S A M A	GTATGGCA	GCGGAGTCACTAGACGTGGGAGT A E V T R R G S
WN/ZKV-25	AAGAAAGA K K R	GGAGGAAGACCGGAATTCAGTCATGATGGCCCTGATGCCCGAGGTATGGCA G G K T G I A V M I G L I T T A M A	AACACACCTATGGCA	GCGGAGTCACTAGACGTGGGAGT A E V T R R G S
WN/ZKV-215	AAGAAAGA K K R	GGAGGAAGACCGGAATTTGGCCCTGCTGACACAGCTATGGCA T S V G I V G L L L T T A M A	GCGGAGTCACTAGACGTGGGAGT	A E V T R R G S

FIG. 2

Type I reporter constructs:

- First C gene box [C1-25 or -35]: contains 1-25 or 1-35 amino acids of C protein: non-codon edited
- Reporter Gene can be ZsGreen, mWasabi, or Luciferase.
- 2A self cleavage peptide could be F2A or P2A
- Second C gene box [C1-25 or 1-35(edited codons)/26- or 36-123 contains entire C gene of WNV, the first 25 or 35 amino acids were codon edited (silent mutations), and rest codons are as wild-type codons of WNV C



Type II reporter constructs:

- Reporter Gene can be ZsGreen, mWasabi, or Luciferase.
- 2A self cleavage peptide could be F2A or P2A
- The reporter cassette is located after the first 3 AA of the WNV signal sequence encoding "GGK".
- The sequence encoding the entire 18 AA of the ZIKV signal sequence (red fonts) are included between 2A and prM

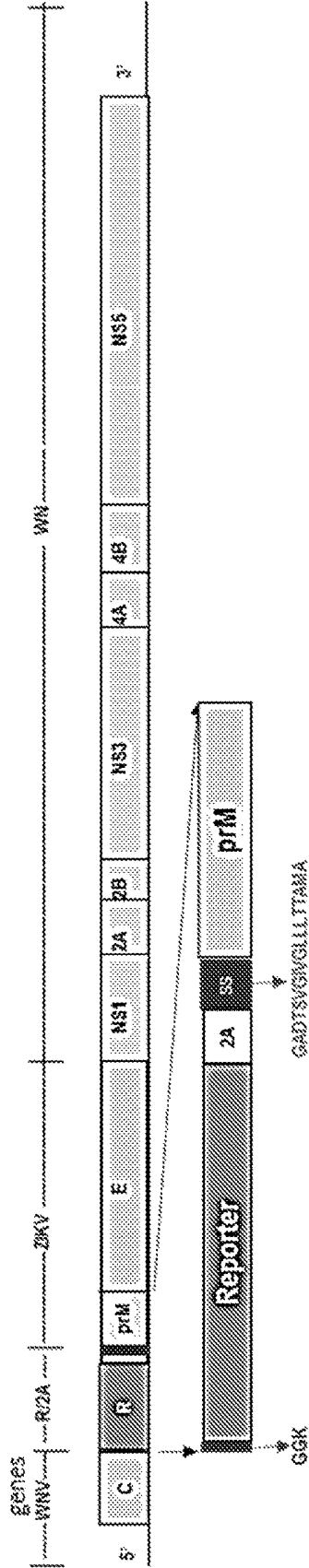


FIG. 3

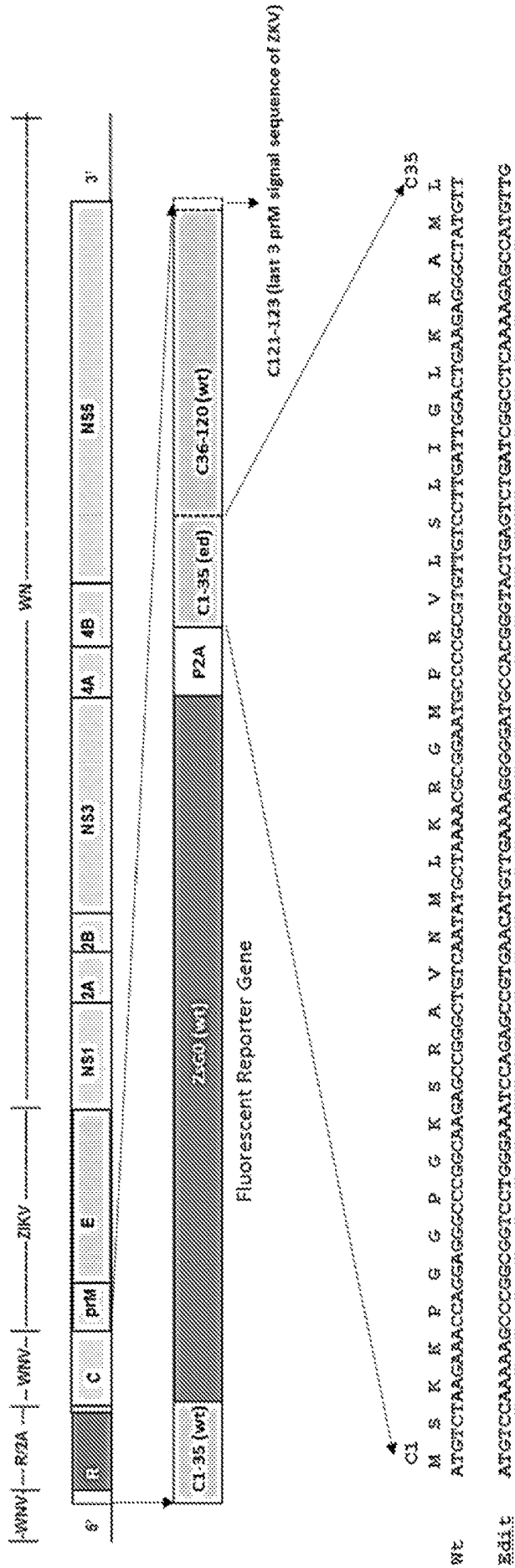
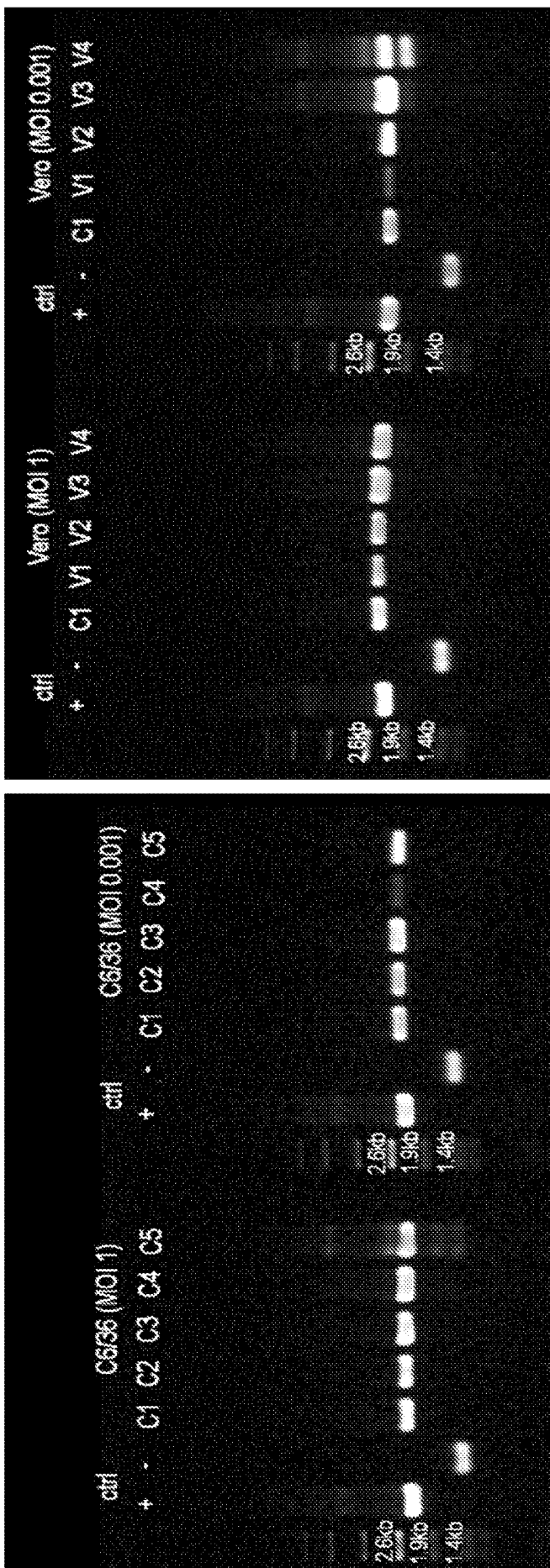


FIG. 4



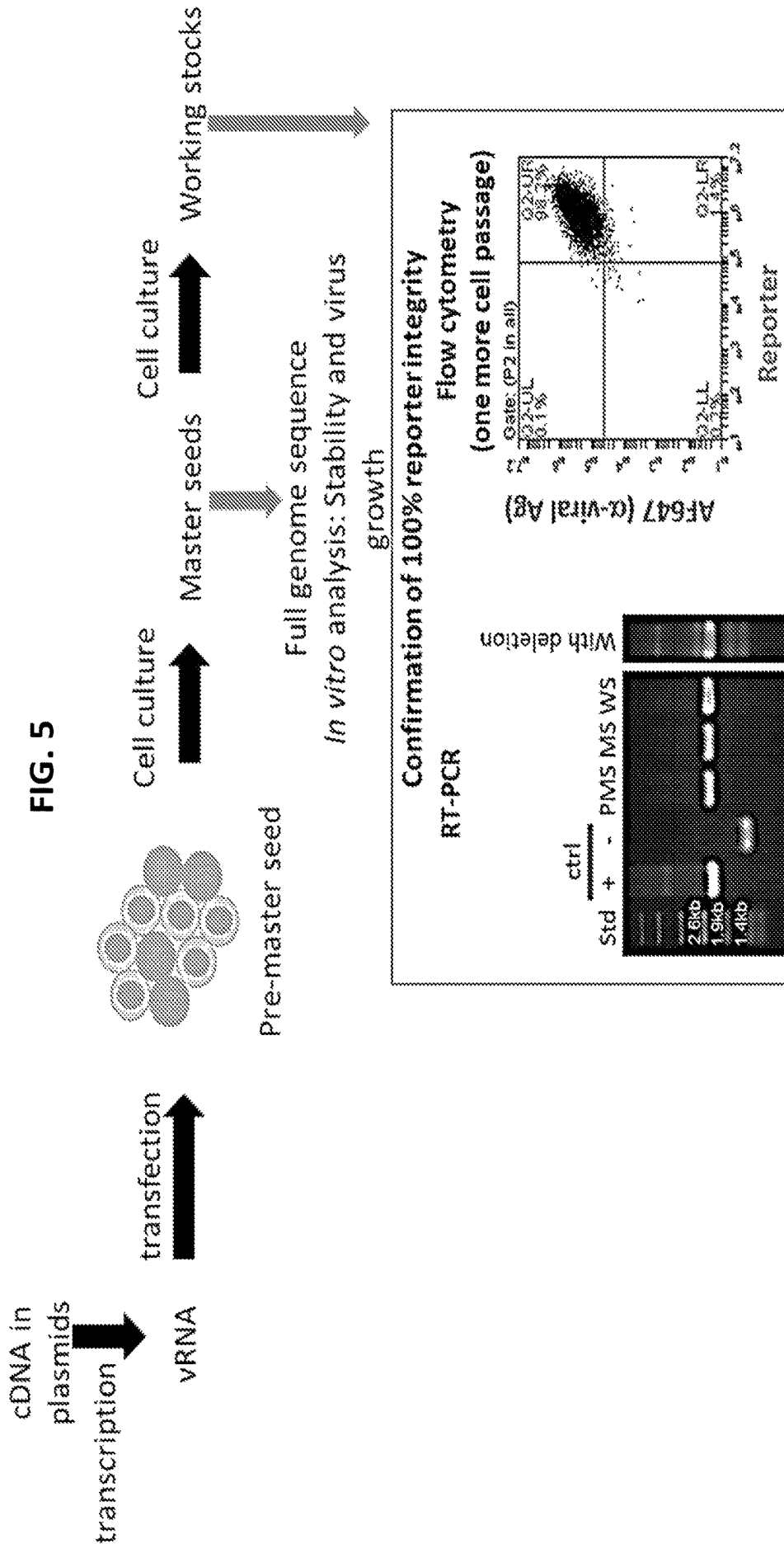


FIG. 6

Comparison of Neutralization Assays

	PRNT	Immuno-mFRNT	Fluoro-mFRNT
Detection	Plaque	Immunospot	Fluorospot
Processing	1-2 overlays	1 overlay	none
	Plaque staining	Fixation and Immunostaining	Live cell image (w/o fixation)
	Plaque visualization	Foci image	
Plate Format	6-, 12-, 24-well	96-, 384-well	96-, 384-well
Labor-intensive	High	High	Low
Estimated minimal time*	WN/ZKV: 72 hours (wt ZKV: 120 hours)	WN/ZKV: 28 hours (wt ZKV: 28/40 hours**)	R-WN/ZKV: 25 hours
Summary	Slow and labor-intensive	Fast and automatic readout, but labor-intensive	Fast and automatic readout, minimum procedures (high-throughput)

* Minimal duration starts from cell infection with virus-Ab complex and ends at result readout

** 40 hours is better than 28 hours

CHIMERIC WEST NILE/ZIKA VIRUSES AND METHODS OF USE**CROSS REFERENCE TO RELATED APPLICATIONS**

This application is the U.S. National Stage of International Application No. PCT/US2017/040818, file Jul. 6, 2017, published in English under PCT Article 21(2), which claims the benefit of U.S. Provisional Application No. 62/359,807, filed Jul. 8, 2016, which is herein incorporated by reference in its entirety.

FIELD

This disclosure concerns chimeric flaviviruses, particularly chimeric West Nile virus/Zika virus constructs. Further, it relates to methods of using the chimeric viruses for therapeutic and diagnostic applications.

BACKGROUND

Zika virus, a flavivirus classified within the Flaviviridae with other important mosquito-borne viruses, including yellow fever, dengue, West Nile and Japanese encephalitis viruses, has spread rapidly in a hemispheric-wide epidemic since the virus was introduced to Brazil in 2015, reaching Central and North Americas, including territories of the United States and now threatening the continental U.S. Initially isolated in 1947 in Uganda, the virus was first linked to human disease in 1952 and has been recognized sporadically as a cause of mild, self-limited febrile illness in Africa and Southeast Asia (Weaver et al., *Antiviral Res* 130:69-80, 2016; Faria et al., *Science* 352(6283):345-349, 2016). However, in 2007, an outbreak appeared in the North Pacific island of Yap, transferred there presumably from Asia, and subsequently disseminated from island to island across the Pacific, leading to an extensive outbreak in 2013-2014 in French Polynesia, with subsequent spread to New Caledonia, the Cook Islands, and ultimately to Easter Island, far to the East. An Asian lineage virus subsequently was transferred to the Western Hemisphere by routes that remain undetermined (Faria et al., *Science* 352(6283):345-349, 2016). The virus is transmitted anthropotically by *Aedes aegypti*, *A. albopictus* and possibly *A. hensilli* and *A. polynesiensis* (Weaver et al., *Antiviral Res* 130:69-80, 2016).

In late 2015, a significant increase in fetal abnormalities (e.g. microcephaly) and Guillain-Barré syndrome (GBS) in areas of widespread Zika virus infection raised concerns that Zika virus might be much more virulent than originally thought and prompted the World Health Organization (WHO) to declare a Public Health Emergency of International Concern (PHEIC) (Heymann et al., *Lancet* 387(10020):719-721, 2016).

SUMMARY

Disclosed herein are chimeric flaviviruses that include non-coding regions, a capsid (C) protein, a portion of a pre-membrane (prM) signal sequence, and non-structural proteins from West Nile virus (WNV); and a portion of a prM signal sequence, a prM protein and an envelope (E) protein from Zika virus (ZIKV). Also disclosed are compositions and methods for eliciting an immune response

directed against ZIKV in a subject. Diagnostic assays that utilize the disclosed chimeric West Nile/Zika viruses are further described.

Provided herein is a nucleic acid chimera that includes nucleic acid sequence from a WNV and nucleic acid sequence from a ZIKV. In some embodiments, the nucleic acid chimera includes a first nucleic acid molecule comprising a 5' non-coding region, a nucleic acid encoding a C protein and non-structural proteins, and a 3' non-coding region, each from a WNV genome, wherein the C protein comprises a portion of a prM signal sequence from the WNV genome and a portion of a prM signal sequence from a ZIKV genome; and a second nucleic acid molecule operably linked to the first nucleic acid molecule, encoding a prM protein and an E protein from the ZIKV genome. In some examples, the portion of the prM signal sequence from the WNV genome includes the first 15 amino acids of the WNV prM signal sequence and the portion of the prM signal sequence from the ZIKV genome includes the last three amino acids of the ZIKV prM signal sequence. In other examples, the portion of the prM signal sequence from the WNV genome includes the first 13 amino acids of the WNV prM signal sequence and the portion of the prM signal sequence from the ZIKV genome includes the last five amino acids of the ZIKV prM signal sequence. In yet other examples, the portion of the prM signal sequence from the WNV genome includes the first three amino acids of the WNV prM signal sequence and the portion of the prM signal sequence from the ZIKV genome includes the last 15 amino acids of the ZIKV prM signal sequence.

Also provided herein is an immunogenic composition that includes an inactivated virus comprising a nucleic acid chimera disclosed herein, and a pharmaceutically acceptable carrier. Further provided is a method of eliciting an immune response against ZIKV in a subject by administering the immunogenic composition.

A method that includes inactivating a virus comprising a nucleic chimera disclosed herein is further provided by the present disclosure. The virus can be inactivated using any means known in the art, such as, but not limited to treating the virus with a chemical inactivation agent, high pressure, ultraviolet irradiation, gamma irradiation, or any combination thereof.

Further provided herein is a nucleic acid chimera that includes a first nucleic acid molecule comprising a 5' non-coding region, a nucleic acid encoding a C protein and non-structural proteins, and a 3' non-coding region, each from a WNV genome, wherein the C protein comprises a portion of a prM signal sequence from the WNV genome and a portion of a prM signal sequence from a ZIKV genome; and a second nucleic acid molecule operably linked to the first nucleic acid molecule, encoding a prM protein and an E protein from the ZIKV genome, and further includes a reporter gene, such as a reporter gene encoding a light-emitting protein, such as a fluorescent or bioluminescent protein.

Further provided herein are chimeric viruses that include a nucleic acid chimera disclosed herein.

Methods of detecting ZIKV-specific antibodies in a sample are also provided herein. In some embodiments, the method includes contacting the sample with a chimeric virus disclosed herein under conditions sufficient to form virus-antibody complexes if ZIKV antibodies are present in the sample; and detecting the virus-antibody complexes, thereby detecting ZIKV-specific antibodies in the sample.

In some embodiments, the method includes contacting the sample with a chimeric virus disclosed herein to form a

virus-sample mixture, wherein virus-antibody complexes are formed in the virus-sample mixture if ZIKV-specific antibodies are present in the sample; inoculating a cell culture with the virus-sample mixture under conditions sufficient to allow plaque formation or micro-focus formation in the cell culture; and detecting a decrease in plaque formation or micro-focus formation in the cell culture as compared to a control cell culture, such as a control cell culture infected with virus only.

In some embodiments, the method includes providing a chimeric virus disclosed herein bound to a solid support; contacting the chimeric virus-bound solid support with the sample under conditions sufficient to form virus-antibody complexes if ZIKV-specific antibodies are present in the sample; contacting the virus-antibody complexes with a secondary antibody; and detecting binding of the secondary antibody to the virus-antibody complexes.

In some embodiments, the method includes providing a secondary antibody bound to a solid support; contacting the secondary antibody-bound solid support with the sample under conditions sufficient to allow binding of the secondary antibody to any ZIKV-specific antibodies present in the sample, thereby forming antibody-antibody complexes; contacting the antibody-antibody complexes with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the ZIKV-specific antibodies, thereby forming immune complexes; and detecting the presence of the immune complexes.

In some embodiments, the method includes providing a ZIKV-specific antibody bound to a solid support; contacting the antibody-bound solid support with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the ZIKV-specific antibody to form antibody-virus complexes; contacting the antibody-virus complexes with the sample to allow binding of any ZIKV-specific antibodies present in the sample to the chimeric virus, thereby forming immune complexes; contacting the immune complexes with a secondary antibody; and detecting binding of the secondary antibody to the immune complexes, thereby detecting ZIKV-specific antibodies present in the sample.

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

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the genomic structure of chimeric West Nile/Zika viruses. Chimeric viruses contain prM-E of ZIKV in the genomic backbone of WNV. The chimeric C/prM junction site is enlarged to show the 3 different junction strategies. The NS2B-3 protease cleavage and signalase cleavage sites are indicated. WNV (NY99) and ZIKV (R103451; also referred to as "103451" in the GenBank database) nucleotide and amino acid sequences are shown. For the three chimeric viruses, boxes indicate the ZIKV portion of the sequence. The sequences shown include WNV NY99 (nucleotides 403-489 of SEQ ID NO: 17; amino acids 103-131 of SEQ ID NO: 18), ZIKV R103451 (nucleotides 411-497 of SEQ ID NO: 13 and amino acids 102-130 of SEQ ID NO: 14), WN/ZKV-Z3 (nucleotides 403-489 of SEQ ID NO: 3; amino acids 103-131 of SEQ ID NO: 4), WN/ZKV-Z5 (nucleotides 403-489 of SEQ ID NO: 5; amino acids 103-131 of SEQ ID NO: 6) and WN/ZKV-Z15 (nucleotides 403-489 of SEQ ID NO: 7; amino acids 103-131 of SEQ ID NO: 8).

FIG. 2 shows the genomic structure of chimeric West Nile/Zika reporter viruses. Two construct strategies (Type I and Type II) are shown in the figure. For Type I reporter constructs, the reporter cassette (including the reporter gene and a 2A peptide encoding sequence) is inserted 5' of the complete C gene, and a partial C gene encoding the first 25 or 35 amino acids is added 5' of the reporter cassette. The partial C gene provides a critical cyclization sequence connected to the 5' non-coding region for competent virus replication. The first 25 or 35 amino acids in the complete C gene is codon edited with silent mutations to minimize homologous recombination potential with the partial C gene. The reporter viruses WN/ZKV-ZsG0 (SEQ ID NOs: 9 and 10) and WN/ZKV-ZsG1 (SEQ ID NOs: 11 and 12) are examples of Type I constructs with ZsGreen and P2A as the reporter cassette for both. For Type II reporter constructs, the reporter cassette is inserted in the signal sequence region at the 3' end of the C gene. The first three amino acids (GGK) of the WNV signal sequence are retained in front of the reporter for correct NS2B-NS3 cleavage, and the entire 18 amino acids of the ZIKV signal sequence (residues 105-122 of SEQ ID NO: 14) are included between the 2A peptide and Zika virus prM for proper prM protein processing.

FIG. 3 is a schematic of the R-WN/ZKV-PR chimeric reporter virus. R-WN/ZKV-PR (also referred to as R-WN/ZKV) is a Type I reporter construct with ZsG0/P2A inserted after C1-35 of WNV and includes a complete WNV C gene downstream of P2A. In order to minimize homologous recombination between the partial C gene (C1-35(wt)) preceding the reporter insert and the complete C gene following the reporter insert, the first 35 amino acids of the downstream C protein (C1-35(ed)) was edited to substitute specific nucleotides (indicated by underline) while maintaining the amino acid sequence.

FIG. 4 shows the genetic stability of ZsG0 in R-WN/ZKV-PR virus. R-WN/ZKV-PR was serially passaged in C6/36 cells (left) or Vero cells (right) at an MOI of 1 or an MOI of 0.001. ZsG0 gene was analyzed by RT-PCR with a primer set for amplifying a 2.27 kb cDNA fragment (nucleotides 1-2272 of R-WN/ZKV-PR), including the full ZsG0 and P2A. The reporter gene was intact after 5 passages in C6/36 cells at an MOI of 0.001, but showed deletion in a portion of the stock at an MOI of 1. In Vero cells, the reporter gene was stable up to 4 passages at an MOI of 1, but a significant portion of the 0.001 MOI passage-4 stock showed partial gene deletion.

FIG. 5 includes a schematic of the production of R-WN/ZKV reporter virus seed lots. Also shown are RT-PCR and flow cytometry analysis of the integrity of the R-WN/ZKV reporter virus.

FIG. 6 is a table showing a comparison of PRNT, immuno-mFRNT and fluoro-mFRNT assays when using WN/ZKV, R-WN/ZKV or wild-type Zika virus.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids, as defined in 37 C.F.R. 1.822. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. The Sequence Listing is submitted as an ASCII text file, created on Jan. 2, 2019 448 KB, which is incorporated by reference herein. In the accompanying sequence listing:

SEQ ID NOs: 1 and 2 are WN/ZKV-3PR nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 3 and 4 are WN/ZKV-3SPH nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 5 and 6 are WN/ZKV-5SPH nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 7 and 8 are WN/ZKV-15SPH nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 9 and 10 are WN/ZKV-ZsG0 reporter nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 11 and 12 are WN/ZKV-ZsG1 reporter nucleotide and amino acid sequences, respectively.

SEQ ID NOs: 13 and 14 are the nucleotide and amino acid sequences of Zika virus strain R103451.

SEQ ID NOs: 15 and 16 are the nucleotide and amino acid sequences of Zika virus strain PRVABC59.

SEQ ID NOs: 17 and 18 are the nucleotide and amino acid sequences of West Nile virus strain NY99, deposited under Genbank Accession No. AF196835.

SEQ ID NOs: 19 and 20 are R-WN/ZKV-PR reporter nucleotide and amino acid sequences, respectively.

DETAILED DESCRIPTION

I. Abbreviations

AST average survival time
 C capsid protein
 C(ss) prM signal sequence portion of C protein
 CPE cytopathic effect
 E envelope glycoprotein
 ELISA enzyme-linked immunosorbent assay
 GBS Guillain-Barré syndrome
 mAb monoclonal antibody
 mFRNT microfocus reduction neutralization test
 NCR non-coding region
 NS non-structural
 Nt Abs neutralization antibodies
 pfu plaque forming unit
 p.i. post-infection
 prM premembrane protein
 PHEIC Public Health Emergency of International Concern
 PRNT plaque reduction neutralization test
 WHO World Health Organization
 WNV West Nile virus
 WN/ZKV West Nile/Zika virus chimera
 ZIKV Zika virus

II. Terms and Methods

Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in *Lewin's Genes X*, ed. Krebs et al, Jones and Bartlett Publishers, 2009 (ISBN 0763766321); Kendrew et al. (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Publishers, 1994 (ISBN 0632021829); Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by Wiley, John & Sons, Inc., 1995 (ISBN 0471186341); and George P. Rédei, *Encyclopedic Dictionary of Genetics, Genomics, Proteomics and Informatics*, 3rd Edition, Springer, 2008 (ISBN: 1402067534).

Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. The singular terms "a," "an," and "the"

include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. It is further to be understood that all base sizes (lengths) or amino acid sizes (lengths), and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety for all purposes. All GenBank Accession Nos. mentioned herein are incorporated by reference in their entirety. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. In case of conflict, the present specification, including explanations of terms, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

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

Adjuvant: A substance or vehicle that non-specifically enhances the immune response to an antigen. Adjuvants can include a suspension of minerals (alum, aluminum hydroxide, or phosphate) on which antigen is adsorbed; or water-in-oil emulsion in which antigen solution is emulsified in mineral oil (for example, Freund's incomplete adjuvant), sometimes with the inclusion of killed mycobacteria (Freund's complete adjuvant) to further enhance antigenicity. Immunostimulatory oligonucleotides (such as those including a CpG motif) can also be used as adjuvants (for example, see U.S. Pat. Nos. 6,194,388; 6,207,646; 6,214,806; 6,218,371; 6,239,116; 6,339,068; 6,406,705; and 6,429,199). Adjuvants also include biological molecules, such as costimulatory molecules. Exemplary biological adjuvants include IL-2, RANTES, GM-CSF, TNF- α , IFN- γ , G-CSF, LFA-3, CD72, B7-1, B7-2, OX-40L and 41 BBL.

Administer: As used herein, administering a composition (e.g. an immunogenic composition, such as a chimeric virus) to a subject means to give, apply or bring the composition into contact with the subject. Administration can be accomplished by any of a number of routes, such as, for example, topical, oral, subcutaneous, intramuscular, intraperitoneal, intravenous, intrathecal and intramuscular.

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

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

As used herein, the term "antibodies" includes intact immunoglobulins as well as a number of well-characterized fragments. For instance, Fabs, Fvs, and single-chain Fvs (scFvs) that bind to target protein (or epitope within a

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

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

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

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

Biological sample: A sample obtained from a subject (such as a human or veterinary subject). Biological samples, include, for example, fluid, cell and/or tissue samples. In some embodiments herein, the biological sample is a fluid sample. Fluid sample include, but are not limited to, serum, blood, plasma, urine, feces, saliva, cerebral spinal fluid (CSF) and bronchoalveolar lavage (BAL) fluid.

Capsid protein (C protein): A flavivirus structural protein that functions to package viral RNA into the nucleocapsid core during virus assembly. The C-terminal portion of the C protein includes an internal signal sequence (referred to herein as either C(ss) or prM signal sequence) for translocation of the prM protein into the endoplasmic reticulum,

where cleavage of the C and prM proteins occurs. This signal sequence varies in length among different flaviviruses. For example, the C(ss) of both WNV and ZIKV is 18 amino acids, while the C(ss) of DEN viruses is 14 amino acids.

Chimera: A molecule (e.g., nucleic acid or protein) composed of parts that are of different origin (such as at least two nucleic acids or polypeptides) that, while typically unjoined in their native state, are joined or linked to form a single continuous molecule. A chimera may include nucleic acids or polypeptides that are joined end-to-end (for example, the amino-terminus of one sequence is joined to the carboxyl-terminus of a second sequence) or may include a sequence from one molecule that is embedded within that of another molecule (for example, the amino-terminus and carboxyl-terminus of the chimera are from one molecule, while an intervening sequence comes from another molecule).

A chimera may include a chimeric protein, for example a protein that is composed of amino acids from more than one protein. A chimera may also include a chimeric nucleic acid composed of nucleic acid sequences from more than one source, such as a chimeric nucleic acid which encodes a chimeric protein. In other examples, a chimera may include a chimeric genome, such as a flavivirus genome, which is composed of sequences from two or more flaviviruses. For example, a chimeric flavivirus genome may comprise nucleic acid sequences from more than one flavivirus genome, such as a West Nile virus and a Zika virus. In some examples, a chimeric flavivirus includes nucleic acids encoding one or more proteins from a first flavivirus and nucleic acids encoding one or more proteins from a second flavivirus. In particular examples, a chimeric flavivirus is composed of a nucleic acid encoding the non-structural proteins and a C protein or a portion thereof from a West Nile virus genome linked to a nucleic acid encoding a prM protein and E protein (and optionally a portion of a C protein) from a Zika virus genome.

Conservative substitution: A substitution of one amino acid residue in a protein sequence for a different amino acid residue having similar biochemical properties. Typically, conservative substitutions have little to no impact on the activity of a resulting polypeptide. For example, ideally, a flavivirus protein (such as a prM, E, or non-structural protein) including one or more conservative substitutions (for example 1-10, 2-5, or 10-20, or no more than 2, 5, 10, 20, 30, 40, or 50 substitutions) retains the structure and function of the wild-type protein. A polypeptide can be produced to contain one or more conservative substitutions by manipulating the nucleotide sequence that encodes that polypeptide using, for example, standard procedures such as site-directed mutagenesis or PCR. In one example, such variants can be readily selected for additional testing by infecting cells with a virus containing a variant protein and determining its ability to replicate, by producing virus containing a variant protein and determining its neurovirulence or neuroinvasion properties, and/or by testing antibody cross-reactivity.

Contacting: Placement in direct physical association; includes both in solid and liquid form. "Contacting" is often used interchangeably with "exposed." In some cases, "contacting" includes transfecting, such as transfecting a nucleic acid molecule into a cell. In other examples, "contacting" refers to incubating a molecule (such as an antibody) with a biological sample.

Control: A reference standard, for example a positive control or negative control. A positive control is known to provide a positive test result. A negative control is known to

provide a negative test result. However, the reference standard can be a theoretical or computed result, for example a result obtained in a population.

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

Flavivirus non-structural protein: There are seven non-structural (NS) proteins of a flavivirus, NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5, which are encoded by the portion of the flavivirus genome that is 3' to the structural proteins. NS1 has been implicated in RNA replication and has been shown to be secreted from infected mammalian cells (Post et al., *Virus Res.* 18:291-302, 1991; Mackenzie et al., *Virology* 220:232-240, 1996; Muylaert et al., *Virology* 222:159-168, 1996). NS1 can elicit strong humoral immune responses and is a potential vaccine candidate (Shlesinger et al., *J. Virol.* 60:1153-1155, 1986; Qu et al., *J. Gen. Virol.* 74:89-97, 1993). NS2 is cleaved into NS2A and NS2B. NS2A is involved in RNA replication and virus particle assembly and secretion and NS2B forms a complex with NS3 and functions as a cofactor for the NS3 protease, which cleaves portions of the virus polyprotein. NS3 also functions as an RNA helicase and is used to unwind viral RNA during replication (Li et al., *J. Virol.* 73:3108-3116, 1999). While the exact functions of NS4A and NS4B remain to be elucidated, they are thought to be involved in RNA replication and RNA trafficking (Lindenbach and Rice, In: *Fields Virology*, Knipe and Howley, eds., Lippincott, Williams, and Wilkins, 991-1041, 2001). Finally, the NS5 protein is an RNA-dependent RNA polymerase involved in genome replication (Rice et al., *Science* 229:726-733, 1985). NS5 also shows methyltransferase activity commonly found in RNA capping enzymes (Koonin, *J. Gen. Virol.* 74:733-740, 1993).

Flavivirus structural protein: The capsid (C), premembrane (prM), and envelope (E) proteins of a flavivirus are the viral structural proteins. Flavivirus genomes consist of positive-sense RNAs that are roughly 11 kb in length. The genome has a 5' cap, but lacks a 3' polyadenylated tail (Wengler et al., *Virology* 89:423-437, 1978) and is translated into one polyprotein. The structural proteins (C, prM, and E) are at the amino-terminal end of the polyprotein followed by the non-structural proteins (NS1-5). The polyprotein is cleaved by virus and host derived proteases into individual proteins. The C protein forms the viral capsid while the prM and E proteins are embedded in the surrounding envelope (Russell et al., *The Togaviruses: Biology, Structure, and Replication*, Schlesinger, ed., Academic Press, 1980). The E protein functions in binding to host cell receptors resulting in receptor-mediated endocytosis. In the low pH of the endosome, the E protein undergoes a conformational change causing fusion between the viral envelope and the endosomal membranes. The prM protein is believed to stabilize the E protein until the virus exits the infected cell, at which time prM is cleaved to the mature M protein (Reviewed in Lindenbach and Rice, In: *Fields Virology*, Knipe and Howley, eds., Lippincott, Williams, and Wilkins, 991-1041, 2001).

Fluorescent protein: A protein that emits light of a certain wavelength when exposed to a particular wavelength of light. Fluorescent proteins include, but are not limited to,

green fluorescent proteins (such as GFP, EGFP, AcGFP1, Emerald, Superfolder GFP, Azami Green, mWasabi, Tag-GFP, TurboGFP and ZsGreen), blue fluorescent proteins (such as EBFP, EBFP2, Sapphire, T-Sapphire, Azurite and mTagBFP), cyan fluorescent proteins (such as ECFP, mECFP, Cerulean, CyPet, AmCyan1, Midori-Ishi Cyan, mTurquoise and mTFP1), yellow fluorescent proteins (EYFP, Topaz, Venus, mCitrine, YPet, TagYFP, PhiYFP, ZsYellow1 and mBanana), orange fluorescent proteins (Kusabira Orange, Kusabira Orange2, mOrange, mOrange2 and mTangerine), red fluorescent proteins (mRuby, mApple, mStrawberry, AsRed2, mRFPI, JRed, mCherry, HcRed1, mRaspberry, dKeima-Tandem, HcRed-Tandem, mPlum, AQ143, tdTomato and E2-Crimson), orange/red fluorescence proteins (dTomato, dTomato-Tandem, TagRFP, TagRFP-T, DsRed, DsRed2, DsRed-Express (TI) and DsRed-Monomer) and modified versions thereof.

Heterologous: Originating from a different genetic sources or species. For example, a chimeric nucleic acid including nucleic acid from two (or more) different genetic sources or from two (or more) otherwise separated segments of sequence from a single genetic source is considered a heterologous nucleic acid. Similarly, a polypeptide including peptides from two (or more) different proteins from a single genetic source or two (or more) proteins from different genetic sources (such as a fusion protein) is considered a heterologous polypeptide. For example, a nucleic acid comprising portions of a WNV genome operably linked to a nucleic acid comprising portions of a ZIKV genome is a heterologous nucleic acid. Similarly, a polypeptide including a WNV polypeptide or portion thereof linked to a ZIKV polypeptide or portion thereof is a heterologous polypeptide.

In another example of use of the term heterologous, a nucleic acid that is heterologous to a cell originates from an organism or species other than the cell in which it is expressed. In one specific, non-limiting example, a heterologous nucleic acid includes a flavivirus nucleic acid that is present or expressed in a bacterial cell (such as an *E. coli* cell) or in an algal, plant, insect (e.g. C6/36), or mammalian (e.g., Vero) cell. Methods for introducing a heterologous nucleic acid into bacterial, algal, plant, insect, and mammalian cells are well known in the art, including infection of a cell with a viral nucleic acid, or transformation with a nucleic acid, for example electroporation, lipofection, and particle gun acceleration.

Immune response: A response of a cell of the immune system, such as a B-cell, T-cell, macrophage or polymorphonucleocyte, to a stimulus such as an antigen. An immune response can include any cell of the body involved in a host defense response for example, an epithelial cell that secretes an interferon or a cytokine. An immune response includes, but is not limited to, an innate immune response or inflammation.

Immunize: To render a subject protected from an infectious disease, such as by vaccination.

Inactivated virus: A virus (such as a viral vaccine) that has been rendered incapable of replication in host cells (and is thus not virulent), but can elicit an immune response. Methods of inactivating a virus (such as a virus including a nucleic acid chimera described herein) include chemical treatment (for example, formaldehyde), physical treatment (such as heat), irradiation, or combinations thereof.

Isolated: An "isolated" or "purified" biological component (such as a nucleic acid, peptide, protein, protein complex, or particle) has been substantially separated, produced apart from, or purified away from other components in a preparation or other biological components in the cell of the

organism in which the component occurs, that is, other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids, peptides and proteins that have been “isolated” or “purified” thus include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids, peptides and proteins prepared by recombinant expression in a host cell, as well as chemically synthesized nucleic acids or proteins. The term “isolated” or “purified” does not require absolute purity; rather, it is intended as a relative term. Thus, for example, an isolated biological component is one in which the biological component is more enriched than the biological component is in its natural environment within a cell, or other production vessel. Preferably, a preparation is purified such that the biological component represents at least 50%, such as at least 70%, at least 90%, at least 95%, or greater, of the total biological component content of the preparation.

Light-emitting protein: Any protein that is capable of emitting light or inducing the emission of light by acting on a particular substrate. Light-emitting proteins include, for example, fluorescent proteins and bioluminescent proteins. Fluorescent proteins include, for example, green fluorescent proteins and variants thereof (including blue, cyan, yellow, orange and red fluorescent proteins) and phycobiliproteins, such as B-phycoerythrin (B-PE), R-phycoerythrin (R-PE) and allophycocyanin (APC). Bioluminescent proteins include, for example, aequorin and luciferase (which acts on the substrate luciferin to emit light).

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

Operably linked: A first nucleic acid is operably linked to a second nucleic acid when the first nucleic acid is placed in a functional relationship with the second nucleic acid. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame. Operably linked nucleic acids include a first nucleic acid contiguous with the 5' or 3' end of a second nucleic acid. In other examples, a second nucleic acid is operably linked to a first nucleic acid when it is embedded within the first nucleic acid, for example, where the nucleic acid construct includes (in order) a portion of the first nucleic acid, the second nucleic acid, and the remainder of the first nucleic acid.

Pharmaceutically acceptable carrier: The pharmaceutically acceptable carriers (vehicles) useful in this disclosure are conventional. *Remington: The Science and Practice of Pharmacy*, The University of the Sciences in Philadelphia, Editor, Lippincott, Williams, & Wilkins, Philadelphia, Pa., 21st Edition (2005), describes compositions and formulations suitable for pharmaceutical delivery of one or more therapeutic compositions, such as a chimeric virus, and additional pharmaceutical agents.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually comprise injectable fluids that include pharmaceutically and physiologi-

cally acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol or the like as a vehicle. For solid compositions (for example, powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

Premembrane protein (prM protein): A flavivirus structural protein. The prM protein is an approximately 25 kDa protein that is the intracellular precursor for the membrane (M) protein. prM is believed to stabilize the E protein during transport of the immature virion to the cell surface. When the virus exits the infected cell, the prM protein is cleaved to the mature M protein, which is part of the viral envelope (Reviewed in Lindenbach and Rice, In: *Fields Virology*, Knipe and Howley, eds., Lippincott, Williams, and Wilkins, 991-1041, 2001).

Preventing, treating or ameliorating a disease: “Preventing” a disease refers to inhibiting the full development of a disease. “Treating” refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition after it has begun to develop. “Ameliorating” refers to the reduction in the number or severity of one or more signs or symptoms of a disease.

Purified: The term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified nucleic acid preparation is one in which the nucleic acid is more enriched than the nucleic acid is in its natural environment (such as within a cell) or in a preparation or production vessel. In other examples, a purified virus preparation is one in which the virus is more enriched than in a cell or organism, a preparation, or a production vessel. A purified nucleic acid or virus also includes one that is substantially free of undesired components, such as an inactivating agent. Preferably, a preparation is purified such that the nucleic acid or virus represents at least 50% of the total content of the preparation. In some embodiments, a purified preparation contains at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or more of the nucleic acid or virus.

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

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

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

The alignment tools ALIGN (Myers and Miller, *CABIOS* 4:11-17, 1989) or LFASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85:2444-2448, 1988) may be used to perform sequence comparisons (Internet Program © 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFASTA compares regions of local similarity. These alignment tools and their respective tutorials are available on the Internet at the NCSA website. Alternatively, for comparisons of amino acid sequences of greater than about 30 amino acids, the "Blast 2 sequences" function can be employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the "Blast 2 sequences" function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). The BLAST sequence comparison system is available, for instance, from the NCBI web site; see also Altschul et al., *J. Mol. Biol.*, 215:403-10, 1990; Gish and States, *Nature Genet.*, 3:266-72, 1993; Madden et al., *Meth. Enzymol.*, 266:131-41, 1996; Altschul et al., *Nucleic Acids Res.*, 25:3389-402, 1997; and Zhang and Madden, *Genome Res.*, 7:649-56, 1997.

Serum: The fluid portion of the blood that separates out from clotted blood. Serum contains many proteins, including antibodies, but does not contain clotting factors.

Subject: Living multi-cellular vertebrate organisms, a category that includes both human and non-human mammals (such as mice, rats, rabbits, sheep, horses, cows, and non-human primates).

Therapeutically effective amount: A quantity of a specified agent (such as a chimeric virus) sufficient to achieve a desired effect in a subject being treated with that agent. For example, this may be the amount of a virus vaccine useful for eliciting an immune response in a subject and/or for preventing infection by the virus. In the context of the present disclosure, a therapeutically effective amount of a Zika virus vaccine, for example, is an amount sufficient to increase resistance to, prevent, ameliorate, and/or treat infection caused by Zika virus in a subject without causing a substantial cytotoxic effect in the subject. The effective amount of a Zika virus vaccine (or Zika virus immunogenic composition) useful for increasing resistance to, preventing, ameliorating, and/or treating infection in a subject will be dependent on, for example, the subject being treated, the manner of administration of the therapeutic composition and other factors.

Transformed: A "transformed" cell is a cell into which has been introduced a nucleic acid molecule (such as a heterologous nucleic acid) by molecular biology techniques. The term encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid

vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Vaccine: A preparation of immunogenic material capable of stimulating an immune response, administered for the prevention, inhibition, amelioration, or treatment of infectious or other types of disease. The immunogenic material may include attenuated or inactivated (killed) microorganisms (such as bacteria or viruses), or antigenic proteins, peptides or DNA derived from them. An attenuated virus is a virulent organism that has been modified to produce a less virulent form, but nevertheless retains the ability to elicit antibodies and cell-mediated immunity against the virulent form. An inactivated (killed) virus is a previously virulent organism that has been inactivated with chemicals, heat, or other treatment, but elicits antibodies against the organism. Vaccines may elicit both prophylactic (preventative or protective) and therapeutic responses. Methods of administration vary according to the vaccine, but may include inoculation, ingestion, inhalation or other forms of administration. Vaccines may be administered with an adjuvant to boost the immune response.

Vector: A vector is a nucleic acid molecule allowing insertion of foreign nucleic acid without disrupting the ability of the vector to replicate and/or integrate in a host cell. A vector can include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. An insertional vector is capable of inserting itself into a host nucleic acid. A vector can also include one or more selectable marker genes and other genetic elements. An expression vector is a vector that contains the necessary regulatory sequences to allow transcription and translation of inserted gene or genes.

West Nile virus (WNV): A member of the virus family Flaviviridae and the genus Flavivirus. Other members of this genus include dengue virus, yellow fever virus, Japanese encephalitis virus (JEV), Zika virus and Spondweni virus. WNV was first isolated from a woman in the West Nile district of Uganda in 1937. The virus was later identified in birds in the Nile delta region in 1953. Human infections attributable to WNV have been reported in many countries for over 50 years. In 1999, a WNV circulating in Israel and Tunisia was imported into New York, producing a large and dramatic outbreak that spread throughout the continental United States in the following years. Human infection is most often the result of bites from infected mosquitoes, but may also be transmitted through contact with other infection animals, their blood or other tissues. Infection with WNV is asymptomatic in about 80% of infected people, but about 20% develop West Nile fever. Symptoms include fever, headache, fatigue, body aches, nausea, vomiting, swollen lymph glands and in some cases, a skin rash. Approximately 1 in 150 of infected individuals develop severe, neuroinvasive disease, such as encephalitis, meningitis or poliomyelitis. Treatment of WNV infection is supportive, such as administration of intravenous fluids, respiratory support and prevention of secondary infections. There is currently no approved vaccine available for humans.

Zika virus (ZIKV): A member of the virus family Flaviviridae and the genus Flavivirus. Other members of this genus include dengue virus, yellow fever virus, Japanese encephalitis virus (JEV), West Nile virus and Spondweni virus. ZIKV is spread by the daytime-active mosquitoes *Aedes aegypti* and *A. albopictus*. This virus was first isolated from a Rhesus macaque from the Zika Forest of Uganda in 1947. Since the 1950s, ZIKV has been known to occur within a narrow equatorial belt from Africa to Asia. The virus spread eastward across the Pacific Ocean in 2013-

2014, resulting in ZIKV outbreaks in Oceania to French Polynesia, New Caledonia, the Cook Islands, and Easter Island. In 2015, ZIKV spread to Mexico, Central America, the Caribbean and South America, where ZIKV has reached pandemic levels. Infection by ZIKV generally causes either no symptoms or mild symptoms, including mild headache, maculopapular rash, fever, malaise, conjunctivitis and joint pain. ZIKV causes symptoms in about 20% of infected individuals, and no deaths from the virus have yet been reported. However, ZIKV infection has been linked to the birth of microcephalic infants following maternal infection, as well as an increase in cases of GBS. Reports have also indicated that ZIKV has the potential for human blood-borne and sexual transmission. ZIKV has also been found in human saliva and breastmilk. There are currently no available medical countermeasures for the treatment or prevention of Zika virus infection (Malone et al., *PLoS Negl Trop Dis* 10(3):e0004530, 2016).

III. West Nile/Zika Virus Chimeras

Although both ZIKV and WNV are flaviviruses, ZIKV replicates more slowly and to lower titers than WNV in cell cultures. This makes production of Zika viruses or viral antigens (for example for development of ZIKV vaccines) more difficult than for WNV. The chimeric West Nile/Zika viruses described herein contain ZIKV antigenic structures on the surface of the virus particles while retaining certain WNV features (such as replication to high titer). The disclosed chimeras can thus be used in the development of immunogenic compositions, such as inactivated virus vaccines, for eliciting an immune response to Zika viruses. Due to their fast and more robust growth than the wild type Zika viruses in cell cultures, these chimeras can be produced in large quantity more efficiently than the wild-type ZIKV for making inactivated virus. The chimeric viruses disclosed herein can also be used as a challenge virus to assess the efficacy of ZIKV candidate vaccines. Furthermore, the chimeric viruses can be used for more rapid and effective ZIKV diagnostic assays.

Disclosed herein are chimeric flaviviruses that include non-coding regions, a C protein, a portion of a prM signal sequence, and non-structural proteins, from WNV; and include a portion of a prM signal sequence, a prM protein and an E protein from ZIKV. Tables 1 and 2 below provide start and stop positions of the particular genes and proteins in exemplary West Nile and Zika viruses. These sequences can serve as reference sequences and may be used to identify particular nucleotide or amino acid positions that correspond to positions referred to in the chimeric nucleic acids disclosed herein, or proteins encoded by the chimeric nucleic acids disclosed herein, for example by producing an alignment of a chimera and one of the virus sequences provided herein.

TABLE 1

Start and stop positions of noncoding regions (NCRs), structural proteins and nonstructural proteins in WNV NY99 (Genbank Accession No. AF196835)		
Region	Nucleotide start/stop position (SEQ ID NO: 17)	Amino acid start/stop position (SEQ ID NO: 18)
5' NCR	1-96	—
C	97-465	1-123
C(ss)	412-465	106-123
prM	466-966	124-290

TABLE 1-continued

Start and stop positions of noncoding regions (NCRs), structural proteins and nonstructural proteins in WNV NY99 (Genbank Accession No. AF196835)		
Region	Nucleotide start/stop position (SEQ ID NO: 17)	Amino acid start/stop position (SEQ ID NO: 18)
M	742-966	216-290
E	967-2469	291-791
NS1	2470-3525	792-1143
NS2A	3526-4218	1144-1374
NS2B	4219-4611	1375-1505
NS3	4612-6468	1506-2124
NS4A	6469-6915	2125-2273
NS4B	6916-7680	2274-2528
NS5	7681-10395	2529-3433
Stop	10396-10398	—
3' NCR	10399-11029	—

TABLE 2

Start and stop positions of NCRs, structural proteins and nonstructural proteins in ZIKV strain R103451		
Region	Nucleotide start/stop position (SEQ ID NO: 13)	Amino acid start/stop position (SEQ ID NO: 14)
5' NCR	1-107	—
C	108-473	1-122
C(ss)	420-473	105-122
prM	474-977	123-290
M	753-977	216-290
E	978-2489	291-794
NS1	2490-3545	795-1146
NS2A	3546-4223	1147-1372
NS2B	4224-4613	1373-1502
NS3	4614-6464	1503-2119
NS4A	6465-6914	2119-2269
NS4B	6915-7667	2270-2520
NS5	7668-10376	2521-3423
Stop	10377-10379	—
3' NCR	10380-100807	—

In some examples disclosed herein, the WNV genome used in the chimera is derived from a particular WNV strain, such as NY99 or KEN-3829. Additional WNV strains are known in the art (see, e.g., Ebel et al. *Emerg. Infect. Dis.* 7:650-653, 2001; American Type Culture Collection (ATCC) catalog numbers VR-82, VR-1267, VR-1507, VR-1510). In particular examples, the WNV genome is WN NY99, for example, SEQ ID NO: 17 (GenBank Accession No. AF196835, incorporated by reference as included in GenBank on Jun. 14, 2016), or with mutations as described in Kinney et al. (*J. Gen. Virol.* 87:3611-3622, 2006), U.S. Pat. No. 8,715,689 and/or PCT Publication No. WO 2015/196094, each of which are incorporated by reference herein in their entirety. In some examples, the WNV genome sequence is modified, for example to introduce restriction sites for cloning purposes. These modifications can be silent mutations (for example, nucleotide sequence changes that do not alter amino acid sequence) or they may change the amino acid sequence.

WNV genome sequences are publicly available. For example, GenBank Accession Nos. AF196835, AY278441, AF202541, AF404754, AF260967, AY660002, AF481864, AY268133, AF404757, AY268132, AF260969, AF317203, AY262283, AY490240, AF260968, AY603654, D00246, M12294, EU068667, AY765264, and AY277251 disclose WNV genomic nucleic acid sequences, all of which are incorporated by reference as included in GenBank on Jun. 14, 2016. In further examples, the WNV genome, or the

non-coding regions, C protein and/or non-structural proteins of the WNV genome are at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a publicly available WNV genome sequence.

In the disclosed nucleic acid chimeras, the ZIKV genome can be from any strain of ZIKV, including an African genotype strain or an Asian genotype strain. In some embodiments, the ZIKV is an African genotype strain, such as MR-766. In other embodiments, the ZIKV is an Asian genotype strain, such as SPH2015, PRVABC59, R103451, P6-740 or FSS 13025. In some embodiments, the ZIKV genome is from strain R103451 (SEQ ID NO: 13). The ZIKV genome may be a wild type strain or an attenuated (or vaccine) strain. In some examples, the ZIKV genome sequence is modified, for example to introduce restriction sites for cloning purposes. These modifications can be silent mutations (for example, nucleotide sequence changes that do not alter amino acid sequence) or they may change the amino acid sequence.

ZIKV sequences are publicly available. For example GenBank Accession Nos. KU321639.1, KU955595.1, KU955594.1, KU955593.1, KU955592.1, KU955591.1, KU681082.3, KU681081.3 and KX247646.1, all of which are incorporated by reference as included in GenBank on Jun. 14, 2016. In additional examples, the ZIKV genome (or the C signal sequence, prM, and/or E protein from the ZIKV genome) are at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a publicly available ZIKV sequence.

In some examples, the disclosed WN/ZKV chimeras include one or more nucleic acid substitutions that result in an amino acid substitution that provides a desirable characteristic, for example, increased stability or replication in cell culture (such as Vero or C6/36 cells), or decreased infectivity or transmission in mosquitoes, compared to the unsubstituted virus or chimera.

The viruses containing the disclosed nucleic acid chimeras can readily be produced by replication in host cells in culture. Methods of producing viruses are well known in the art (see e.g. *Fields Virology*, Knipe and Howley, eds., Lippincott, Williams, and Wilkins, 2001; Flint et al., *Principles of Virology*, ASM Press, 2000). Host cell lines are generally selected to be easy to infect with virus or transfect with viral genomic RNA, capable of stably maintaining foreign RNA with an unarranged sequence, and have the necessary cellular components for efficient transcription, translation, post-translation modification, virus assembly, and secretion of the protein or virus particle. In addition, cells are typically those having simple media component requirements which can be adapted for growth in suspension culture. In some examples, the host cell line is a mammalian cell line that is adapted to growth in low serum or serum-free medium. Exemplary suitable host cell lines include Vero (monkey), C6/36 (mosquito), BHK21 (hamster), LLC-MK2 (monkey) SK6 (swine), L292 (mouse), HeLa (human), HEK (human), 2fTGH cells (human), HepG2 (human), and PDK (dog) cells. Suitable cell lines can be obtained from the American Type Culture Collection (ATCC), Manassas, Va.

In some examples, the disclosed chimeric WN/ZKV replicate in cell culture more rapidly than wild type Zika viruses. In some examples, plaques formed by WN/ZKV chimeric viruses form on cell cultures (such as Vero, LLC-MK2 or BHK21 cells) sooner than ZIKVs (such as at least one day, two days, three days, four days, or five days post-infection sooner). In other examples, WN/ZKV chimeric viruses form larger plaques than ZIKVs, for example, plaques that are at least 25% larger to about 10 times larger

than Zika viruses (such as at least 50% larger, two-fold, three-fold, four-fold, five-fold, or up to 10-fold larger).

The disclosure also provides WN/ZKV chimeras having one or more nucleic acid or amino acid substitutions, insertions, deletions, or combinations thereof, such that the resulting chimera has improved characteristics. In some examples, the improved characteristic of the chimera includes but is not limited to increased virus titer, increased replication rate, increased plaque size, or increased stability in cell culture compared to a wild type virus. In additional examples, the improved characteristic of the chimera includes increased infectivity or virulence in a subject (such as mice or non-human primates) or decreased infectivity or transmissibility in mosquitoes as compared to a wild type virus. For example, to decrease infectivity or transmissibility in mosquitoes, the WN/ZKV chimeras may include one or more miRNAs specific to mosquito cells, such as but not limited to, miRNA-14, miRNA-184 or miRNA-1175.

Manipulation of the nucleotide sequence of the disclosed chimeric flaviviruses by standard procedures, including for instance site-directed mutagenesis or PCR and M13 primer mutagenesis, can be used to produce variants with improved characteristics (such as increased virus titer or stability in cell culture). Details of these techniques are well known. For instances, protocols are provided in Sambrook et al. (ed.), *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989. The simplest modifications involve the substitution of one or more amino acids for amino acids having similar physiochemical and/or structural properties. These so-called conservative substitutions are likely to have minimal impact on the activity and/or structure of the resultant protein. Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Examples of conservative substitutions are shown below.

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

The substitutions which in general are expected to produce the greatest changes in protein properties will be non-conservative, for instance changes in which (a) a hydrophilic residue, for example, seryl or threonyl, is substituted for (or by) a hydrophobic residue, for example, leucyl, isoleucyl, phenylalanyl, valyl or alanyl (or vice versa); (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, for example, lysyl, arginyl, or histadyl, is substituted for (or

by) an electronegative residue, for example, glutamyl or aspartyl (or vice versa); or (d) a residue having a bulky side chain, for example, phenylalanine, is substituted for (or by) one not having a side chain, for example, glycine (or vice versa).

In addition to targeted mutagenesis to produce variants of the disclosed WN/ZKV chimeras, mutations may accrue upon passage in cell culture that result in variants, some with desirable characteristics. Nucleic acid and amino acid substitutions, insertions, and/or deletions that accrue in chimeric viruses during cell culture passages are readily determined by sequence analysis of the virus amplified from isolated plaques of the virus seed, and can be engineered into infectious clones to generate WN/ZKV chimera variants that have improved characteristics (such as replication to high titer or production of uniform large plaques in cells). Consistent mutations identified from multiple seeds or isolated plaques are one indication of a desirable substitution of the chimera in the cell type. Previous studies have successfully identified substitutions which occurred in cell culture and engineered these into different chimeric virus constructs to produce chimeric viruses with improved characteristics (e.g., Huang et al., *J. Virol.* 77:11436-11447, 2003; Huang et al., *J. Virol.* 12:7300-7310, 2005; U.S. Pat. No. 8,715,689; and WO 2015/196094).

A. Nucleic Acid Chimeras

Provided herein are flavivirus nucleic acid chimeras. In some embodiments, the nucleic acid chimera includes a first nucleic acid molecule comprising a 5' non-coding region, a nucleic acid encoding a C protein and non-structural proteins, and a 3' non-coding region, each from a West Nile virus genome, wherein the C protein comprises a portion of a prM signal sequence from the West Nile virus genome and a portion of the prM signal sequence from a Zika virus genome; and a second nucleic acid molecule operably linked to the first nucleic acid molecule, encoding a prM protein and an E protein from the Zika virus genome.

In some examples, the portion of the prM signal sequence from the West Nile virus genome includes the first 15 amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome includes the last three amino acids of the Zika virus prM signal sequence. In specific non-limiting examples, the first 15 amino acids of the West Nile virus prM signal sequence includes amino acids 106-120 of SEQ ID NOS: 2 and 4 and/or the last three amino acids of the Zika virus prM signal sequence includes AMA (amino acids 121-123 of SEQ ID NOS: 2 and 4).

In other examples, the portion of the prM signal sequence from the West Nile virus genome includes the first 13 amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome includes the last five amino acids of the Zika virus prM signal sequence. In specific non-limiting examples, the first 13 amino acids of the West Nile virus prM signal sequence includes amino acids 106-118 of SEQ ID NO: 6 and/or the last five amino acids of the Zika virus prM signal sequence includes amino acids 119-123 of SEQ ID NO: 6.

In yet other examples, the portion of the prM signal sequence from the West Nile virus genome includes the first three amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome includes the last 15 amino acids of the Zika virus prM signal sequence. In specific non-limiting examples, the first three amino acids of the West Nile virus prM signal sequence includes amino acids GGK (amino acids 106-108 of SEQ ID NO: 8) and/or the last 15 amino

acids of the Zika virus prM signal sequence includes amino acids 109-123 of SEQ ID NO: 8.

In some embodiments, the West Nile virus is strain NY99 or KEN-3829.

In some embodiments, the Zika virus is an African genotype virus, such as strain MR-766. In other embodiments, the Zika virus is an Asian genotype virus, such as strain SPH2015, PRVABC59, R103451, P6-740 or FSS 13025.

In some embodiments, the nucleic acid chimera includes a nucleic acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7. In some examples, the nucleic acid chimera includes the nucleic acid sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7.

In some embodiments, the nucleic acid chimera encodes an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8. In some examples, the nucleic acid chimera encodes the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8.

In some embodiments, the nucleic acid chimera further includes a reporter gene. In some examples, the reporter gene encodes a light-emitting protein. In some examples, the light-emitting protein is a fluorescent protein, such as a green, blue, cyan, yellow, orange or red fluorescent protein. In other examples, the light-emitting protein is a bioluminescent protein, such as luciferase. In particular non-limiting examples, the reporter gene encodes a green fluorescent protein, such as ZsGreen or mWasabi.

In some examples, the reporter gene is inserted upstream (5') of a complete C gene, and an additional nucleic acid sequence encoding a portion of the C protein (such as the first 25 or 35 amino acids of the C protein) is inserted between the 5' non-coding region and the reporter gene (see FIG. 2, Type I reporter construct). In specific non-limiting examples, the nucleic acid sequence encoding the portion of the C protein is human codon optimized or modified with multiple silent mutations to enhance the genetic stability of the reporter virus by decreasing homologous sequences between the complete and partial C genes. In particular examples, the nucleic acid sequence of the reporter gene (such as ZsGreen) is human codon optimized.

In some examples, a nucleic acid sequence encoding a self-cleaving 2A peptide (such as F2A or P2A) is placed at the 3' end of the reporter gene (see FIG. 2, Type II reporter construct). In particular examples, the reporter gene and 2A peptide coding sequence are inserted in the signal sequence region at the 3' end of the C gene. In specific non-limiting examples, the reporter gene and 2A peptide coding sequence are flanked by a nucleic acid sequence encoding the first three amino acids (GGK) of the WNV signal sequence at the 5' end and a nucleic acid sequence encoding the 18 amino acid ZIKV signal sequence at the 3' end (see FIG. 2, Type II reporter construct).

In some examples, the nucleic acid sequence encoding the report construct is human codon optimized.

In some examples, the nucleic acid chimera includes a nucleic acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 9, SEQ ID NO: 11 or SEQ ID NO: 19. In specific examples, the nucleic acid

chimera includes the nucleic acid sequence of SEQ ID NO: 9, SEQ ID NO: 11 or SEQ ID NO: 19.

In some examples, the nucleic acid chimera encodes an amino acid sequence at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to SEQ ID NO: 10, SEQ ID NO: 12 or SEQ ID NO: 20. In specific examples, the nucleic acid chimera encodes the amino acid sequence of SEQ ID NO: 10, SEQ ID NO: 12 or SEQ ID NO: 20.

Also provided herein are chimeric flaviviruses that comprise a nucleic acid chimera disclosed herein. Compositions, such as immunogenic compositions, that include the chimeric flaviviruses are also provided by the present disclosure.

B. Inactivated Virus, Methods of Use and Methods of Making

Further provided herein are inactivated chimeric flaviviruses. In particular, provided are chimeric West Nile/Zika viruses that have been inactivated using any method known to one of skill in the art. The chimeric West/Nile Zika viruses have a chimeric nucleic acid that includes a first nucleic acid molecule comprising a 5' non-coding region, a nucleic acid encoding a C protein and non-structural proteins, and a 3' non-coding region, each from a West Nile virus genome, wherein the C protein comprises a portion of a prM signal sequence from the West Nile virus genome and a portion of a prM signal sequence from a Zika virus genome; and a second nucleic acid molecule operably linked to the first nucleic acid molecule, encoding a prM protein and an E protein from the Zika virus genome, as described in the above section.

Also provided are immunogenic compositions that include an inactivated flavivirus comprising a nucleic acid chimera disclosed herein and a pharmaceutically acceptable carrier. In some embodiments, the inactivated virus is purified.

In some embodiments, the inactivated virus is inactivated by one or more of chemical inactivation, high pressure inactivation, ultraviolet or gamma irradiation, or any combination thereof.

Further provided herein is a method of eliciting an immune response against Zika virus in a subject by administering to the subject an inactivated virus or immunogenic composition disclosed herein. The immune response may include, for example, induction of ZIKV-specific antibodies (such as IgM and/or IgG antibodies) or induction of a virus-specific T cell response. In some examples, the immune response is a protective immune response.

In some embodiments, the subject is a human.

In some embodiments, the method includes administering one to five doses (such as 1, 2, 3, 4 or 5 doses) of the immunogenic composition to the subject. In some examples, the method further includes administering one or more adjuvants to the subject.

Also provided is a method of immunizing a subject against ZIKV by administering to the subject an inactivated virus or immunogenic composition disclosed herein. In some embodiments, the subject is a human.

Further provided is a method that includes inactivating a virus that includes a nucleic acid chimera disclosed herein. In some embodiments, inactivating the virus includes treating the virus with a chemical inactivation agent, high pressure, ultraviolet irradiation, gamma irradiation, or any combination thereof. In some examples, the method further includes purifying the inactivated virus. In some examples, the method further includes administering the inactivated virus to a subject

C. Methods of Detecting Zika Virus Infection

Methods of detecting ZIKV-specific antibodies in a sample are also provided herein. In some embodiments, the method includes contacting the sample with a chimeric virus disclosed herein under conditions sufficient to form virus-antibody complexes if ZIKV antibodies are present in the sample; and detecting the virus-antibody complexes, thereby detecting ZIKV-specific antibodies in the sample.

In some embodiments, the method includes contacting the sample with a chimeric virus disclosed herein to form a virus-sample mixture, wherein virus-antibody complexes are formed in the virus-sample mixture if ZIKV-specific antibodies are present in the sample; inoculating a cell culture with the virus-sample mixture under conditions sufficient to allow plaque formation or micro-focus formation in the cell culture; and detecting a decrease in plaque formation or micro-focus formation in the cell culture as compared to a virus-infected control cell culture.

In some embodiments, the method includes providing a chimeric virus disclosed herein bound to a solid support; contacting the chimeric virus-bound solid support with the sample under conditions sufficient to form virus-antibody complexes if ZIKV-specific antibodies are present in the sample; contacting the virus-antibody complexes with a secondary antibody; and detecting binding of the secondary antibody to the virus-antibody complexes.

In some embodiments, the method includes providing a secondary antibody bound to a solid support; contacting the secondary antibody-bound solid support with the sample under conditions sufficient to allow binding of the secondary antibody to any ZIKV-specific antibodies present in the sample, thereby forming antibody-antibody complexes; contacting the antibody-antibody complexes with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the ZIKV-specific antibodies, thereby forming immune complexes; and detecting the presence of the immune complexes. In some examples, detecting the presence of the immune complexes includes contacting the immune complexes with an antibody that specifically binds the chimeric virus and comprises a detectable label.

In some embodiments, the method includes providing a ZIKV-specific antibody bound to a solid support; contacting the antibody-bound solid support with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the ZIKV-specific antibody to form antibody-virus complexes; contacting the antibody-virus complexes with the sample to allow binding of any ZIKV-specific antibodies present in the sample to the chimeric virus, thereby forming immune complexes; contacting the immune complexes with a secondary antibody; and detecting binding of the secondary antibody to the immune complexes, thereby detecting ZIKV-specific antibodies present in the sample.

In some examples of the detection methods, the secondary antibody is an anti-IgM antibody. In other examples, the secondary antibody is an anti-IgG antibody. In specific examples, the secondary antibody includes an anti-human IgM antibody or an anti-human IgG antibody.

In some examples, the sample includes a biological fluid samples, such as serum, blood or plasma. In particular non-limiting examples, the sample includes serum.

In some examples, the ZIKV-specific antibody is cross-reactive with other flaviviruses.

In some examples, the ZIKV-specific antibody is a neutralizing antibody.

IV. Compositions and Methods for Eliciting an Immune Response

Due to its robust replication in Vero cells, the chimeric viruses disclosed herein can be readily utilized for producing

inactivated virus vaccine from vaccine-production certified Vero cells. Inactivated flavivirus vaccines, such as Japanese encephalitis virus vaccine and tick-borne encephalitis vaccine, have previously been used successfully in humans. An inactivated ZIKV vaccine may be a safe vaccine option for pregnant woman to prevent ZIKV-caused microcephaly in the fetus. Large quantities of virus are required for purification and inactivation procedures to make an inactivated vaccine. Thus, the chimeric West Nile/Zika viruses disclosed herein are advantageous due to their ability to produce very high titers for many days, which will significantly enhance Zika virus vaccine production.

Provided herein are methods of eliciting an immune response in a subject by administering an inactivated viruses including a WN/ZKV chimeric nucleic acid to the subject. In a particular example, the subject is a human. The inactivated virus comprising a WN/ZKV nucleic acid chimera is used to produce an immune response that prevents or inhibits infection with a ZIKV, and can also be used to treat or inhibit infection with ZIKV.

In some examples, the method further includes selecting a subject in need of enhanced immunity to ZIKV. Subjects in need of enhanced immunity to ZIKV include subjects who are at risk of ZIKV infection, and subjects who have been previously vaccinated with a ZIKV vaccine. Residents of, or travelers to, countries or regions where ZIKV is endemic are at risk of contracting ZIKV. Additional factors that contribute to risk of infection with ZIKV include the characteristics of the area, presence of ZIKV in the area, exposure to mosquitoes, and lack of preventive measures (such as insect repellent).

In some examples, the chimeric virus is inactivated, for example, using chemical inactivation, high pressure inactivation, ultraviolet or gamma irradiation, or any combination thereof. For example, chemical inactivation includes exposing the virus to one or more of formaldehyde (e.g., formalin), β -propiolactone, aziridines, hydrogen peroxide, organic solvents, surfactants (e.g., sarkosyl) or non-ionic detergents (e.g., Triton®-X100), or ascorbic acid for a time sufficient to inactivate the virus. In one example, the virus is inactivated using an oxidizing agent such as hydrogen peroxide, for example, treatment with about 0.05-5% hydrogen peroxide (such as about 0.1-1% about 0.5-3%, about 1-5%) at room temperature for about 1-24 hours (such as about 1-16 hours, about 2-12 hours, about 4-8 hours, about 1-6 hours, for example, about 1 hour, about 2 hours, about 3 hours, about 4 hours, about 6 hours, about 8 hours, about 12 hours, about 16 hours, or about 24 hours). See, e.g., WO 2008/039171; Amanna et al., *Nat. Med* 18:974-979, 2012; Pinto et al., *J. Virol.* 87:1926-1936, 2013. One of ordinary skill in the art can determine optimal hydrogen peroxide concentrations and conditions for inactivation for different starting viral titers or volumes.

In a particular, non-limiting example, the virus is treated with about 0.001-0.5% sarkosyl (such as about 0.005-0.4%, about 0.025-0.2%, or about 0.01-0.4% sarkosyl, for example, about 0.005%, about 0.01%, about 0.025%, about 0.05%, about 0.1%, about 0.2%, about 0.3%, about 0.4%, or about 0.5% sarkosyl) at about 20-37° C. (for example, about 20-37° C., about 22-30° C., about 30-37° C., or about room temperature) for a sufficient time to inactivate the virus (such as about 15 minutes to 3 hours, about 30 minutes to 2 hours, about 1-2 hours or about 30 minutes to 90 minutes). One of ordinary skill in the art can determine optimal detergent concentrations and conditions for inactivation for other detergents and/or different starting viral titers or volumes. In some examples, longer inactivation times are used at lower

temperatures (such as room temperature) than at higher temperatures (such as 37° C.). One of ordinary skill in the art can determine inactivation times based on the temperature of treatment and routine experimentation.

In other examples, the virus is exposed to an ultraviolet light source (such as a UV-C light source of 254 nm) or a radioactive source (such as cobalt-60) for a time sufficient to inactivate the virus. In some examples, the virus (such as a WN/ZIKV chimera disclosed herein) is exposed to about 350-700 $\mu\text{W}/\text{cm}^2$ (such as about 350-680 $\mu\text{W}/\text{cm}^2$, about 400-670 $\mu\text{W}/\text{cm}^2$, about 670-685 $\mu\text{W}/\text{cm}^2$, or about 350 $\mu\text{W}/\text{cm}^2$, about 670 $\mu\text{W}/\text{cm}^2$, or about 680 $\mu\text{W}/\text{cm}^2$) of UV-254 nm for about 10 minutes to 2 hours (such as about 15 minutes to 1 hour, about 15-45 minutes, about 1-2 hours, about 15 minutes, about 30 minutes, about 45 minutes, about 1 hour, or more). In other examples, the virus is exposed to about 0.1-200 mW/cm^2 (such as about 0.5-5 mW/cm^2 , about 1-10 mW/cm^2 , about 10-50 mW/cm^2 , about 25-100 mW/cm^2 , about 100-200 mW/cm^2 , for example, about 2 mW/cm^2 , about 5 mW/cm^2 , about 10 mW/cm^2 , about 50 mW/cm^2 , about 100 mW/cm^2 , about 150 mW/cm^2 , or about 200 mW/cm^2) for about 10 minutes to 8 hours (such as about 30 minutes to 1 hour, about 1-6 hours, about 2-4 hours, about 15 minutes, about 30 minutes, about 1 hour, about 2 hours, about 3 hours, about 4 hours, about 6 hours, about 8 hours). In some examples, the virus is kept cool (for example at 4° C. or on ice) during UV treatment. In particular examples, small volumes (such as less than about 1 ml) are treated at 670 $\mu\text{W}/\text{cm}^2$ for 15 minutes or 350 $\mu\text{W}/\text{cm}^2$ for 45 minutes and larger volumes (such as about 1 ml or more, for example about 2-5 ml, about 1-3 ml, or more) are treated at 680 $\mu\text{W}/\text{cm}^2$ for 45 minutes or more. One of ordinary skill in the art can determine optimal UV power and conditions for inactivation for other volumes or different starting viral titers.

In additional examples, the virus is inactivated by photochemical inactivation. The methods include exposure of the virus to UV radiation (365 nm) in the presence of photo-activatable chemicals, such as 1,5-indonaphthylazide (INA), 4'-aminomethyl-trioxsalen (AMT), 8-methoxypsoralen (MOP), 4,5',8-trimethylpsoralen (TMP), or psoralen. See, e.g., Raviprakash et al., *Hum Vaccines Immunother.* 9:2336-2341, 2013; Raviv et al., *J. Virol.* 82:4612-4619, 2008; Sharma et al., *Vaccine* 29:953-959, 2011; Hanson et al., *J. Gen. Virol.* 40:345-358, 1978. In particular examples, the virus is exposed to about 0.1-200 mW/cm^2 (such as about 0.1-1 mW/cm^2 , about 0.5-5 mW/cm^2 , about 1-100 mW/cm^2 , about 100-200 mW/cm^2 , for example, about 2 mW/cm^2 , about 100 mW/cm^2 , about 145 mW/cm^2 , about 180 mW/cm^2 , or about 200 mW/cm^2) of UV-365 nm for about 1 minute to about 6 hours (such as about 2-15 minutes, about 5-30 minutes, about 15 minutes to 1 hour, about 15-45 minutes, about 1-2 hours, about 90 minutes to 4 hours, about 2-6 hours, about 2 minutes, about 5 minutes, about 10 minutes, about 15 minutes, about 30 minutes, about 45 minutes, about 1 hour, about 2 hours, about 4 hours, about 6 hours, or more) in the presence of INA, AMT, MOP, TMP, or psoralen. One of ordinary skill in the art can determine optimal UV power and conditions for inactivation using particular compounds, virus volumes, or starting viral titers.

Before or after the chimeric virus has been inactivated, the virus may be purified. Purification methods include filtration or diafiltration, chromatography (e.g., size exclusion, ion exchange, or immunoaffinity chromatography), density-gradient centrifugation, glycerol-cushion centrifugation, or Cel-lufine® sulfate media chromatography. In other examples, the chimeric virus is purified prior to inactivation. If purified

virus is inactivated, an additional purification step may be included following inactivation, for example, to remove a chemical inactivation agent (such as detergent), for example using filtration or buffer exchange. Preparations of purified inactivated WN/ZIKV chimeras may include both inactivated whole virus and inactivated virus-like particles.

In some examples, chimeras are purified (for example, through polyethylene glycol 8000 (PEG8000) precipitation and gradient-density centrifugation, glycerol cushion centrifugation, and/or Cellufine® sulfate media chromatography) before inactivation. Inactivated viruses may be further purified by filtration to remove inactivating reagent, for example, if necessary. In particular examples, detergent (such as sarkosyl) is removed after inactivation by filtration, detergent removal spin columns (such as Millipore Detergent-OUT™ kits), dialysis, or ion-exchange chromatography. Final product may be tested for infectivity in cell cultures, antigenicity (for example, by ELISA; as discussed in Section VI, below), and/or protein concentration (for example, by Bradford or bicinchoninic acid protein assay).

One or more purified inactivated viruses comprising a WN/ZKV nucleic acid chimera (for example in the form of a pharmaceutical or immunogenic composition) are administered to a subject by any of the routes normally used for introducing a composition into a subject. Methods of administration include, but are not limited to, intradermal, intramuscular, intraperitoneal, parenteral, intravenous, subcutaneous, vaginal, rectal, intranasal, inhalation or oral. Parenteral administration, such as subcutaneous, intravenous or intramuscular administration, is generally achieved by injection. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. Administration can be systemic or local.

Immunogenic compositions are administered in any suitable manner, such as with pharmaceutically acceptable carriers. Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. See, e.g., *Remington: The Science and Practice of Pharmacy*, The University of the Sciences in Philadelphia, Editor, Lippincott, Williams, & Wilkins, Philadelphia, Pa., 21st Edition (2005). Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present disclosure.

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous 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.

In some examples, the compositions disclosed herein include one or more adjuvants. In other examples, an adjuvant is not included in the composition, but is separately administered to a subject (for example, in combination with

a composition disclosed herein) before, after, or substantially simultaneously with administration of one or more of the compositions disclosed herein. Adjuvants are agents that increase or enhance an immune response in a subject administered an antigen, compared to administration of the antigen in the absence of an adjuvant. One example of an adjuvant is an aluminum salt, such as aluminum hydroxide, aluminum phosphate, aluminum potassium sulfate, or aluminum hydroxyphosphate. Other adjuvants include biological adjuvants, such as cytokines (for example, IL-2, IL-6, IL-12, RANTES, GM-CSF, TNF- α , or IFN- γ), growth factors (for example, GM-CSF or G-CSF), one or more molecules such as OX-40L or 4-1 BBL, immunostimulatory oligonucleotides (for example, CpG oligonucleotides), Toll-like receptor agonists (for example, TLR2, TLR4, TLR7/8, or TLR9 agonists), and bacterial lipopolysaccharides or their derivatives (such as 3D-MPL). Additional adjuvants include oil and water emulsions, squalene, or other agents. In one example, the adjuvant is a mixture of stabilizing detergents, micelle-forming agent, and oil available under the name PROVAX® (IDEC Pharmaceuticals, San Diego, Calif.). One of skill in the art can select a suitable adjuvant or combination of adjuvants to be included in the compositions disclosed herein or administered to a subject in combination with the compositions disclosed herein.

Administration is accomplished by single or multiple doses. The dose administered to a subject in the context of the present disclosure should be sufficient to induce a beneficial therapeutic response in a subject over time, or to inhibit or prevent ZIKV infection. The dose required will vary from subject to subject depending on the species, age, weight and general condition of the subject, the severity of the infection being treated, the particular immunogenic composition being used, and its mode of administration. An appropriate dose can be determined by one of ordinary skill in the art using only routine experimentation. In some examples, the dose of inactivated virus (such as in an immunogenic composition) administered to the subject is about 0.1 μg to about 100 μg . For example, a dose of the immunogenic composition can contain at least 0.1 μg , at least 0.2 μg , at least 0.25 μg , at least 0.3 μg , at least 0.33 μg , at least 0.4 μg , at least 0.5 μg , at least 1.0 μg , at least 2.0 μg , at least 3.0 μg , at least 5.0 μg , at least 10.0 μg , at least 20 μg , at least 40 μg , at least 80 μg , or at least 100 μg (or any amount between 0.1 and 10.0 μg) of inactivated chimeric virus.

Repeated immunizations may be necessary to produce an immune response in a subject. When administered in multiple doses, the booster doses are administered at various time intervals, such as weeks or months to years. In other examples, the inactivated WN/ZKV chimeric viruses are used as a booster following administration of one or more ZIKV vaccines. In one example, a subject is administered a prime dose of a live-attenuated ZIKV vaccine followed by at least one boost dose of the inactivated WN/ZKV chimeric viruses disclosed herein. In some examples, the boost dose is administered about 14, 30, 60, 90, or more days after administration of the prime dose. Additional boosters (of live-attenuated ZIKV or inactivated WN/ZKV chimeras) can be administered at subsequent time points, if determined to be necessary or beneficial. Immunization protocols (such as amount of immunogen, number of doses and timing of administration) can be determined experimentally, for example by using animal models (such as mice or non-human primates), followed by clinical testing in humans.

V. Preparation of Viruses

Methods of cell culture, viral replication, plaque titration, and virus or virus particle purification are well known in the

art. See e.g. Obijeski et al., *J. Gen. Virol.* 22:21-33, 1974; Beaty et al., *Diagnostic Procedures for Viral, Rickettsial, and Chlamydial Infections*, pp. 189-212, Lennette et al. (eds.), 7th Edition, American Public Health Association, 1995; *Virology Methods Manual*, Mahy and Kangro (eds.), Academic Press, 1996.

The chimeric viruses of the present disclosure can be made using standard methods known and recognized in the art. For example, an RNA molecule corresponding to the genome of a virus, or a chimeric virus, can be introduced into primary cells, chick embryos, or diploid cell lines, from which (or the supernatants of which) progeny virus can then be purified. Another method that can be used to produce the viruses employs heteroploid cells, such as Vero cells (Yasumura et al., *Nihon Rinsho* 21:1201-1215, 1963) or C6/36 cells. In this method, a nucleic acid molecule (e.g., an RNA molecule) corresponding to the genome of a virus or chimeric virus is introduced into the heteroploid cells and virus is harvested from the medium in which the cells have been cultured. The harvested virus can be further amplified in cell cultures and then concentrated (e.g., by PEG 8000 precipitation, use of ultrafiltration, such as a filter having a molecular weight cut-off of, e.g., 50-500 kDa (e.g., Amicon ultra-centrifugal filter, tangential flow filtration cassette, or Pellicon-2 Mini ultrafilter cassette)), diafiltered against MEME without phenol red or FBS, formulated by the addition of lactose, and filtered into a sterile container. Details of a method of virus production are provided in WO 03/060088. Viruses optionally are further purified, for example by density gradient centrifugation, glycerol cushion centrifugation, and/or Cellufine® sulfate media chromatography.

VI. Detection of Flavivirus Antibodies

The present disclosure further provides a method of detecting a Zika virus-reactive antibody in a sample (such as a sample from a subject, for example, a blood or serum sample), including contacting the sample with a chimeric virus disclosed herein under conditions sufficient to form virus-antibody complexes if Zika virus antibodies are present in the sample; and detecting formation of the complexes, thereby detecting Zika virus antibody in the sample. An advantage of the disclosed WN/ZKV chimeras is that they grow faster and to higher titers and produce larger and more well-defined plaques or micro-foci than wild type ZIKV. It is disclosed herein that chimeric WN/ZIKV expresses authentic ZIKV neutralization epitopes that result in neutralization assay results that are equivalent to the neutralization assay using wt ZIKV (Table 3). In addition, the chimeric virus can speed up the traditional PRNT from 5-6 days to 3-4 days, and plaque morphology of the WN/ZIKV is more uniform for consistent counting. Therefore, the disclosure provides methods of detecting ZIKV-reactive antibody in a sample that are faster and more accurate (consistent) than methods utilizing wild type ZIKV.

The methods of detecting Zika virus-specific antibodies in a sample are performed, for example, by contacting a fluid or tissue sample from a subject with a chimeric virus of this disclosure and detecting the binding of at least one polypeptide encoded by the virus to the antibody. A fluid sample of this method includes any biological fluid which could contain the antibody, such as cerebrospinal fluid, blood, bile plasma, serum, saliva and urine. Other possible examples of body fluids include sputum, mucus and the like.

In one example, the presence of a ZIKV antibody is detected in a sample from a subject utilizing a disclosed

chimeric flavivirus in a plaque-reduction neutralization test (PRNT) or micro-focus reduction neutralization test (mFRNT). In the PRNT or mFRNT assay, a sample is contacted with a virus encoded by a chimeric flavivirus disclosed herein. A suitable cell culture (such as Vero, C6/36, LLC-MK2 or BHK cells) is inoculated with the virus-sample mixture to infect the cells. The cell culture is incubated under conditions sufficient to allow plaque or micro-focus formation and the number of plaques or micro-foci formed in a culture inoculated with the chimeric virus-sample mixture is compared to the number of plaques or micro-foci formed in a control culture (such as cells inoculated with virus alone). A reduction in the number of plaques or micro-foci in the cell culture inoculated with the chimeric virus-sample mixture as compared to the control culture (for example a decrease of at least 50%, 60%, 70%, 80%, 90%, 95%, or 99% compared with the control sample) indicates the presence of a ZIKV antibody, such as a neutralizing antibody, in the sample.

Chimeric WN/ZKVs encoding a fluorescent reporter (Zs-Green) are also disclosed herein (referred to as WN/ZKV-ZsG0 and WN/ZKV-ZsG1). The reporter viruses can be used to improve the micro-neutralization assay because the viral foci (infected cells) can be directly imaged and automatically counted, for example, by an ELISPOT reader. This eliminates the time-consuming and labor-intensive procedure required for immunostaining of viral foci.

The robust growth characteristics of the chimeric virus disclosed herein can also be useful in the production of ZIKV particles for use in a variety of diagnostic assays. For example, viral particles and/or antigens are required in various serology assays, such as traditional IgM antibody capture (MAC)-ELISA or IgG antibody capture (GAC)-ELISA, indirect ELISA and rapid lateral flow assays. Other immunoassays, such as immunofluorescence assay and immunoblotting can also be readily adapted for the detection of Zika virus antibodies in a sample according to the methods of this disclosure. An ELISA method effective for the detection of the antibodies includes, for example, binding the chimeric virus or virus particles to a substrate; contacting the bound chimeric virus with a fluid or tissue sample containing the antibody; contacting the above with a secondary antibody, which is reactive with the bound antibody, bound to a detectable moiety (for example, horseradish peroxidase enzyme or alkaline phosphatase enzyme); contacting the above with the substrate for the enzyme; contacting the above with a color reagent; and observing/measuring color change or development.

The immune response following a flavivirus infection includes the production of IgM and IgG antibodies, which are primarily directed against the flavivirus E protein. IgM antibody capture (MAC) or IgG antibody capture (GAC) ELISAs are commonly used to detect the level of IgM or IgG (respectively) in serum samples of patients suspected of having a flavivirus (such as a Zika virus) infection. In these assays, anti-human IgM or anti-human IgG serves as a capture antibody and is coated onto an appropriate assay plate, such as a multi-well plate. After blocking of the plate, such as with nonfat dry milk, diluted human sera are reacted with the anti-human IgM or IgG. In the context of the present disclosure, chimeric virus, which serves as the antigen, is added to the plates. A ZIKV antigen-specific antibody conjugated to a detectable label (for example, an enzyme or fluorophore) is then reacted with the immobilized virus. The detectable label is then measured to detect the presence of ZIKV-specific antibodies that were present in the serum sample. Serial dilutions of positive sera can be

evaluated. The maximum dilution that exhibits positive signal is the titer for the serum. The titer of the MAC-ELISA or GAC-ELISA can be compared with the titers of other tests, such as hemagglutination inhibition tests (HIT) or PRNT. Serum samples can also be tested on control antigen in addition to viral antigen, to reduce the number of false-positive results due to non-specific binding of the serum or other factors (U.S. Patent Application Publication No. 2006/0115896).

Indirect ELISAs to detect the presence of virus-specific antibodies are typically carried out by coating a microtiter plate with an antigen-specific antibody (such as a flavivirus-cross reactive or ZIKV-specific antibody), blocking the plates to prevent non-specific binding to the plate surface, and adding virus antigen (such as a chimeric virus disclosed herein) to allow binding of the antigen to the virus-specific antibody. After several washes, diluted human sera is added to allow binding of any antibodies present in the sample to the immobilized viral antigens (e.g. the chimeric virus antigens). IgM or IgG antibodies that were present in the sample are then detected using a labelled secondary antibody, such as anti-human IgG or anti-human IgM conjugated to a detectable label (such as an enzyme or fluorophore). The presence of ZIKV-specific antibody is detected by measuring the detectable label (for example, by measuring fluorescence, optical density or colorimetric absorbance).

In some embodiments herein, detection of Zika virus-specific antibodies in a sample is performed by providing a chimeric virus disclosed herein bound to a solid support; contacting the chimeric virus-bound solid support with the sample under conditions sufficient to form virus-antibody complexes if Zika virus-specific antibodies are present in the sample; contacting the virus-antibody complexes with a secondary antibody; and detecting binding of the secondary antibody to the virus-antibody complexes.

In other embodiments herein, detection Zika virus-specific antibodies in a sample is carried out by providing a secondary antibody bound to a solid support; contacting the secondary antibody-bound solid support with the sample under conditions sufficient to allow binding of the secondary antibody to any Zika virus-specific antibodies present in the sample, thereby forming antibody-antibody complexes; contacting the antibody-antibody complexes with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibodies, thereby forming immune complexes; and detecting the presence of the immune complexes, thereby detecting Zika virus-specific antibodies in the sample. In some examples, detecting the presence of the immune complexes includes contacting the immune complexes with an antibody that specifically binds the chimeric virus and comprises a detectable label.

In yet other embodiments, detection of Zika virus-specific antibodies in a sample includes the steps of providing a Zika virus-specific antibody bound to a solid support; contacting the antibody-bound solid support with a chimeric virus disclosed herein under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibody to form antibody-virus complexes; contacting the antibody-virus complexes with the sample to allow binding of any Zika virus-specific antibodies present in the sample to the chimeric virus, thereby forming immune complexes; contacting the immune complexes with a secondary antibody; and detecting binding of the secondary antibody to the immune complexes, thereby detecting Zika virus-specific antibodies present in the sample.

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

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

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

In yet another example, a microsphere-based immunoassay can be used to detect the presence of flavivirus antibodies in a sample. Microsphere immunoassays (MIAs) are becoming increasingly popular for laboratory diagnosis of many diseases (Earley et al., *Cytometry* 50:239-242, 2002; Kellar et al., *Cytometry* 45:27-36, 2001). The technology involves the detection and analysis of a reaction (such as an antibody or other ligand) attached to microspheres or beads. The detecting instrument is a simplified flow cytometer, and lasers simultaneously identify the microsphere sets and measure the fluorescence associated with the reaction. The speed at which these tests can be performed and the ability to multiplex make this methodology particularly useful.

A MIA can be used to detect the presence of Zika virus-specific antibodies in a sample. In some embodiments, microsphere beads are coated with a ZIKV-specific antibody and contacted with a chimeric virus (as disclosed herein) such that the chimeric viruses bind to the microsphere-bound Zika virus-specific antibodies. The microsphere immune complexes are mixed with a serum sample such that antibodies in the sample that are specifically reactive with the chimeric viruses bind the viruses bound (indirectly) to the microsphere. The bead-bound immune complexes are allowed to react with fluorescent-dye labeled anti-species antibody (such as PE-labeled anti-human IgM or anti-human

IgG), and are measured using a microsphere reader (such as a Luminex instrument). In an alternative embodiment, microsphere beads are coated directly with the chimeric viruses and virus-bound microspheres are contacted with the serum samples.

Lateral flow assays (LFAs) are another method by which antigen-specific antibodies (or pathogen-specific antigens) can be detected in biological samples. These assays are generally very rapid and enable point of care testing. LFA is performed over a strip, different parts of which are assembled on a plastic backing. These parts are sample application pad, conjugate pad, nitrocellulose membrane and adsorption pad. Nitrocellulose membrane is further divided into test and control lines. Pre-immobilized reagents at different parts of the strip become active upon flow of liquid sample. LFA combines the unique advantages of biorecognition probes and chromatography.

Several designs have been developed for lateral flow assays. Generally LFAs include a porous support strip (such as a strip of cellulose) with a number of separate regions spaced horizontally along the support. The solid support need not be identical in all regions of a strip. Typically, the first region is a sample pad where a biological fluid is applied to flow laterally through the support to the remaining regions. The second region generally contains a labeling moiety that can be bound to the analyte of interest (such as an antibody or protein) in the sample if present. Downstream of the labeling region is a capture or "test" region where the labeled analyte (for example, antibody or peptide) is retained in the strip. It is in this test region where detection is generally performed. In addition to the test region, the strip may contain a control region either in the same flow path as that of the test region, or in a parallel path on the strip. There may also be a reservoir downstream of the various regions to absorb the sample that has traversed the test strip.

LFAs can be direct assays, forming sandwiches in proportion to the level of analyte present, or may be competition assays where analyte in the sample diminishes the amount of label detected in the detection zone. In direct sandwich assays, for example, the sample may be labeled by colored particles that are coupled to affinity reagents such as secondary antibodies that bind ZIKV-specific antibodies present in the sample, forming complexes which are then carried to the test region for capture by an additional reagent. The detectable label in the test region will be directly proportional to the level of peptide in the sample.

In competitive assays, the labeling region may contain labeled reagents, for example, that are already coupled to the target analyte (e.g. antibody) or an analog thereof, and the analytes in the sample compete with this labeled material for capture by the capture reagent in the test region. In this case, the detectable label in the test region will be inversely proportional to the quantity of analyte in the sample itself.

Simple visual detection is the most common means of reading an LFA, however, there are commercially available lateral flow readers that can quantitate the detectable label in the test region.

LFAs can be used, for example, to detect antigen-specific antibodies present in a biological sample (such as a serum sample) that specifically recognize ZIKV.

VII. Peripheral Challenge Model and Evaluation of Candidate Vaccine Efficacy

The chimeric viruses disclosed herein can also be used in the development of a peripheral challenge mouse model for ZIKV vaccine evaluation. It has been shown that mouse

models established for ZIKV infection have limitations. In particular, many strains of mice are not susceptible to most wt ZIKV challenge by peripheral injection routes. Since the chimeric WN/ZKV disclosed herein are based on the WNV genetic backbone that is highly infective in many strains of mouse at any age, the chimeric viruses could be used as challenge viruses that are virulent in some of the mouse strain that are resistant to wt ZIKV infection.

Thus, the chimeric flaviviruses disclosed herein may be used in methods to assess the efficacy of candidate vaccines, such as ZIKV vaccine candidates. In some examples, the efficacy of candidate ZIKV vaccines are tested by inoculating subjects (for example, mice or non-human primates (such as rhesus monkeys)) with a candidate vaccine, followed by challenge with a virulent ZIKV strain. The disclosed WN/ZKV chimeras are virulent and/or generate significant viremia in non-immunized mice, therefore they can be used as the challenge dose in previously inoculated subjects.

In one particular embodiment, a set of subjects (such as mice) is inoculated with a candidate ZIKV vaccine. Administration of the candidate vaccine strain virus may be carried out by any suitable means, including by parenteral injection (such as intraperitoneal, subcutaneous, or intramuscular injection). In a particular example, the subjects are inoculated intraperitoneally with candidate vaccine virus in a vehicle such as phosphate buffered saline. Multiple inoculations (such as boosters) may be carried out, separated by a suitable period of time, such as at least two weeks, four weeks, eight weeks, twelve weeks, or more.

Subjects that have been test vaccinated with the candidate vaccine are challenged with a virulent or lethal dose of a WN/ZKV chimera disclosed herein following a suitable period of time to allow immunity based on the vaccination to develop (such as at least two weeks, four weeks, eight weeks, twelve weeks, or more). The challenge dose is administered by any suitable route including those above, and optionally is administered by the same or a different route as the vaccinating dose. Following the challenge dose, subjects are monitored for development of morbidity (such as fever, rash, vomiting, loss of appetite, rough fur, hunched back, lethargy, unbalanced or irritable movement, dehydration, weight loss, or signs of paralysis) or mortality. In addition, blood is collected from subjects after challenge for measurement of viremia levels. A decrease in viremia levels, signs of morbidity and/or mortality compared to a set of control subjects which is not inoculated with the candidate vaccine (for example, a decrease of at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 99% in a test vaccinated population compared with a control population) indicates the effectiveness of the candidate vaccine.

The following examples are provided to illustrate certain particular features and/or embodiments. These examples should not be construed to limit the disclosure to the particular features or embodiments described.

EXAMPLES

Example 1: Construction of Chimeric West Nile/Zika Viruses

This example describes the construction of chimeric West Nile/Zika viruses (WN/ZKVs) that include the prM and E genes from Zika virus in a WNV backbone.

Engineering and Deriving Chimeric WN/ZKVs

Using previously engineered infectious clones of WNV (Kinney et al., *J Gen Virol* 87: 3611-3622, 2006), several

chimeric WN/ZKVs that contain the prM and E genes of a Zika virus (ZIKV) in the genomic background of the WNV NY99 virus were engineered. The chimeric WN/ZKV expresses the entire ZIKV viral envelope on the virion surface, and can be used as a surrogate for ZIKV for multiple applications.

Flaviviruses encode a signal sequence (SS) at the C-terminal end of the capsid protein that serves as a signal peptide for prM during protein processing. The junction site of the chimeric constructs within the SS requires empirical investigation to obtain the most viable and stable chimeric virus. The amino acid (AA) sequences of the SS between WNV and ZIKV are not highly conserved, but both are 18 AA in length (FIG. 1). Based in part on knowledge obtained from the previous construction of various chimeric flaviviruses (U.S. Pat. No. 8,715,689 and PCT Publication No. WO 2015/196094, which are herein incorporated by reference in their entirety), three junction strategies were designed for the chimeric constructs (FIG. 1). The Z3 chimeric construct contains 15 AA of the SS from WNV and 3 AA of the SS from ZIKV; the Z5 construct contains 13 AA of the SS from WNV and 5 AA from ZIKV; and the Z15 construct contains 3 AA of the SS from WNV and 15 AA from ZIKV.

All three chimeric viruses were successfully recovered from C6/36 cells transfected with chimeric viral RNA which was in vitro transcribed from engineered chimeric cDNA. Virus seeds were designated as C6/36-0 seeds when recovered from transfected C6/36 cells, and were amplified one more time in C6/36 and Vero cells to obtain the working virus seeds, C6/36-1 and C6/36-0/Vero-1, for further characterization.

Genome Sequencing of Chimeric WN/ZKVs

Initial chimeric constructs (WN/ZKV-3SPH, WN/ZKV-5SPH, and WN/ZKV-15SPH) were made using the prM-E gene sequence of the ZIKV SPH2015 strain obtained from Genbank (Accession No. KU321639.1), prior to when the PRVABC59 and R103451 strains were isolated from travelers acquiring ZIKV infection during the 2015 outbreak by the CDC diagnostic lab at Fort Collins, Colo. The R103451 (GenBank Accession No. KX262887.1; SEQ ID NO: 13) and PRVABC59 (GenBank Accession No. KU501215.1; SEQ ID NO: 15) strains were available as wild-type (wt) ZIKV controls to CDC labs, but the SPH2015 strain was not. There is only 1 amino acid residue that differs between SPH2015 and R103451/PRVABC59 within the prM-E gene region included in the WN/ZIKV chimeric constructs. The difference is at E protein amino acid position 23 (E23), with an isoleucine (Ile) in the SPH2015 strain and a valine (Val) in the PRVABC59 and R103451 strains. Although the difference from Ile to Val is quite conserved, the E23 amino acid was changed to Val in one of the Z3 chimeric constructs (WN/ZKV-3PR) to make the entire prM-E amino acid sequence identical to the R103451 and PRVABC59 strains that will be used as wt ZIKV controls. For the nucleotide sequences of the prM-E, there is one nucleotide that differs (silent) between the chimeras and strain R103251, and six silent differences between the chimeras and the PRVABC59 strain. Except for the 5' and 3' 24-base termini of the viral genome, the genomes of the chimeric virus working seeds have been sequenced, and it has been verified that all of the seeds contain the correct recombinant genome sequences. The following constructs have been sequenced:

WN/ZKV-3PR (SEQ ID NOs: 1 and 2)—contains 15 AA of the SS from WNV and 3 AA of the SS from ZIKV; the nucleotide and amino sequences of this construct were modified to substitute Ile for Val at position 23 of the E

protein (E23; residue 314 of SEQ ID NO: 2) to correspond to the sequence of strain PRVABC59 and R103451.

WN/ZKV-3SPH (SEQ ID NOs: 3 and 4)—contains 15 AA of the SS from WNV and 3 AA of the SS from ZIKV; includes Ile at position E23 (residue 314 of SEQ ID NO: 4), which corresponds to strain SPH2015.

WN/ZKV-5SPH (SEQ ID NOs: 5 and 6)—contains 13 AA of the SS from WNV and 5 AA of the SS from ZIKV; includes Ile at position E23 (residue 314 of SEQ ID NO: 6), which corresponds to strain SPH2015.

WN/ZKV-15SPH (SEQ ID NOs: 7 and 8)—contains 3 AA of the SS from WNV and 15 AA of the SS from ZIKV; includes Ile at position E23 (residue 314 of SEQ ID NO: 8), which corresponds to strain SPH2015.

Chimeric Virus Growth in Cells

All three types of chimeric constructs yielded viable viruses that replicated competently and reached very high titers (ranging from 10^8 - 10^9 pfu/ml) in C6/36 cells as early as day 3 post-infection (p.i.). In C6/36 cell cultures, rapid replication to high titer permitted the chimeric viruses to be harvested daily from day 3 to day 14. In Vero cells, the chimeric viruses caused significant cytopathic effect (CPE) starting at day 3, but still achieved high virus titers (10^7 - 10^8 pfu/ml) that could be harvested daily from day 2 to day 10 p.i. All three types of chimeric constructs demonstrated similar infectivity and replication efficiency in cell cultures.

When comparing plaque size of chimeric WN/ZKV with its wt ZIKV, the chimeric plaques were significantly larger and more uniform than wt ZIKV plaques. Plaques of chimeric WN/ZKV could be clearly counted on day 3 p.i., while wt ZIKV R103451 plaques could not be readily counted until day 5-6 p.i.

PRNT Titers of Human Serum Against Chimeric WN/ZKV

In view of the faster replication rate of chimeric WN/ZKV compared to wt ZIKV, the chimeric viruses were evaluated as a ZIKV surrogate for the development of faster neutralization assays. Wild type ZIKV and chimeric WN/ZKV-3SPH were compared in the traditional plaque reduction neutralization test (PRNT). The results confirmed that chimeric WN/ZKV expressed authentic ZIKV neutralization epitopes that resulted in neutralization assay results that were equivalent to the neutralization assay using wt ZIKV (Table 3). The chimeric virus can speed up the traditional PRNT from 5-6 days to 3-4 days.

TABLE 3

Similar PRNT (90% virus reduction) titers of 13 human serum samples against chimeric WN/ZKV-3SPH virus and wt ZIKV PRVABC59

Serum ID	PRNT90	
	wt ZIKV (PRVABC59)	WN/ZKV
1	5120	5120
2	10	20
3	2560	2560
4	320	640
5	10,240	10240
6	40	80
7	2560	2560
8	640	1280
9	<10	<10
10	<10	<10
13	160	640
14	160	320
15	320	640

Live Chimeric Reporter Viruses

A fluorescent reporter gene (ZsGreen) was inserted into the chimeric WN/ZKV virus construct to generate live chimeric WN/ZKV reporter viruses. Reporter viruses were successfully generated for WN/ZKV-3SPH by insertion of the ZsGreen linked with P2A using strategy 1 (FIG. 2, Type I reporter construct). The nucleotide and amino acid sequences of two reporter viruses (WN/ZKV-ZsG0 and WN/ZKV-ZsG1) are set forth herein as SEQ ID NOs: 9-12. The nucleotide sequence of the ZsGreen in WN/ZKV-ZsG1 (SEQ ID NO: 11) is codon-optimized for expression in human cells. The first 35 amino acid codons of the C gene immediately after ZsGreen-P2A in both chimeric constructs were edited (not human codon optimized) to make multiple silent mutations in order to minimize homologous recombination potential with the partial C35 gene upstream of ZsGreen. The C sequence was edited instead of human codon optimized because the codon optimization could result in more homologous recombination potential with the human optimized ZsGreen gene. Decreasing homologous recombination potential is expected to enhance the genetic stability of the reporter viruses. An alternative reporter virus strategy is shown in FIG. 2 (see Type II reporter construct). Genetic Stability

Chimeric viruses are passaged serially in Vero cell cultures to determine their genetic stability. The chimeric virus exhibiting the greatest genetic stability are chosen for applications that require serial cell passages during virus production (for example, production of inactivated vaccine).

Example 2: Characterization of Chimeric WN/ZKV and R-WN/ZKV Constructs

This example describes the generation and characterization of an additional WN/ZKV reporter virus (R-WN/ZKV). Stability of WN/ZKV and R-WN/ZKV Constructs

Example 1 describes the successful recovery of chimeric WN/ZKV's using all three of the strategies illustrated in FIG. 1. All three types of chimeric viruses replicated efficiently in both Vero and C6/36 cells and, based on their similar plaque phenotypes in Vero cells between 1 to 10 serial passages, all three chimeric constructs appeared to be similarly stable in Vero cells. The chimeric WN/ZKV-Z3 constructs WN/ZKV-3SPH and WN/ZKV-3PR were genome sequenced after serial passages in Vero cells. Both chimeric viral genomes were quite stable after serial passage. The WN/ZKV-3SPH acquired 3 amino acid (AA) mutations, and WN/ZKV-3PR acquired only 2 AA mutations after the 10 passages.

The reporter chimeric virus constructs disclosed herein are based on WN/ZKV-3SPH or WN/ZKV-3PR. First, two reporter viruses (WN/ZKV-ZsG0 and WN/ZKV-ZsG1) based on WN/ZKV-3SPH were recovered. After genome sequencing both reporter chimeras recovered from transfection and 1 more passage in C6/36 cells, WN/ZKV-ZsG0 was found to have the expected sequence, including the full ZsGreen gene, while a small portion of the WN/ZKV-ZsG1 reporter seed lost the ZsGreen gene. After RT-PCR analysis, it was estimated that about 10% of the WN/ZKV-ZsG1 suffered deletion of the ZsGreen gene. Therefore, the WN/ZKV-ZsG0 construct was used to make the reporter chimera R-WN/ZKV-PR (based on WN/ZKV-3PR).

Similar to WN/ZKV-ZsG0, R-WN/ZKV-PR was constructed with the type 1 reporter construct shown in FIG. 2. The reporter genome contains WNV 5'NCR, WNV partial C gene (first 35 AA with wt sequence), ZsGreen gene (wt) linked with a self-cleavage 2A peptide from porcine teschovirus-1 (P2A), a full WNV C gene with its first 35 AA codon

edited, the first 15 AA of the WNV prM signal sequence and the last 3 AA of the ZIKV prM signal sequence, the prM and E genes of ZIKV, and all of the NS genes and the 3'NCR of WNV (FIG. 3). The nucleotide and amino acid sequences of R-WN/ZKV-PR are set forth herein as SEQ ID NO: 19 and SEQ ID NO: 20, respectively. Serial passaging of R-WN/ZKV-PR indicated that the ZsG0 gene in the construct was stable up to 4 passages in Vero cells and 5 passages in C6/36 cells (FIG. 4). Therefore, it was determined that the working stock of the reporter virus should be limited to low cell passage levels, less than a total of three passages after deriving the virus from transfection of the in vitro transcribed recombinant viral RNA (FIG. 5).

In addition, every reporter virus lot generated is confirmed for ZsGreen gene stability and expression by dual-fluorescent flow cytometry analysis. Cells infected with pre-master seed (PMS), master seed (MS), or working stock (WS) of the R-WN/ZKV-PR were immunostained with a rabbit monoclonal WNV capsid Ab followed by a goat anti-rabbit Ab conjugated with Alexa Fluor 647 (AF647) fluorophore after 24-48 hours of infection. Flow cytometry results in FIG. 5 show an example in which 98% of infected cells co-expressed both WNV C protein (AF647) and ZsG0 protein (ZsGreen), while only 0.1% of cells showed low positivity to WNV C protein only, and only 1.4% of cells showed positivity to ZsG0 only. Using RT-PCR and flow cytometry, the PMS, MS, and WS lots of R-WN/ZKV-PR were analyzed, and all three lots had an intact ZsG0 gene and showed a high level of co-expression of WNV C and ZsG0 proteins in the infected cells. These two assays serve as quality control assays for each lot of reporter virus generated.

Chimeric WN/ZKV and WN/DENVs for Fast and Synchronized PRNT and mFRNT to ZIKV and DENVs

The WNV NY99 strain replicates significantly faster than wt DENV and ZIKV in multiple cell cultures, including Vero, LLC-MK2, and BHK-21 cells that are widely used for cell based neutralization antibody assays. Unlike ELISA that measures all types of antibodies, the neutralization test measures antibodies capable of neutralizing the viruses. Because it is more specific than ELISA, the neutralization test has been used as a confirmative serological assay after positive results of ELISA in diagnosis.

Upon binding to viruses, the neutralization antibodies (Nt Abs) block virus infection of cells (mostly during virus entry stage) and are the most important B cell immune response product in directly fighting many viral infections. Therefore, the neutralization test is also one of the most important functional immunological assays in analyses of vaccine efficacy. However, most of the cell-based neutralization tests are time-consuming and labor-intensive. The traditional gold-standard plaque-reduction neutralization test (PRNT) used in detecting Nt Abs to many flaviviruses typically has used 6- to 24-well plates, and required multiple days of cell infection before the virus plaques formed on the infected cell sheet under an agarose medium overlay can be stained and become visible for counting. The faster micro-focus neutralization test (mFRNT) typically uses 96-well micro plates, and the viral micro-foci can be detected and counted by microplate reader (such as ELISPOT reader or image-based cytometry reader) after immunostaining by viral Abs of the cell sheet within 1-2 days post infection.

Because ZIKV and DENVs are transmitted by the same mosquito vectors, *Ae. aegypti* and *Ae. albopictus*, most recent ZIKV outbreaks happen in areas that are also endemic for DENVs. Due to significant cross-reactivity of flavivirus antibodies, it is very difficult to differentiate infection among

ZIKV and the four types of DENV in secondary ZIKV- or DENV-infected cases. For example, during confirmative diagnosis by PRNT for recent ZIKV outbreaks, it is necessary to conduct a PRNT assay against ZIKV and multiple types (typically at least 2) of DENV for the same clinical samples. Because DENVs and ZIKV have different replication rates in Vero cells, the duration of PRNT for each virus is different. Such differential testing schedule complicates the streaming of diagnostic effort. By using chimeric WN/DENVs and WN/ZKV for the PRNT, it is possible to synchronize the assay duration to three days post infection (pi). As indicated in the Table 4, wt DENVs require 6 to 9 days, depending on the DENV strain, to produce visible plaques, while the wt ZIKV takes at least 5 days p.i. to show countable plaques. On the other hand, all chimeric WN/DENVs and WN/ZKV produced clear plaques by 3 days p.i. Therefore, using the chimeric viruses, it was possible to decrease the PRNT duration by approximately 50% and obtain results for all viruses on the same day. A panel of human serum specimens were tested to confirm that use of the chimeric WN/DENVs and WN/ZIKV resulted in similar PRNT titers as those that were obtained when using wt DENVs and wt ZIKV (Table 3 shows WN/ZKV vs ZIKV results).

TABLE 4

Chimeric viruses form plaques faster than wt parental viruses in Vero cells			
Visible Plaques (day p.i.)			
WNV	3		
DENV-1	6-8	WN/DENV-1	3
DENV-2	7-9	WN/DENV-2	3
DENV-3	6-8	WN/DENV-3	3
DENV-4	6-8	WN/DENV-4	3
ZIKV	5-7	WN/ZIKV	3

R-WN/ZKV-PR for Fast, Easy, and High-Throughput Fluoro-mFRNT or Cell Infection Rate Reduction Assay

Although much faster and higher throughput than the PRNT, the typical mFRNT is still labor intensive. The procedures include adding and removing the carboxyl methyl cellulose overlays from cell plates, cell fixation, and multiple immunostaining procedures. R-WN/ZKV-PR was used to largely simplify and optimize the mFRNT to a fluoro-mFRNT that can be live-imaged by an image-based cytometry plate reader to detect the fluorescent viral foci on infected cell sheets. Due to the fast replication efficiency of the WN/ZKV and strong ZsG0 reporter signal, the infected cells can be measured within 24 hours p.i. With a live-imaging capable cytometry plate reader, it was possible to directly read the infected 96-well plate without any CMC overly, cell fixation, or immunostaining process. FIG. 6 shows a comparison of the PRNT, mFRNT, and fluoro-mFRNT procedures.

A small panel of human serum specimens were tested with the fluoro-mFRNT using R-WN/ZKV-PR. The neutralizing Ab titer results were very comparable to the traditional gold-standard PRNT using wt ZIKV (Table 5). In addition to the fluoro-mFRNT, R-WN/ZKV-PR can also be used in other cytometry-based neutralization assays, which measure reduction of the percent cell infection rate instead of the reduction in viral foci formation. The same image-cytometry plate reader was used to evaluate such an assay with R-WN/ZKV-PR, and the results indicated that a wide linear range of the cell infection rate can be easily achieved by R-WN/ZKV-PR, suggesting its utility for the percent cell infection reduction-based Nt assay.

TABLE 5

Comparable results between PRNT using wt ZIKV and Fluoro-mFRNT using R-WN/ZKV		
Serum ID	wt ZIKV PRNT90*	R-WN/ZKV F-mFRNT90*
20	1280	640/1280
21	10240	2560/5120
22	2560	1280
23	5120	1280/2860
30	160	320/640
32	2560	1280
33	20480	10240/20480
38	640	640/1280
39	1280	2560
44	320	640

*At least 90% reduction

Mouse Challenge Study

WN/ZKV-3PR was tested in CD-1 and AG129 mice. The results showed that the CD-1 immune competent, outbred mice were not susceptible to WN/ZKV-3PR or wt ZIKV, but were highly susceptible to wt WNV (Table 6). In the interferon- α , - β , - γ receptor knockout AG129 mice, WN/ZKV was also attenuated relative to WNV, but caused a mortality rate similar to or somewhat higher than that of wt ZIKV (Table 7). AG129 mice infected with WN/ZKV had significantly shorter survival time than wt ZIKV-infected AG129. Overall, the results showed that WN/ZKV was more similar to the BSL-2 wt ZIKV in mice than the BSL-3 WNV. Therefore, these results support laboratory containment at BSL-2 when working with chimeric WN/ZKV.

TABLE 6

Three week-old CD-1 mice by intra-peritoneal challenge		
Virus/dose (pfu)	Survival	AST* \pm SD
ZIKV PRVABC59/10 ⁶	100%	NA
WN/ZIKV-3PR/10 ⁶	100%	NA
WN/ZIKV-3PR/10 ⁵	100%	NA
WN/ZIKV-3PR/10 ⁴	100%	NA
WN/ZIKV-3PR/10 ³	100%	NA
WN NY99/10 ³	0%	8 \pm 0

*AST = Average Survival Time

TABLE 7

AG129 mice (\geq 20 week-old) by intraperitoneal challenge		
Virus/dose (pfu)	Survival	AST* \pm SD
ZIKV PRVABC59/10 ⁴	0%	13.6 \pm 1.2
ZIKV PRVABC59/10 ³	0%	18.6 \pm 3.5
ZIKV PRVABC59/10 ²	40%	19.7 \pm 1.89
WN/ZIKV-3PR/10 ³	0%	5.2 \pm 0.4
WN/ZIKV-3PR/10 ²	20%	6 \pm 0
WN/ZIKV-3PR/10	40%	7.3 \pm 2.6
WN NY99/10 ²	0%	3.1 \pm 0.4
WN NY99/10	20%	3.8 \pm 0.4

*AST = Average Survival Time

Mosquito Study

A mosquito infection experiment was initiated with the chimeric viruses WN/ZKV-3PR and R-WN/ZKV-PR. Results from a small number of infected mosquitoes have shown an absence of infectivity or very low infectivity of the chimeric viruses for the Culex mosquito vector of WNV. To further reduce the potential for infection of mosquitoes, miRNAs specific to mosquito cells are incorporated into

WN/ZKV and R-WN/ZKV to evaluate whether such miRNA can be used to eliminate any potential of mosquito transmission of the virus. Specifically, miRNA-14, miRNA-184, and miRNA-1175 are investigated.

In view of the many possible embodiments to which the principles of the disclosed invention may be applied, it

should be recognized that the illustrated embodiments are only preferred examples of the invention and should not be taken as limiting the scope of the invention. Rather, the scope of the invention is defined by the following claims. We therefore claim as our invention all that comes within the scope and spirit of these claims.

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<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 2

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Ala Leu Leu Ala Phe Phe Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala
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Val Leu Asp Arg Trp Arg Gly Val Asn Lys Gln Thr Ala Met Lys His
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Leu Leu Ser Phe Lys Lys Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn
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Arg Arg Ser Ser Lys Gln Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala
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Val Met Ile Gly Leu Ile Ala Ser Ala Met Ala Ala Glu Val Thr Arg
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Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
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Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
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Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
           165          170          175

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
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Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
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Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
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Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
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Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
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Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
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Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
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Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
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Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
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Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
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Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
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Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
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Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
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Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
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Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
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His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser
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Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
 465 470 475 480

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
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Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
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Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
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Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
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Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
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Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
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Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
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Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
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Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
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Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
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Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
 660 665 670

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
 675 680 685

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
 690 695 700

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
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Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
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His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser
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Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu
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Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly
 770 775 780

Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Ser Gly Cys Ala
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Ile Asp Ile Ser Arg Gln Glu Leu Arg Cys Gly Ser Gly Val Phe Ile
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His Asn Asp Val Glu Ala Trp Met Asp Arg Tyr Lys Tyr Tyr Pro Glu
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Thr Pro Gln Gly Leu Ala Lys Ile Ile Gln Lys Ala His Lys Glu Gly
 835 840 845

Val Cys Gly Leu Arg Ser Val Ser Arg Leu Glu His Gln Met Trp Glu
 850 855 860

Ala Val Lys Asp Glu Leu Asn Thr Leu Leu Lys Glu Asn Gly Val Asp
 865 870 875 880

Leu Ser Val Val Val Glu Lys Gln Glu Gly Met Tyr Lys Ser Ala Pro
 885 890 895

Lys Arg Leu Thr Ala Thr Thr Glu Lys Leu Glu Ile Gly Trp Lys Ala
 900 905 910

Trp Gly Lys Ser Ile Leu Phe Ala Pro Glu Leu Ala Asn Asn Thr Phe
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Val Val Asp Gly Pro Glu Thr Lys Glu Cys Pro Thr Gln Asn Arg Ala
 930 935 940

Trp Asn Ser Leu Glu Val Glu Asp Phe Gly Phe Gly Leu Thr Ser Thr
 945 950 955 960

Arg Met Phe Leu Lys Val Arg Glu Ser Asn Thr Thr Glu Cys Asp Ser
 965 970 975

Lys Ile Ile Gly Thr Ala Val Lys Asn Asn Leu Ala Ile His Ser Asp
 980 985 990

Leu Ser Tyr Trp Ile Glu Ser Arg Leu Asn Asp Thr Trp Lys Leu Glu
 995 1000 1005

Arg Ala Val Leu Gly Glu Val Lys Ser Cys Thr Trp Pro Glu Thr
 1010 1015 1020

His Thr Leu Trp Gly Asp Gly Ile Leu Glu Ser Asp Leu Ile Ile
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Pro Val Thr Leu Ala Gly Pro Arg Ser Asn His Asn Arg Arg Pro
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Gly Tyr Lys Thr Gln Asn Gln Gly Pro Trp Asp Glu Gly Arg Val
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Glu Ile Asp Phe Asp Tyr Cys Pro Gly Thr Thr Val Thr Leu Ser
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Glu Ser Cys Gly His Arg Gly Pro Ala Thr Arg Thr Thr Thr Glu
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Ser Gly Lys Leu Ile Thr Asp Trp Cys Cys Arg Ser Cys Thr Leu
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Pro Pro Leu Arg Tyr Gln Thr Asp Ser Gly Cys Trp Tyr Gly Met
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Glu Ile Arg Pro Gln Arg His Asp Glu Lys Thr Leu Val Gln Ser
 1130 1135 1140

Gln Val Asn Ala Tyr Asn Ala Asp Met Ile Asp Pro Phe Gln Leu
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Gly Leu Leu Val Val Phe Leu Ala Thr Gln Glu Val Leu Arg Lys
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Arg Trp Thr Ala Lys Ile Ser Met Pro Ala Ile Leu Ile Ala Leu
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Leu Val Leu Val Phe Gly Gly Ile Thr Tyr Thr Asp Val Leu Arg
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Tyr Val Ile Leu Val Gly Ala Ala Phe Ala Glu Ser Asn Ser Gly
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Gly Asp Val Val His Leu Ala Leu Met Ala Thr Phe Lys Ile Gln

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Ala Tyr Tyr Asp Ala Arg Gln Ile Leu Leu Trp Glu Ile Pro Asp 1265 1270 1275		
Val Leu Asn Ser Leu Ala Val Ala Trp Met Ile Leu Arg Ala Ile 1280 1285 1290		
Thr Phe Thr Thr Thr Ser Asn Val Val Val Pro Leu Leu Ala Leu 1295 1300 1305		
Leu Thr Pro Gly Leu Arg Cys Leu Asn Leu Asp Val Tyr Arg Ile 1310 1315 1320		
Leu Leu Leu Met Val Gly Ile Gly Ser Leu Ile Arg Glu Lys Arg 1325 1330 1335		
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Leu Ala Ser Thr Gly Leu Phe Asn Pro Met Ile Leu Ala Ala Gly 1355 1360 1365		
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Glu Val Met Thr Ala Val Gly Leu Met Phe Ala Ile Val Gly Gly 1385 1390 1395		
Leu Ala Glu Leu Asp Ile Asp Ser Met Ala Ile Pro Met Thr Ile 1400 1405 1410		
Ala Gly Leu Met Phe Ala Ala Phe Val Ile Ser Gly Lys Ser Thr 1415 1420 1425		
Asp Met Trp Ile Glu Arg Thr Ala Asp Ile Ser Trp Glu Ser Asp 1430 1435 1440		
Ala Glu Ile Thr Gly Ser Ser Glu Arg Val Asp Val Arg Leu Asp 1445 1450 1455		
Asp Asp Gly Asn Phe Gln Leu Met Asn Asp Pro Gly Ala Pro Trp 1460 1465 1470		
Lys Ile Trp Met Leu Arg Met Val Cys Leu Ala Ile Ser Ala Tyr 1475 1480 1485		
Thr Pro Trp Ala Ile Leu Pro Ser Val Val Gly Phe Trp Ile Thr 1490 1495 1500		
Leu Gln Tyr Thr Lys Arg Gly Gly Val Leu Trp Asp Thr Pro Ser 1505 1510 1515		
Pro Lys Glu Tyr Lys Lys Gly Asp Thr Thr Thr Gly Val Tyr Arg 1520 1525 1530		
Ile Met Thr Arg Gly Leu Leu Gly Ser Tyr Gln Ala Gly Ala Gly 1535 1540 1545		
Val Met Val Glu Gly Val Phe His Thr Leu Trp His Thr Thr Lys 1550 1555 1560		
Gly Ala Ala Leu Met Ser Gly Glu Gly Arg Leu Asp Pro Tyr Trp 1565 1570 1575		
Gly Ser Val Lys Glu Asp Arg Leu Cys Tyr Gly Gly Pro Trp Lys 1580 1585 1590		
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Val Glu Pro Gly Arg Asn Val Lys Asn Val Gln Thr Lys Pro Gly 1610 1615 1620		

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1640						1645					1650			
Asp	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Ile	Met	Pro	Asn	Gly
1655						1660					1665			
Ser	Tyr	Ile	Ser	Ala	Ile	Val	Gln	Gly	Glu	Arg	Met	Asp	Glu	Pro
1670						1675					1680			
Ile	Pro	Ala	Gly	Phe	Glu	Pro	Glu	Met	Leu	Arg	Lys	Lys	Gln	Ile
1685						1690					1695			
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1700						1705					1710			
Leu	Pro	Gln	Ile	Ile	Lys	Glu	Ala	Ile	Asn	Arg	Arg	Leu	Arg	Thr
1715						1720					1725			
Ala	Val	Leu	Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Ala	Glu
1730						1735					1740			
Ala	Leu	Arg	Gly	Leu	Pro	Ile	Arg	Tyr	Gln	Thr	Ser	Ala	Val	Pro
1745						1750					1755			
Arg	Glu	His	Asn	Gly	Asn	Glu	Ile	Val	Asp	Val	Met	Cys	His	Ala
1760						1765					1770			
Thr	Leu	Thr	His	Arg	Leu	Met	Ser	Pro	His	Arg	Val	Pro	Asn	Tyr
1775						1780					1785			
Asn	Leu	Phe	Val	Met	Asp	Glu	Ala	His	Phe	Thr	Asp	Pro	Ala	Ser
1790						1795					1800			
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Gln	Leu	Asn	Arg	Lys	Ser	Tyr	Glu	Thr	Glu	Tyr	Pro	Lys	Cys	Lys
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Val	Lys	Pro	Thr	Ile	Ile	Thr	Glu	Gly	Glu	Gly	Arg	Val	Ile	Leu
1940						1945					1950			
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1955						1960					1965			
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Tyr	Gly	Gly	His	Thr	Asn	Glu	Asp	Asp	Ser	Asn	Phe	Ala	His	Trp
1985						1990					1995			
Thr	Glu	Ala	Arg	Ile	Met	Leu	Asp	Asn	Ile	Asn	Met	Pro	Asn	Gly
2000						2005					2010			

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Lys Val 2060	Ala Ala Ala Gly	Val 2065	Ser Tyr His Asp Arg	Arg Trp Cys 2070
Phe Asp 2075	Gly Pro Arg Thr	Asn 2080	Thr Ile Leu Glu Asp	Asn Asn Glu 2085
Val Glu 2090	Val Ile Thr Lys	Leu 2095	Gly Glu Arg Lys Ile	Leu Arg Pro 2100
Arg Trp 2105	Ile Asp Ala Arg	Val 2110	Tyr Ser Asp His Gln	Ala Leu Lys 2115
Ala Phe 2120	Lys Asp Phe Ala	Ser 2125	Gly Lys Arg Ser Gln	Ile Gly Leu 2130
Ile Glu 2135	Val Leu Gly Lys	Met 2140	Pro Glu His Phe Met	Gly Lys Thr 2145
Trp Glu 2150	Ala Leu Asp Thr	Met 2155	Tyr Val Val Ala Thr	Ala Glu Lys 2160
Gly Gly 2165	Arg Ala His Arg	Met 2170	Ala Leu Glu Glu Leu	Pro Asp Ala 2175
Leu Gln 2180	Thr Ile Ala Leu	Ile 2185	Ala Leu Leu Ser Val	Met Thr Met 2190
Gly Val 2195	Phe Phe Leu Leu	Met 2200	Gln Arg Lys Gly Ile	Gly Lys Ile 2205
Gly Leu 2210	Gly Gly Ala Val	Leu 2215	Gly Val Ala Thr Phe	Phe Cys Trp 2220
Met Ala 2225	Glu Val Pro Gly	Thr 2230	Lys Ile Ala Gly Met	Leu Leu Leu 2235
Ser Leu 2240	Leu Leu Met Ile	Val 2245	Leu Ile Pro Glu Pro	Glu Lys Gln 2250
Arg Ser 2255	Gln Thr Asp Asn	Gln 2260	Leu Ala Val Phe Leu	Ile Cys Val 2265
Met Thr 2270	Leu Val Ser Ala	Val 2275	Ala Ala Asn Glu Met	Gly Trp Leu 2280
Asp Lys 2285	Thr Lys Ser Asp	Ile 2290	Ser Ser Leu Phe Gly	Gln Arg Ile 2295
Glu Val 2300	Lys Glu Asn Phe	Ser 2305	Met Gly Glu Phe Leu	Leu Asp Leu 2310
Arg Pro 2315	Ala Thr Ala Trp	Ser 2320	Leu Tyr Ala Val Thr	Thr Ala Val 2325
Leu Thr 2330	Pro Leu Leu Lys	His 2335	Leu Ile Thr Ser Asp	Tyr Ile Asn 2340
Thr Ser 2345	Leu Thr Ser Ile	Asn 2350	Val Gln Ala Ser Ala	Leu Phe Thr 2355
Leu Ala 2360	Arg Gly Phe Pro	Phe 2365	Val Asp Val Gly Val	Ser Ala Leu 2370
Leu Leu 2375	Ala Ala Gly Cys	Trp 2380	Gly Gln Val Thr Leu	Thr Val Thr 2385
Val Thr 2390	Ala Ala Thr Leu	Leu 2395	Phe Cys His Tyr Ala	Tyr Met Val 2400
Pro Gly	Trp Gln Ala Glu Ala	Met Arg Ser Ala Gln	Arg Arg Thr	

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Val Val Asn Pro Ser Val Lys Thr Val Arg Glu Ala Gly Ile Leu 2465 2470		2475
Ile Thr Ala Ala Ala Val Thr Leu Trp Glu Asn Gly Ala Ser Ser 2480 2485		2490
Val Trp Asn Ala Thr Thr Ala Ile Gly Leu Cys His Ile Met Arg 2495 2500		2505
Gly Gly Trp Leu Ser Cys Leu Ser Ile Thr Trp Thr Leu Ile Lys 2510 2515		2520
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Arg Ser Ala Ala Lys His Ala Arg Lys Glu Gly Asn Val Thr Gly 2570 2575		2580
Gly His Pro Val Ser Arg Gly Thr Ala Lys Leu Arg Trp Leu Val 2585 2590		2595
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Val Gln Glu Val Arg Gly Tyr Thr Lys Gly Gly Pro Gly His Glu 2630 2635		2640
Glu Pro Gln Leu Val Gln Ser Tyr Gly Trp Asn Ile Val Thr Met 2645 2650		2655
Lys Ser Gly Val Asp Val Phe Tyr Arg Pro Ser Glu Cys Cys Asp 2660 2665		2670
Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Ser Ala Glu Val 2675 2680		2685
Glu Glu His Arg Thr Ile Arg Val Leu Glu Met Val Glu Asp Trp 2690 2695		2700
Leu His Arg Gly Pro Arg Glu Phe Cys Val Lys Val Leu Cys Pro 2705 2710		2715
Tyr Met Pro Lys Val Ile Glu Lys Met Glu Leu Leu Gln Arg Arg 2720 2725		2730
Tyr Gly Gly Gly Leu Val Arg Asn Pro Leu Ser Arg Asn Ser Thr 2735 2740		2745
His Glu Met Tyr Trp Val Ser Arg Ala Ser Gly Asn Val Val His 2750 2755		2760
Ser Val Asn Met Thr Ser Gln Val Leu Leu Gly Arg Met Glu Lys 2765 2770		2775
Arg Thr Trp Lys Gly Pro Gln Tyr Glu Glu Asp Val Asn Leu Gly 2780 2785		2790
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gtggagaaac tcacaaaagc gaaaggaccc aaagtcagga cctggctggt tgagaatggg	9660
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gatcgctttg ccacctcgt ccacttctc aatgctatgt caaaggctcg caaagacatc	9780
caagagtga aacctcaac tggatggtat gattggcagc aggttccatt ttgctcaaac	9840
catttcactg aattgatcat gaaagatgga agaactcgg tggttccatg ccgaggacag	9900
gatgaattgg taggcagac tcgcataatc ccaggggccc gatggaactg ccgagacact	9960
gcttgtctgg ctaagtctta tgcccagatg tggctcttc tgtacttcca cagaagagac	10020
ctgcgctca tggccaacgc catttctcc gctgtccctg tgaattgggt cctaccgga	10080
agaaccacgt ggtccatcca tgcaggagga gactggatga caacagagga catgttgag	10140

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gtctggaacc gtgtttgat agaggagaat gaatggatgg aagacaaaac cccagtggag 10200
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acaactttgg ttgaggacac agtactgtag atatttaatc aattgtaaat agacaatata 10440
agtatgcata aaagtgtag tttatagtag tatttagtgg tgtagtgta aatagttaag 10500
aaaattttga ggagaaagtc aggccgggaa gttcccgcca ccggaagtgg agtagacggt 10560
gctgcctgcg actcaacccc agggaggactg ggtgaacaaa gcccggaagt gatccatgta 10620
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actgggtaa caaaggcaaa ccaacgcccc acgcccgcct agccccgta atggtgtaa 10800
ccagggcgaa aggactagag gttagaggag accccgcggt ttaaagtca cgcccagcc 10860
tggctgaagc tgtaggtcag ggaaggact agaggttagt ggagaccctg tgccacaaaa 10920
caccacaaca aaacagcata ttgacacctg ggatagacta ggagatcttc tgctctgcac 10980
aaccagccac acggcacagt gcgcccacaa tgggtggctgg tggtagcaga acacaggatc 11040
t 11041

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<210> SEQ ID NO 4
<211> LENGTH: 3437
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

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<400> SEQUENCE: 4

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20            25            30
Ala Met Leu Ser Leu Ile Asp Gly Lys Gly Pro Ile Arg Phe Val Leu
35            40            45
Ala Leu Leu Ala Phe Phe Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala
50            55            60
Val Leu Asp Arg Trp Arg Gly Val Asn Lys Gln Thr Ala Met Lys His
65            70            75            80
Leu Leu Ser Phe Lys Lys Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn
85            90            95
Arg Arg Ser Ser Lys Gln Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala
100           105           110
Val Met Ile Gly Leu Ile Ala Ser Ala Met Ala Ala Glu Val Thr Arg
115           120           125
Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
130           135           140
Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
145           150           155           160
Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
165           170           175
Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
180           185           190

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Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
 195 200 205

Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser
 210 215 220

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
 225 230 235 240

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
 245 250 255

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
 260 265 270

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

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
 290 295 300

Gly Met Ser Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly
 305 310 315 320

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
 325 330 335

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
 340 345 350

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
 355 360 365

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
 370 375 380

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
 385 390 395 400

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
 405 410 415

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
 420 425 430

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
 435 440 445

His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser
 450 455 460

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
 465 470 475 480

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
 485 490 495

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
 500 505 510

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
 515 520 525

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
 530 535 540

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
 545 550 555 560

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
 565 570 575

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
 580 585 590

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
 595 600 605

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala

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Pro Val	Thr Leu Ala Gly	Pro Arg Ser Asn His Asn	Arg Arg Pro	
1040		1045	1050	
Gly Tyr	Lys Thr Gln Asn	Gln Gly Pro Trp Asp Glu	Gly Arg Val	
1055		1060	1065	
Glu Ile	Asp Phe Asp Tyr Cys	Pro Gly Thr Thr Val	Thr Leu Ser	
1070		1075	1080	
Glu Ser	Cys Gly His Arg Gly	Pro Ala Thr Arg Thr	Thr Thr Glu	
1085		1090	1095	
Ser Gly	Lys Leu Ile Thr Asp	Trp Cys Cys Arg Ser	Cys Thr Leu	
1100		1105	1110	
Pro Pro	Leu Arg Tyr Gln Thr	Asp Ser Gly Cys Trp	Tyr Gly Met	
1115		1120	1125	
Glu Ile	Arg Pro Gln Arg His	Asp Glu Lys Thr Leu	Val Gln Ser	
1130		1135	1140	
Gln Val	Asn Ala Tyr Asn Ala	Asp Met Ile Asp Pro	Phe Gln Leu	
1145		1150	1155	
Gly Leu	Leu Val Val Phe Leu	Ala Thr Gln Glu Val	Leu Arg Lys	
1160		1165	1170	
Arg Trp	Thr Ala Lys Ile Ser	Met Pro Ala Ile Leu	Ile Ala Leu	
1175		1180	1185	
Leu Val	Leu Val Phe Gly Gly	Ile Thr Tyr Thr Asp	Val Leu Arg	
1190		1195	1200	
Tyr Val	Ile Leu Val Gly Ala	Ala Phe Ala Glu Ser	Asn Ser Gly	
1205		1210	1215	
Gly Asp	Val Val His Leu Ala	Leu Met Ala Thr Phe	Lys Ile Gln	
1220		1225	1230	
Pro Val	Phe Met Val Ala Ser	Phe Leu Lys Ala Arg	Trp Thr Asn	
1235		1240	1245	
Gln Glu	Asn Ile Leu Leu Met	Leu Ala Ala Val Phe	Phe Gln Met	
1250		1255	1260	
Ala Tyr	Tyr Asp Ala Arg Gln	Ile Leu Leu Trp Glu	Ile Pro Asp	
1265		1270	1275	
Val Leu	Asn Ser Leu Ala Val	Ala Trp Met Ile Leu	Arg Ala Ile	
1280		1285	1290	
Thr Phe	Thr Thr Thr Ser Asn	Val Val Val Pro Leu	Leu Ala Leu	
1295		1300	1305	
Leu Thr	Pro Gly Leu Arg Cys	Leu Asn Leu Asp Val	Tyr Arg Ile	
1310		1315	1320	
Leu Leu	Leu Met Val Gly Ile	Gly Ser Leu Ile Arg	Glu Lys Arg	
1325		1330	1335	
Ser Ala	Ala Ala Lys Lys Lys	Gly Ala Ser Leu Leu	Cys Leu Ala	
1340		1345	1350	
Leu Ala	Ser Thr Gly Leu Phe	Asn Pro Met Ile Leu	Ala Ala Gly	
1355		1360	1365	
Leu Ile	Ala Cys Asp Pro Asn	Arg Lys Arg Gly Trp	Pro Ala Thr	
1370		1375	1380	
Glu Val	Met Thr Ala Val Gly	Leu Met Phe Ala Ile	Val Gly Gly	
1385		1390	1395	
Leu Ala	Glu Leu Asp Ile Asp	Ser Met Ala Ile Pro	Met Thr Ile	
1400		1405	1410	
Ala Gly	Leu Met Phe Ala Ala	Phe Val Ile Ser Gly	Lys Ser Thr	
1415		1420	1425	

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Asp Met 1430	Trp Ile Glu Arg	Thr 1435	Ala Asp Ile Ser	Trp 1440	Glu Ser Asp
Ala Glu 1445	Ile Thr Gly Ser	Ser 1450	Glu Arg Val Asp	Val 1455	Arg Leu Asp
Asp Asp 1460	Gly Asn Phe Gln	Leu 1465	Met Asn Asp Pro	Gly 1470	Ala Pro Trp
Lys Ile 1475	Trp Met Leu Arg	Met 1480	Val Cys Leu Ala	Ile 1485	Ser Ala Tyr
Thr Pro 1490	Trp Ala Ile Leu	Pro 1495	Ser Val Val Gly	Phe 1500	Trp Ile Thr
Leu Gln 1505	Tyr Thr Lys Arg	Gly 1510	Gly Val Leu Trp	Asp 1515	Thr Pro Ser
Pro Lys 1520	Glu Tyr Lys Lys	Gly 1525	Asp Thr Thr Thr	Gly 1530	Val Tyr Arg
Ile Met 1535	Thr Arg Gly Leu	Leu 1540	Gly Ser Tyr Gln	Ala 1545	Gly Ala Gly
Val Met 1550	Val Glu Gly Val	Phe 1555	His Thr Leu Trp	His 1560	Thr Thr Lys
Gly Ala 1565	Ala Leu Met Ser	Gly 1570	Glu Gly Arg Leu	Asp 1575	Pro Tyr Trp
Gly Ser 1580	Val Lys Glu Asp	Arg 1585	Leu Cys Tyr Gly	Gly 1590	Pro Trp Lys
Leu Gln 1595	His Lys Trp Asn	Gly 1600	Gln Asp Glu Val	Gln 1605	Met Ile Val
Val Glu 1610	Pro Gly Arg Asn	Val 1615	Lys Asn Val Gln	Thr 1620	Lys Pro Gly
Val Phe 1625	Lys Thr Pro Glu	Gly 1630	Glu Ile Gly Ala	Val 1635	Thr Leu Asp
Phe Pro 1640	Thr Gly Thr Ser	Gly 1645	Ser Pro Ile Val	Asp 1650	Lys Asn Gly
Asp Val 1655	Ile Gly Leu Tyr	Gly 1660	Asn Gly Val Ile	Met 1665	Pro Asn Gly
Ser Tyr 1670	Ile Ser Ala Ile	Val 1675	Gln Gly Glu Arg	Met 1680	Asp Glu Pro
Ile Pro 1685	Ala Gly Phe Glu	Pro 1690	Glu Met Leu Arg	Lys 1695	Lys Gln Ile
Thr Val 1700	Leu Asp Leu His	Pro 1705	Gly Ala Gly Lys	Thr 1710	Arg Arg Ile
Leu Pro 1715	Gln Ile Ile Lys	Glu 1720	Ala Ile Asn Arg	Arg 1725	Leu Arg Thr
Ala Val 1730	Leu Ala Pro Thr	Arg 1735	Val Val Ala Ala	Glu 1740	Met Ala Glu
Ala Leu 1745	Arg Gly Leu Pro	Ile 1750	Arg Tyr Gln Thr	Ser 1755	Ala Val Pro
Arg Glu 1760	His Asn Gly Asn	Glu 1765	Ile Val Asp Val	Met 1770	Cys His Ala
Thr Leu 1775	Thr His Arg Leu	Met 1780	Ser Pro His Arg	Val 1785	Pro Asn Tyr
Asn Leu 1790	Phe Val Met Asp	Glu 1795	Ala His Phe Thr	Asp 1800	Pro Ala Ser
Ile Ala 1805	Ala Arg Gly Tyr	Ile 1810	Ser Thr Lys Val	Glu 1815	Leu Gly Glu
Ala Ala	Ala Ile Phe Met	Thr	Ala Thr Pro Pro	Gly	Thr Ser Asp

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1820	1825	1830
Pro Phe 1835	Pro Glu Ser Asn Ser 1840	Pro Ile Ser Asp Leu Gln Thr Glu 1845
Ile Pro 1850	Asp Arg Ala Trp Asn Ser Gly Tyr Glu 1855	Trp Ile Thr Glu 1860
Tyr Thr 1865	Gly Lys Thr Val Trp Phe Val Pro Ser Val 1870	Lys Met Gly 1875
Asn Glu 1880	Ile Ala Leu Cys Leu Gln Arg Ala Gly Lys 1885	Lys Val Val 1890
Gln Leu 1895	Asn Arg Lys Ser Tyr Glu Thr Glu Tyr Pro 1900	Lys Cys Lys 1905
Asn Asp 1910	Asp Trp Asp Phe Val Ile Thr Thr Asp 1915	Ile Ser Glu Met 1920
Gly Ala 1925	Asn Phe Lys Ala Ser Arg Val Ile Asp Ser 1930	Arg Lys Ser 1935
Val Lys 1940	Pro Thr Ile Ile Thr Glu Gly Glu Gly Arg 1945	Val Ile Leu 1950
Gly Glu 1955	Pro Ser Ala Val Thr Ala Ala Ser Ala Ala 1960	Gln Arg Arg 1965
Gly Arg 1970	Ile Gly Arg Asn Pro Ser Gln Val Gly Asp 1975	Glu Tyr Cys 1980
Tyr Gly 1985	Gly His Thr Asn Glu Asp Asp Ser Asn Phe 1990	Ala His Trp 1995
Thr Glu 2000	Ala Arg Ile Met Leu Asp Asn Ile Asn Met 2005	Pro Asn Gly 2010
Leu Ile 2015	Ala Gln Phe Tyr Gln Pro Glu Arg Glu Lys 2020	Val Tyr Thr 2025
Met Asp 2030	Gly Glu Tyr Arg Leu Arg Gly Glu Glu Arg 2035	Lys Asn Phe 2040
Leu Glu 2045	Leu Leu Arg Thr Ala Asp Leu Pro Val Trp 2050	Leu Ala Tyr 2055
Lys Val 2060	Ala Ala Ala Gly Val Ser Tyr His Asp Arg 2065	Arg Trp Cys 2070
Phe Asp 2075	Gly Pro Arg Thr Asn Thr Ile Leu Glu Asp 2080	Asn Asn Glu 2085
Val Glu 2090	Val Ile Thr Lys Leu Gly Glu Arg Lys Ile 2095	Leu Arg Pro 2100
Arg Trp 2105	Ile Asp Ala Arg Val Tyr Ser Asp His Gln 2110	Ala Leu Lys 2115
Ala Phe 2120	Lys Asp Phe Ala Ser Gly Lys Arg Ser Gln 2125	Ile Gly Leu 2130
Ile Glu 2135	Val Leu Gly Lys Met Pro Glu His Phe Met 2140	Gly Lys Thr 2145
Trp Glu 2150	Ala Leu Asp Thr Met Tyr Val Val Ala Thr 2155	Ala Glu Lys 2160
Gly Gly 2165	Arg Ala His Arg Met Ala Leu Glu Glu Leu 2170	Pro Asp Ala 2175
Leu Gln 2180	Thr Ile Ala Leu Ile Ala Leu Leu Ser Val 2185	Met Thr Met 2190
Gly Val 2195	Phe Phe Leu Leu Met Gln Arg Lys Gly Ile 2200	Gly Lys Ile 2205
Gly Leu 2210	Gly Gly Ala Val Leu Gly Val Ala Thr Phe 2215	Phe Cys Trp 2220

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Met	Ala	Glu	Val	Pro	Gly	Thr	Lys	Ile	Ala	Gly	Met	Leu	Leu	Leu
2225						2230					2235			
Ser	Leu	Leu	Leu	Met	Ile	Val	Leu	Ile	Pro	Glu	Pro	Glu	Lys	Gln
2240						2245					2250			
Arg	Ser	Gln	Thr	Asp	Asn	Gln	Leu	Ala	Val	Phe	Leu	Ile	Cys	Val
2255						2260					2265			
Met	Thr	Leu	Val	Ser	Ala	Val	Ala	Ala	Asn	Glu	Met	Gly	Trp	Leu
2270						2275					2280			
Asp	Lys	Thr	Lys	Ser	Asp	Ile	Ser	Ser	Leu	Phe	Gly	Gln	Arg	Ile
2285						2290					2295			
Glu	Val	Lys	Glu	Asn	Phe	Ser	Met	Gly	Glu	Phe	Leu	Leu	Asp	Leu
2300						2305					2310			
Arg	Pro	Ala	Thr	Ala	Trp	Ser	Leu	Tyr	Ala	Val	Thr	Thr	Ala	Val
2315						2320					2325			
Leu	Thr	Pro	Leu	Leu	Lys	His	Leu	Ile	Thr	Ser	Asp	Tyr	Ile	Asn
2330						2335					2340			
Thr	Ser	Leu	Thr	Ser	Ile	Asn	Val	Gln	Ala	Ser	Ala	Leu	Phe	Thr
2345						2350					2355			
Leu	Ala	Arg	Gly	Phe	Pro	Phe	Val	Asp	Val	Gly	Val	Ser	Ala	Leu
2360						2365					2370			
Leu	Leu	Ala	Ala	Gly	Cys	Trp	Gly	Gln	Val	Thr	Leu	Thr	Val	Thr
2375						2380					2385			
Val	Thr	Ala	Ala	Thr	Leu	Leu	Phe	Cys	His	Tyr	Ala	Tyr	Met	Val
2390						2395					2400			
Pro	Gly	Trp	Gln	Ala	Glu	Ala	Met	Arg	Ser	Ala	Gln	Arg	Arg	Thr
2405						2410					2415			
Ala	Ala	Gly	Ile	Met	Lys	Asn	Ala	Val	Val	Asp	Gly	Ile	Val	Ala
2420						2425					2430			
Thr	Asp	Val	Pro	Glu	Leu	Glu	Arg	Thr	Thr	Pro	Ile	Met	Gln	Lys
2435						2440					2445			
Lys	Val	Gly	Gln	Ile	Met	Leu	Ile	Leu	Val	Ser	Leu	Ala	Ala	Val
2450						2455					2460			
Val	Val	Asn	Pro	Ser	Val	Lys	Thr	Val	Arg	Glu	Ala	Gly	Ile	Leu
2465						2470					2475			
Ile	Thr	Ala	Ala	Ala	Val	Thr	Leu	Trp	Glu	Asn	Gly	Ala	Ser	Ser
2480						2485					2490			
Val	Trp	Asn	Ala	Thr	Thr	Ala	Ile	Gly	Leu	Cys	His	Ile	Met	Arg
2495						2500					2505			
Gly	Gly	Trp	Leu	Ser	Cys	Leu	Ser	Ile	Thr	Trp	Thr	Leu	Ile	Lys
2510						2515					2520			
Asn	Met	Glu	Lys	Pro	Gly	Leu	Lys	Arg	Gly	Gly	Ala	Lys	Gly	Arg
2525						2530					2535			
Thr	Leu	Gly	Glu	Val	Trp	Lys	Glu	Arg	Leu	Asn	Gln	Met	Thr	Lys
2540						2545					2550			
Glu	Glu	Phe	Thr	Arg	Tyr	Arg	Lys	Glu	Ala	Ile	Ile	Glu	Val	Asp
2555						2560					2565			
Arg	Ser	Ala	Ala	Lys	His	Ala	Arg	Lys	Glu	Gly	Asn	Val	Thr	Gly
2570						2575					2580			
Gly	His	Pro	Val	Ser	Arg	Gly	Thr	Ala	Lys	Leu	Arg	Trp	Leu	Val
2585						2590					2595			
Glu	Arg	Arg	Phe	Leu	Glu	Pro	Val	Gly	Lys	Val	Ile	Asp	Leu	Gly
2600						2605					2610			

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Cys Gly	Arg Gly Gly Trp	Cys Tyr Tyr Met Ala Thr	Gln Lys Arg
2615		2620	2625
Val Gln	Glu Val Arg Gly Tyr	Thr Lys Gly Gly Pro	Gly His Glu
2630		2635	2640
Glu Pro	Gln Leu Val Gln Ser	Tyr Gly Trp Asn Ile	Val Thr Met
2645		2650	2655
Lys Ser	Gly Val Asp Val Phe	Tyr Arg Pro Ser Glu	Cys Cys Asp
2660		2665	2670
Thr Leu	Leu Cys Asp Ile Gly	Glu Ser Ser Ser Ser	Ala Glu Val
2675		2680	2685
Glu Glu	His Arg Thr Ile Arg	Val Leu Glu Met Val	Glu Asp Trp
2690		2695	2700
Leu His	Arg Gly Pro Arg Glu	Phe Cys Val Lys Val	Leu Cys Pro
2705		2710	2715
Tyr Met	Pro Lys Val Ile Glu	Lys Met Glu Leu Leu	Gln Arg Arg
2720		2725	2730
Tyr Gly	Gly Gly Leu Val Arg	Asn Pro Leu Ser Arg	Asn Ser Thr
2735		2740	2745
His Glu	Met Tyr Trp Val Ser	Arg Ala Ser Gly Asn	Val Val His
2750		2755	2760
Ser Val	Asn Met Thr Ser Gln	Val Leu Leu Gly Arg	Met Glu Lys
2765		2770	2775
Arg Thr	Trp Lys Gly Pro Gln	Tyr Glu Glu Asp Val	Asn Leu Gly
2780		2785	2790
Ser Gly	Thr Arg Ala Val Gly	Lys Pro Leu Leu Asn	Ser Asp Thr
2795		2800	2805
Ser Lys	Ile Lys Asn Arg Ile	Glu Arg Leu Arg Arg	Glu Tyr Ser
2810		2815	2820
Ser Thr	Trp His His Asp Glu	Asn His Pro Tyr Arg	Thr Trp Asn
2825		2830	2835
Tyr His	Gly Ser Tyr Asp Val	Lys Pro Thr Gly Ser	Ala Ser Ser
2840		2845	2850
Leu Val	Asn Gly Val Val Arg	Leu Leu Ser Lys Pro	Trp Asp Thr
2855		2860	2865
Ile Thr	Asn Val Thr Thr Met	Ala Met Thr Asp Thr	Thr Pro Phe
2870		2875	2880
Gly Gln	Gln Arg Val Phe Lys	Glu Lys Val Asp Thr	Lys Ala Pro
2885		2890	2895
Glu Pro	Pro Glu Gly Val Lys	Tyr Val Leu Asn Glu	Thr Thr Asn
2900		2905	2910
Trp Leu	Trp Ala Phe Leu Ala	Arg Glu Lys Arg Pro	Arg Met Cys
2915		2920	2925
Ser Arg	Glu Glu Phe Ile Arg	Lys Val Asn Ser Asn	Ala Ala Leu
2930		2935	2940
Gly Ala	Met Phe Glu Glu Gln	Asn Gln Trp Arg Ser	Ala Arg Glu
2945		2950	2955
Ala Val	Glu Asp Pro Lys Phe	Trp Glu Met Val Asp	Glu Glu Arg
2960		2965	2970
Glu Ala	His Leu Arg Gly Glu	Cys His Thr Cys Ile	Tyr Asn Met
2975		2980	2985
Met Gly	Lys Arg Glu Lys Lys	Pro Gly Glu Phe Gly	Lys Ala Lys
2990		2995	3000
Gly Ser	Arg Ala Ile Trp Phe	Met Trp Leu Gly Ala	Arg Phe Leu

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3005		3010		3015	
Glu Phe	Glu Ala Leu Gly	Phe Leu Asn Glu Asp	His Trp Leu Gly		
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Arg Lys	Asn Ser Gly Gly	Gly Val Glu Gly Leu Gly	Leu Gln Lys		
3035		3040	3045		
Leu Gly	Tyr Ile Leu Arg	Glu Val Gly Thr Arg Pro	Gly Gly Lys		
3050		3055	3060		
Ile Tyr	Ala Asp Asp Thr	Ala Gly Trp Asp Thr Arg	Ile Thr Arg		
3065		3070	3075		
Ala Asp	Leu Glu Asn Glu	Ala Lys Val Leu Glu Leu	Leu Asp Gly		
3080		3085	3090		
Glu His	Arg Arg Leu Ala	Arg Ala Ile Ile Glu Leu	Thr Tyr Arg		
3095		3100	3105		
His Lys	Val Val Lys Val	Met Arg Pro Ala Ala Asp	Gly Arg Thr		
3110		3115	3120		
Val Met	Asp Val Ile Ser	Arg Glu Asp Gln Arg Gly	Ser Gly Gln		
3125		3130	3135		
Val Val	Thr Tyr Ala Leu	Asn Thr Phe Thr Asn Leu	Ala Val Gln		
3140		3145	3150		
Leu Val	Arg Met Met Glu	Gly Glu Gly Val Ile Gly	Pro Asp Asp		
3155		3160	3165		
Val Glu	Lys Leu Thr Lys	Gly Lys Gly Pro Lys Val	Arg Thr Trp		
3170		3175	3180		
Leu Phe	Glu Asn Gly Glu	Glu Arg Leu Ser Arg Met	Ala Val Ser		
3185		3190	3195		
Gly Asp	Asp Cys Val Val	Lys Pro Leu Asp Asp Arg	Phe Ala Thr		
3200		3205	3210		
Ser Leu	His Phe Leu Asn	Ala Met Ser Lys Val Arg	Lys Asp Ile		
3215		3220	3225		
Gln Glu	Trp Lys Pro Ser	Thr Gly Trp Tyr Asp Trp	Gln Gln Val		
3230		3235	3240		
Pro Phe	Cys Ser Asn His	Phe Thr Glu Leu Ile Met	Lys Asp Gly		
3245		3250	3255		
Arg Thr	Leu Val Val Pro	Cys Arg Gly Gln Asp Glu	Leu Val Gly		
3260		3265	3270		
Arg Ala	Arg Ile Ser Pro	Gly Ala Gly Trp Asn Val	Arg Asp Thr		
3275		3280	3285		
Ala Cys	Leu Ala Lys Ser	Tyr Ala Gln Met Trp Leu	Leu Leu Tyr		
3290		3295	3300		
Phe His	Arg Arg Asp Leu	Arg Leu Met Ala Asn Ala	Ile Cys Ser		
3305		3310	3315		
Ala Val	Pro Val Asn Trp	Val Pro Thr Gly Arg Thr	Thr Trp Ser		
3320		3325	3330		
Ile His	Ala Gly Gly Glu	Trp Met Thr Thr Glu Asp	Met Leu Glu		
3335		3340	3345		
Val Trp	Asn Arg Val Trp	Ile Glu Glu Asn Glu Trp	Met Glu Asp		
3350		3355	3360		
Lys Thr	Pro Val Glu Lys	Trp Ser Asp Val Pro Tyr	Ser Gly Lys		
3365		3370	3375		
Arg Glu	Asp Ile Trp Cys	Gly Ser Leu Ile Gly Thr	Arg Ala Arg		
3380		3385	3390		
Ala Thr	Trp Ala Glu Asn	Ile Gln Val Ala Ile Asn	Gln Val Arg		
3395		3400	3405		

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Ala Ile Ile Gly Asp Glu Lys Tyr Val Asp Tyr Met Ser Ser Leu
 3410 3415 3420

Lys Arg Tyr Glu Asp Thr Thr Leu Val Glu Asp Thr Val Leu
 3425 3430 3435

<210> SEQ ID NO 5
 <211> LENGTH: 11041
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 5

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His Asn Asp Val Glu Ala Trp Met Asp Arg Tyr Lys Tyr Tyr Pro Glu
 820 825 830

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Thr Pro Gln Gly Leu Ala Lys Ile Ile Gln Lys Ala His Lys Glu Gly
 835 840 845

Val Cys Gly Leu Arg Ser Val Ser Arg Leu Glu His Gln Met Trp Glu
 850 855 860

Ala Val Lys Asp Glu Leu Asn Thr Leu Leu Lys Glu Asn Gly Val Asp
 865 870 875 880

Leu Ser Val Val Val Glu Lys Gln Glu Gly Met Tyr Lys Ser Ala Pro
 885 890 895

Lys Arg Leu Thr Ala Thr Thr Glu Lys Leu Glu Ile Gly Trp Lys Ala
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Trp Gly Lys Ser Ile Leu Phe Ala Pro Glu Leu Ala Asn Asn Thr Phe
 915 920 925

Val Val Asp Gly Pro Glu Thr Lys Glu Cys Pro Thr Gln Asn Arg Ala
 930 935 940

Trp Asn Ser Leu Glu Val Glu Asp Phe Gly Phe Gly Leu Thr Ser Thr
 945 950 955 960

Arg Met Phe Leu Lys Val Arg Glu Ser Asn Thr Thr Glu Cys Asp Ser
 965 970 975

Lys Ile Ile Gly Thr Ala Val Lys Asn Asn Leu Ala Ile His Ser Asp
 980 985 990

Leu Ser Tyr Trp Ile Glu Ser Arg Leu Asn Asp Thr Trp Lys Leu Glu
 995 1000 1005

Arg Ala Val Leu Gly Glu Val Lys Ser Cys Thr Trp Pro Glu Thr
 1010 1015 1020

His Thr Leu Trp Gly Asp Gly Ile Leu Glu Ser Asp Leu Ile Ile
 1025 1030 1035

Pro Val Thr Leu Ala Gly Pro Arg Ser Asn His Asn Arg Arg Pro
 1040 1045 1050

Gly Tyr Lys Thr Gln Asn Gln Gly Pro Trp Asp Glu Gly Arg Val
 1055 1060 1065

Glu Ile Asp Phe Asp Tyr Cys Pro Gly Thr Thr Val Thr Leu Ser
 1070 1075 1080

Glu Ser Cys Gly His Arg Gly Pro Ala Thr Arg Thr Thr Thr Glu
 1085 1090 1095

Ser Gly Lys Leu Ile Thr Asp Trp Cys Cys Arg Ser Cys Thr Leu
 1100 1105 1110

Pro Pro Leu Arg Tyr Gln Thr Asp Ser Gly Cys Trp Tyr Gly Met
 1115 1120 1125

Glu Ile Arg Pro Gln Arg His Asp Glu Lys Thr Leu Val Gln Ser
 1130 1135 1140

Gln Val Asn Ala Tyr Asn Ala Asp Met Ile Asp Pro Phe Gln Leu
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Gly Leu Leu Val Val Phe Leu Ala Thr Gln Glu Val Leu Arg Lys
 1160 1165 1170

Arg Trp Thr Ala Lys Ile Ser Met Pro Ala Ile Leu Ile Ala Leu
 1175 1180 1185

Leu Val Leu Val Phe Gly Gly Ile Thr Tyr Thr Asp Val Leu Arg
 1190 1195 1200

Tyr Val Ile Leu Val Gly Ala Ala Phe Ala Glu Ser Asn Ser Gly
 1205 1210 1215

Gly Asp Val Val His Leu Ala Leu Met Ala Thr Phe Lys Ile Gln
 1220 1225 1230

Pro Val Phe Met Val Ala Ser Phe Leu Lys Ala Arg Trp Thr Asn

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1235	1240	1245
Gln Glu Asn Ile Leu Leu Met 1250 1255	Leu Ala Ala Val Phe 1255	Phe Gln Met 1260
Ala Tyr Tyr Asp Ala Arg 1265	Gln Ile Leu Leu Trp 1270	Glu Ile Pro Asp 1275
Val Leu Asn Ser Leu Ala 1280	Val Ala Trp Met Ile 1285	Leu Arg Ala Ile 1290
Thr Phe Thr Thr Thr Ser 1295	Asn Val Val Val Pro 1300	Leu Leu Ala Leu 1305
Leu Thr Pro Gly Leu Arg 1310	Cys Leu Asn Leu Asp 1315	Val Tyr Arg Ile 1320
Leu Leu Leu Met Val Gly 1325	Ile Gly Ser Leu Ile 1330	Arg Glu Lys Arg 1335
Ser Ala Ala Ala Lys Lys 1340	Lys Gly Ala Ser Leu 1345	Leu Cys Leu Ala 1350
Leu Ala Ser Thr Gly Leu 1355	Phe Asn Pro Met Ile 1360	Leu Ala Ala Gly 1365
Leu Ile Ala Cys Asp Pro 1370	Asn Arg Lys Arg Gly 1375	Trp Pro Ala Thr 1380
Glu Val Met Thr Ala Val 1385	Gly Leu Met Phe Ala 1390	Ile Val Gly Gly 1395
Leu Ala Glu Leu Asp Ile 1400	Asp Ser Met Ala Ile 1405	Pro Met Thr Ile 1410
Ala Gly Leu Met Phe Ala 1415	Ala Phe Val Ile Ser 1420	Gly Lys Ser Thr 1425
Asp Met Trp Ile Glu Arg 1430	Thr Ala Asp Ile Ser 1435	Trp Glu Ser Asp 1440
Ala Glu Ile Thr Gly Ser 1445	Ser Glu Arg Val Asp 1450	Val Arg Leu Asp 1455
Asp Asp Gly Asn Phe Gln 1460	Leu Met Asn Asp Pro 1465	Gly Ala Pro Trp 1470
Lys Ile Trp Met Leu Arg 1475	Met Val Cys Leu Ala 1480	Ile Ser Ala Tyr 1485
Thr Pro Trp Ala Ile Leu 1490	Pro Ser Val Val Gly 1495	Phe Trp Ile Thr 1500
Leu Gln Tyr Thr Lys Arg 1505	Gly Gly Val Leu Trp 1510	Asp Thr Pro Ser 1515
Pro Lys Glu Tyr Lys Lys 1520	Gly Asp Thr Thr Thr 1525	Gly Val Tyr Arg 1530
Ile Met Thr Arg Gly Leu 1535	Leu Gly Ser Tyr Gln 1540	Ala Gly Ala Gly 1545
Val Met Val Glu Gly Val 1550	Phe His Thr Leu Trp 1555	His Thr Thr Lys 1560
Gly Ala Ala Leu Met Ser 1565	Gly Glu Gly Arg Leu 1570	Asp Pro Tyr Trp 1575
Gly Ser Val Lys Glu Asp 1580	Arg Leu Cys Tyr Gly 1585	Gly Pro Trp Lys 1590
Leu Gln His Lys Trp Asn 1595	Gly Gln Asp Glu Val 1600	Gln Met Ile Val 1605
Val Glu Pro Gly Arg Asn 1610	Val Lys Asn Val Gln 1615	Thr Lys Pro Gly 1620
Val Phe Lys Thr Pro Glu 1625	Gly Glu Ile Gly Ala 1630	Val Thr Leu Asp 1635

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Phe	Pro	Thr	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Val	Asp	Lys	Asn	Gly
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1655						1660					1665			
Ser	Tyr	Ile	Ser	Ala	Ile	Val	Gln	Gly	Glu	Arg	Met	Asp	Glu	Pro
1670						1675					1680			
Ile	Pro	Ala	Gly	Phe	Glu	Pro	Glu	Met	Leu	Arg	Lys	Lys	Gln	Ile
1685						1690					1695			
Thr	Val	Leu	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Arg	Arg	Ile
1700						1705					1710			
Leu	Pro	Gln	Ile	Ile	Lys	Glu	Ala	Ile	Asn	Arg	Arg	Leu	Arg	Thr
1715						1720					1725			
Ala	Val	Leu	Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met	Ala	Glu
1730						1735					1740			
Ala	Leu	Arg	Gly	Leu	Pro	Ile	Arg	Tyr	Gln	Thr	Ser	Ala	Val	Pro
1745						1750					1755			
Arg	Glu	His	Asn	Gly	Asn	Glu	Ile	Val	Asp	Val	Met	Cys	His	Ala
1760						1765					1770			
Thr	Leu	Thr	His	Arg	Leu	Met	Ser	Pro	His	Arg	Val	Pro	Asn	Tyr
1775						1780					1785			
Asn	Leu	Phe	Val	Met	Asp	Glu	Ala	His	Phe	Thr	Asp	Pro	Ala	Ser
1790						1795					1800			
Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr	Lys	Val	Glu	Leu	Gly	Glu
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1835						1840					1845			
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1850						1855					1860			
Tyr	Thr	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Val	Lys	Met	Gly
1865						1870					1875			
Asn	Glu	Ile	Ala	Leu	Cys	Leu	Gln	Arg	Ala	Gly	Lys	Lys	Val	Val
1880						1885					1890			
Gln	Leu	Asn	Arg	Lys	Ser	Tyr	Glu	Thr	Glu	Tyr	Pro	Lys	Cys	Lys
1895						1900					1905			
Asn	Asp	Asp	Trp	Asp	Phe	Val	Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met
1910						1915					1920			
Gly	Ala	Asn	Phe	Lys	Ala	Ser	Arg	Val	Ile	Asp	Ser	Arg	Lys	Ser
1925						1930					1935			
Val	Lys	Pro	Thr	Ile	Ile	Thr	Glu	Gly	Glu	Gly	Arg	Val	Ile	Leu
1940						1945					1950			
Gly	Glu	Pro	Ser	Ala	Val	Thr	Ala	Ala	Ser	Ala	Ala	Gln	Arg	Arg
1955						1960					1965			
Gly	Arg	Ile	Gly	Arg	Asn	Pro	Ser	Gln	Val	Gly	Asp	Glu	Tyr	Cys
1970						1975					1980			
Tyr	Gly	Gly	His	Thr	Asn	Glu	Asp	Asp	Ser	Asn	Phe	Ala	His	Trp
1985						1990					1995			
Thr	Glu	Ala	Arg	Ile	Met	Leu	Asp	Asn	Ile	Asn	Met	Pro	Asn	Gly
2000						2005					2010			
Leu	Ile	Ala	Gln	Phe	Tyr	Gln	Pro	Glu	Arg	Glu	Lys	Val	Tyr	Thr
2015						2020					2025			

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Met Asp 2030	Gly Glu Tyr Arg	Leu 2035	Arg Gly Glu Glu Arg	Lys Asn Phe 2040
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Lys Val 2060	Ala Ala Ala Gly	Val 2065	Ser Tyr His Asp Arg	Arg Trp Cys 2070
Phe Asp 2075	Gly Pro Arg Thr	Asn 2080	Thr Ile Leu Glu Asp	Asn Asn Glu 2085
Val Glu 2090	Val Ile Thr Lys	Leu 2095	Gly Glu Arg Lys Ile	Leu Arg Pro 2100
Arg Trp 2105	Ile Asp Ala Arg	Val 2110	Tyr Ser Asp His Gln	Ala Leu Lys 2115
Ala Phe 2120	Lys Asp Phe Ala	Ser 2125	Gly Lys Arg Ser Gln	Ile Gly Leu 2130
Ile Glu 2135	Val Leu Gly Lys	Met 2140	Pro Glu His Phe Met	Gly Lys Thr 2145
Trp Glu 2150	Ala Leu Asp Thr	Met 2155	Tyr Val Val Ala Thr	Ala Glu Lys 2160
Gly Gly 2165	Arg Ala His Arg	Met 2170	Ala Leu Glu Glu Leu	Pro Asp Ala 2175
Leu Gln 2180	Thr Ile Ala Leu	Ile 2185	Ala Leu Leu Ser Val	Met Thr Met 2190
Gly Val 2195	Phe Phe Leu Leu	Met 2200	Gln Arg Lys Gly Ile	Gly Lys Ile 2205
Gly Leu 2210	Gly Gly Ala Val	Leu 2215	Gly Val Ala Thr Phe	Phe Cys Trp 2220
Met Ala 2225	Glu Val Pro Gly	Thr 2230	Lys Ile Ala Gly Met	Leu Leu Leu 2235
Ser Leu 2240	Leu Leu Met Ile	Val 2245	Leu Ile Pro Glu Pro	Glu Lys Gln 2250
Arg Ser 2255	Gln Thr Asp Asn	Gln 2260	Leu Ala Val Phe Leu	Ile Cys Val 2265
Met Thr 2270	Leu Val Ser Ala	Val 2275	Ala Ala Asn Glu Met	Gly Trp Leu 2280
Asp Lys 2285	Thr Lys Ser Asp	Ile 2290	Ser Ser Leu Phe Gly	Gln Arg Ile 2295
Glu Val 2300	Lys Glu Asn Phe	Ser 2305	Met Gly Glu Phe Leu	Leu Asp Leu 2310
Arg Pro 2315	Ala Thr Ala Trp	Ser 2320	Leu Tyr Ala Val Thr	Thr Ala Val 2325
Leu Thr 2330	Pro Leu Leu Lys	His 2335	Leu Ile Thr Ser Asp	Tyr Ile Asn 2340
Thr Ser 2345	Leu Thr Ser Ile	Asn 2350	Val Gln Ala Ser Ala	Leu Phe Thr 2355
Leu Ala 2360	Arg Gly Phe Pro	Phe 2365	Val Asp Val Gly Val	Ser Ala Leu 2370
Leu Leu 2375	Ala Ala Gly Cys	Trp 2380	Gly Gln Val Thr Leu	Thr Val Thr 2385
Val Thr 2390	Ala Ala Thr Leu	Leu 2395	Phe Cys His Tyr Ala	Tyr Met Val 2400
Pro Gly 2405	Trp Gln Ala Glu	Ala 2410	Met Arg Ser Ala Gln	Arg Arg Thr 2415
Ala Ala	Gly Ile Met Lys Asn	Ala Val Val Asp Gly	Ile Val Ala	

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2420	2425	2430
Thr Asp Val Pro Glu Leu Glu Arg Thr Thr Pro Ile Met Gln Lys 2435	2440	2445
Lys Val Gly Gln Ile Met Leu Ile Leu Val Ser Leu Ala Ala Val 2450	2455	2460
Val Val Asn Pro Ser Val Lys Thr Val Arg Glu Ala Gly Ile Leu 2465	2470	2475
Ile Thr Ala Ala Ala Val Thr Leu Trp Glu Asn Gly Ala Ser Ser 2480	2485	2490
Val Trp Asn Ala Thr Thr Ala Ile Gly Leu Cys His Ile Met Arg 2495	2500	2505
Gly Gly Trp Leu Ser Cys Leu Ser Ile Thr Trp Thr Leu Ile Lys 2510	2515	2520
Asn Met Glu Lys Pro Gly Leu Lys Arg Gly Gly Ala Lys Gly Arg 2525	2530	2535
Thr Leu Gly Glu Val Trp Lys Glu Arg Leu Asn Gln Met Thr Lys 2540	2545	2550
Glu Glu Phe Thr Arg Tyr Arg Lys Glu Ala Ile Ile Glu Val Asp 2555	2560	2565
Arg Ser Ala Ala Lys His Ala Arg Lys Glu Gly Asn Val Thr Gly 2570	2575	2580
Gly His Pro Val Ser Arg Gly Thr Ala Lys Leu Arg Trp Leu Val 2585	2590	2595
Glu Arg Arg Phe Leu Glu Pro Val Gly Lys Val Ile Asp Leu Gly 2600	2605	2610
Cys Gly Arg Gly Gly Trp Cys Tyr Tyr Met Ala Thr Gln Lys Arg 2615	2620	2625
Val Gln Glu Val Arg Gly Tyr Thr Lys Gly Gly Pro Gly His Glu 2630	2635	2640
Glu Pro Gln Leu Val Gln Ser Tyr Gly Trp Asn Ile Val Thr Met 2645	2650	2655
Lys Ser Gly Val Asp Val Phe Tyr Arg Pro Ser Glu Cys Cys Asp 2660	2665	2670
Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Ser Ala Glu Val 2675	2680	2685
Glu Glu His Arg Thr Ile Arg Val Leu Glu Met Val Glu Asp Trp 2690	2695	2700
Leu His Arg Gly Pro Arg Glu Phe Cys Val Lys Val Leu Cys Pro 2705	2710	2715
Tyr Met Pro Lys Val Ile Glu Lys Met Glu Leu Leu Gln Arg Arg 2720	2725	2730
Tyr Gly Gly Gly Leu Val Arg Asn Pro Leu Ser Arg Asn Ser Thr 2735	2740	2745
His Glu Met Tyr Trp Val Ser Arg Ala Ser Gly Asn Val Val His 2750	2755	2760
Ser Val Asn Met Thr Ser Gln Val Leu Leu Gly Arg Met Glu Lys 2765	2770	2775
Arg Thr Trp Lys Gly Pro Gln Tyr Glu Glu Asp Val Asn Leu Gly 2780	2785	2790
Ser Gly Thr Arg Ala Val Gly Lys Pro Leu Leu Asn Ser Asp Thr 2795	2800	2805
Ser Lys Ile Lys Asn Arg Ile Glu Arg Leu Arg Arg Glu Tyr Ser 2810	2815	2820

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Ser	Thr	Trp	His	His	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	Trp	Asn
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2840						2845					2850			
Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	Asp	Thr
2855						2860					2865			
Ile	Thr	Asn	Val	Thr	Thr	Met	Ala	Met	Thr	Asp	Thr	Thr	Pro	Phe
2870						2875					2880			
Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Lys	Ala	Pro
2885						2890					2895			
Glu	Pro	Pro	Glu	Gly	Val	Lys	Tyr	Val	Leu	Asn	Glu	Thr	Thr	Asn
2900						2905					2910			
Trp	Leu	Trp	Ala	Phe	Leu	Ala	Arg	Glu	Lys	Arg	Pro	Arg	Met	Cys
2915						2920					2925			
Ser	Arg	Glu	Glu	Phe	Ile	Arg	Lys	Val	Asn	Ser	Asn	Ala	Ala	Leu
2930						2935					2940			
Gly	Ala	Met	Phe	Glu	Glu	Gln	Asn	Gln	Trp	Arg	Ser	Ala	Arg	Glu
2945						2950					2955			
Ala	Val	Glu	Asp	Pro	Lys	Phe	Trp	Glu	Met	Val	Asp	Glu	Glu	Arg
2960						2965					2970			
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2975						2980					2985			
Met	Gly	Lys	Arg	Glu	Lys	Lys	Pro	Gly	Glu	Phe	Gly	Lys	Ala	Lys
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Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	Leu	Gly
3020						3025					3030			
Arg	Lys	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	Gln	Lys
3035						3040					3045			
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Ala	Asp	Leu	Glu	Asn	Glu	Ala	Lys	Val	Leu	Glu	Leu	Leu	Asp	Gly
3080						3085					3090			
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3110						3115					3120			
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3125						3130					3135			
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Val	Glu	Lys	Leu	Thr	Lys	Gly	Lys	Gly	Pro	Lys	Val	Arg	Thr	Trp
3170						3175					3180			
Leu	Phe	Glu	Asn	Gly	Glu	Glu	Arg	Leu	Ser	Arg	Met	Ala	Val	Ser
3185						3190					3195			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Leu	Asp	Asp	Arg	Phe	Ala	Thr
3200						3205					3210			

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Ser	Leu	His	Phe	Leu	Asn	Ala	Met	Ser	Lys	Val	Arg	Lys	Asp	Ile
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3245						3250					3255			
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3260						3265					3270			
Arg	Ala	Arg	Ile	Ser	Pro	Gly	Ala	Gly	Trp	Asn	Val	Arg	Asp	Thr
3275						3280					3285			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Leu	Leu	Leu	Tyr
3290						3295					3300			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3305						3310					3315			
Ala	Val	Pro	Val	Asn	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3320						3325					3330			
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3335						3340					3345			
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3350						3355					3360			
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3365						3370					3375			
Arg	Glu	Asp	Ile	Trp	Cys	Gly	Ser	Leu	Ile	Gly	Thr	Arg	Ala	Arg
3380						3385					3390			
Ala	Thr	Trp	Ala	Glu	Asn	Ile	Gln	Val	Ala	Ile	Asn	Gln	Val	Arg
3395						3400					3405			
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<210> SEQ ID NO 7

<211> LENGTH: 11041

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

<400> SEQUENCE: 7

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

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<400> SEQUENCE: 10

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          20          25          30
Ala Met Leu Met Ala Gln Ser Lys His Gly Leu Thr Lys Glu Met Thr
          35          40          45
Met Lys Tyr Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile
          50          55          60
Thr Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn
 65          70          75          80
Leu Cys Val Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu
          85          90          95
Ser Ala Ala Phe Met Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln
          100          105          110
Asp Ile Ala Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp
          115          120          125
Asp Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala
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Asp Ile Thr Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys
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Phe Tyr Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met
          165          170          175
Thr Asp Asn Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys
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Gln Gly Ile Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp
          195          200          205
Gly Gly Arg Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser
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Val Pro Arg Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr
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Arg Glu Asp Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu
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Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro

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Ala	Ile	Ser	Phe	Pro	Thr	Thr	Leu	Gly	Met	Asn	Lys	Cys	Tyr	Ile	Gln
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Pro	Met	Leu	Asp	Glu	Gly	Val	Glu	Pro	Asp	Asp	Val	Asp	Cys	Trp	Cys
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Asn	Thr	Thr	Ser	Thr	Trp	Val	Val	Tyr	Gly	Thr	Cys	His	His	Lys	Lys
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Gly	Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser
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Tyr	Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro
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Thr	Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro
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Val	Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr
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Glu	Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln
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Arg	Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly
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Lys	Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met
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Asn Thr	Leu Leu Lys Glu Asn	Gly Val Asp Leu Ser	Val Val Val
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Glu Lys	Gln Glu Gly Met Tyr	Lys Ser Ala Pro Lys	Arg Leu Thr
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Ala Thr	Thr Glu Lys Leu Glu	Ile Gly Trp Lys Ala	Trp Gly Lys
1190		1195	1200
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Lys Leu	Glu Arg Ala Val Leu	Gly Glu Val Lys Ser	Cys Thr Trp
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1385		1390	1395
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Phe Gln	Leu Gly Leu Leu Val	Val Val Phe Leu Ala Thr	Gln Glu Val
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Val Leu	Arg Tyr Val Ile Leu	Val Gly Ala Ala Phe	Ala Glu Ser
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2075						2080					2085			
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2090						2095					2100			
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Glu	Tyr	Cys	Tyr	Gly	Gly	His	Thr	Asn	Glu	Asp	Asp	Ser	Asn	Phe
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Ala	His	Trp	Thr	Glu	Ala	Arg	Ile	Met	Leu	Asp	Asn	Ile	Asn	Met
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Arg Trp	Cys Phe Asp Gly	Pro	Arg Thr Asn Thr	Ile	Leu Glu Asp
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Asn Asn	Glu Val Glu Val	Ile	Thr Lys Leu Gly	Glu	Arg Lys Ile
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Gly Lys	Thr Trp Glu Ala	Leu	Asp Thr Met Tyr	Val	Val Ala Thr
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Pro Asp	Ala Leu Gln Thr	Ile	Ala Leu Ile Ala	Leu	Leu Ser Val
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Gly Lys	Ile Gly Leu Gly	Gly	Ala Val Leu Gly	Val	Ala Thr Phe
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Glu Lys	Gln Arg Ser Gln	Thr	Asp Asn Gln Leu	Ala	Val Phe Leu
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Ile Cys	Val Met Thr Leu	Val	Ser Ala Val Ala	Ala	Asn Glu Met
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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic construct

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<223> OTHER INFORMATION: Synthetic polypeptide

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<400> SEQUENCE: 12

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20           25           30

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

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

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Gly	Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser
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Thr	Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro
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Ala	Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu
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Cys	Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu
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Glu	Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln
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Gly	Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys
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Lys	Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met
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Thr	Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu
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Ser	Val	His	Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly
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His	Glu	Thr	Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser
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Pro	Arg	Ala	Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp
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Cys	Glu	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr
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785					790					795					800
Pro	Leu	Pro	Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn
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		820						825					830		
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Gly Thr Asp Gly	Pro Cys Lys Val	Pro Ala Gln Met Ala Val	Asp Met
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Gln Thr Leu Thr	Pro Val Gly Arg	Leu Ile Thr Ala Asn	Pro Val Ile
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His His Trp His	Arg Ser Gly Ser	Thr Ile Gly Lys Ala	Phe Glu Ala
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Gly Ser Gly Val	Phe Ile His Asn	Asp Val Glu Ala	Trp Met Asp
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Arg Tyr Lys Tyr	Tyr Pro Glu Thr	Pro Gln Gly Leu	Ala Lys Ile
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Ile Gln Lys Ala	His Lys Glu Gly	Val Cys Gly Leu	Arg Ser Val
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Ala Thr Thr Glu	Lys Leu Glu Ile	Gly Trp Lys Ala	Trp Gly Lys
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Ser Ile Leu Phe	Ala Pro Glu Leu	Ala Asn Asn Thr	Phe Val Val
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Thr Thr	Glu Ser Gly Lys	Leu	Ile Thr Asp Trp Cys	Cys Arg Ser	
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Cys Thr	Leu Pro Pro Leu	Arg	Tyr Gln Thr Asp Ser	Gly Cys Trp	
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Tyr Gly	Met Glu Ile Arg	Pro	Gln Arg His Asp Glu	Lys Thr Leu	
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Val Gln	Ser Gln Val Asn	Ala	Tyr Asn Ala Asp Met	Ile Asp Pro	
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Cys Leu	Ala Leu Ala Ser	Thr	Gly Leu Phe Asn Pro	Met Ile Leu	
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Gly Lys 2495	Ile Gly Leu Gly 2500	Gly 2500	Ala Val Leu Gly Val 2505	Ala Thr Phe
Phe Cys 2510	Trp Met Ala Glu 2515	Val 2515	Pro Gly Thr Lys Ile 2520	Ala Gly Met
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Glu Lys 2540	Gln Arg Ser Gln 2545	Thr 2545	Asp Asn Gln Leu Ala 2550	Val Phe Leu
Ile Cys 2555	Val Met Thr Leu 2560	Val 2560	Ser Ala Val Ala Ala 2565	Asn Glu Met
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Gln Arg 2585	Ile Glu Val Lys 2590	Glu 2590	Asn Phe Ser Met Gly 2595	Glu Phe Leu
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Thr Ala 2615	Val Leu Thr Pro 2620	Leu 2620	Leu Lys His Leu Ile 2625	Thr Ser Asp
Tyr Ile 2630	Asn Thr Ser Leu 2635	Thr 2635	Ser Ile Asn Val Gln 2640	Ala Ser Ala
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<210> SEQ ID NO 14

<211> LENGTH: 3423

<212> TYPE: PRT

<213> ORGANISM: Zika virus strain R103451

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<400> SEQUENCE: 14

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 Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
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 Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45
 Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60
 Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80
 Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95
 Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110
 Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125
 Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140
 Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160
 Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175
 Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190
 Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205
 Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220
 Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240
 Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255
 Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270
 Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
 275 280 285
 Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
 290 295 300
 Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
 305 310 315 320
 Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
 325 330 335
 Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
 340 345 350
 Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
 355 360 365
 Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380
 Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400
 Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
 405 410 415

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Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
 450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
 675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
 690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
 705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
 725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
 740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
 755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
 770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
 785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
 805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
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1235	1240	1245
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Ile Ser Ala Leu Glu Gly 1265	Asp Leu Met Val Leu 1270	Ile Asn Gly Phe 1275
Ala Leu Ala Trp Leu Ala 1280	Ile Arg Ala Met Val 1285	Val Pro Arg Thr 1290
Asp Asn Ile Thr Leu Ala 1295	Ile Leu Ala Ala Leu 1300	Thr Pro Leu Ala 1305
Arg Gly Thr Leu Leu Val 1310	Ala Trp Arg Ala Gly 1315	Leu Ala Thr Cys 1320
Gly Gly Phe Met Leu Leu 1325	Ser Leu Lys Gly Lys 1330	Gly Ser Val Lys 1335
Lys Asn Leu Pro Phe Val 1340	Met Ala Leu Gly Leu 1345	Thr Ala Val Arg 1350
Leu Val Asp Pro Ile Asn 1355	Val Val Gly Leu Leu 1360	Leu Leu Thr Arg 1365
Ser Gly Lys Arg Ser Trp 1370	Pro Pro Ser Glu Val 1375	Leu Thr Ala Val 1380
Gly Leu Ile Cys Ala Leu 1385	Ala Gly Gly Phe Ala 1390	Lys Ala Asp Ile 1395
Glu Met Ala Gly Pro Met 1400	Ala Ala Val Gly Leu 1405	Leu Ile Val Ser 1410
Tyr Val Val Ser Gly Lys 1415	Ser Val Asp Met Tyr 1420	Ile Glu Arg Ala 1425
Gly Asp Ile Thr Trp Glu 1430	Lys Asp Ala Glu Val 1435	Thr Gly Asn Ser 1440
Pro Arg Leu Asp Val Ala 1445	Leu Asp Glu Ser Gly 1450	Asp Phe Ser Leu 1455
Val Glu Asp Asp Gly Pro 1460	Pro Met Arg Glu Ile 1465	Ile Leu Lys Val 1470
Val Leu Met Thr Ile Cys 1475	Gly Met Asn Pro Ile 1480	Ala Ile Pro Phe 1485
Ala Ala Gly Ala Trp Tyr 1490	Val Tyr Val Lys Thr 1495	Gly Lys Arg Ser 1500
Gly Ala Leu Trp Asp Val 1505	Pro Ala Pro Lys Glu 1510	Val Lys Lys Gly 1515
Glu Thr Thr Asp Gly Val 1520	Tyr Arg Val Met Thr 1525	Arg Arg Leu Leu 1530
Gly Ser Thr Gln Val Gly 1535	Val Gly Val Met Gln 1540	Glu Gly Val Phe 1545
His Thr Met Trp His Val 1550	Thr Lys Gly Ser Ala 1555	Leu Arg Ser Gly 1560
Glu Gly Arg Leu Asp Pro 1565	Tyr Trp Gly Asp Val 1570	Lys Gln Asp Leu 1575
Val Ser Tyr Cys Gly Pro 1580	Trp Lys Leu Asp Ala 1585	Ala Trp Asp Gly 1590
His Ser Glu Val Gln Leu 1595	Leu Ala Val Pro Pro 1600	Gly Glu Arg Ala 1605
Arg Asn Ile Gln Thr Leu 1610	Pro Gly Ile Phe Lys 1615	Thr Lys Asp Gly 1620
Asp Ile Gly Ala Val Ala 1625	Leu Asp Tyr Pro Ala 1630	Gly Thr Ser Gly 1635

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Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			

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Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Leu	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro

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2420	2425	2430
Gln Val Glu Lys Lys Met Gly 2435	Gln Val Leu Leu Ile Ala Val Ala 2440	Ala Val Ala 2445
Val Ser Ser Ala Ile Leu Ser 2450	Arg Thr Ala Trp Gly 2455	Trp Gly Glu 2460
Ala Gly Ala Leu Ile Thr 2465	Ala Thr Ser Thr Leu 2470	Trp Gly Glu 2475
Ser Pro Asn Lys Tyr Trp 2480	Asn Ser Ser Thr Ala Thr 2485	Ser Leu Cys 2490
Asn Ile Phe Arg Gly Ser 2495	Tyr Leu Ala Gly Ala Ser 2500	Leu Ile Tyr 2505
Thr Val Thr Arg Asn Ala 2510	Gly Leu Val Lys Arg Arg 2515	Gly Gly Gly 2520
Thr Gly Glu Thr Leu Gly 2525	Glu Lys Trp Lys Ala Arg 2530	Leu Asn Gln 2535
Met Ser Ala Leu Glu Phe 2540	Tyr Ser Tyr Lys Lys Ser 2545	Gly Ile Thr 2550
Glu Val Cys Arg Glu Glu 2555	Ala Arg Arg Ala Leu Lys 2560	Asp Gly Val 2565
Ala Thr Gly Gly His Ala 2570	Val Ser Arg Gly Ser Ala 2575	Lys Leu Arg 2580
Trp Leu Val Glu Arg Gly 2585	Tyr Leu Gln Pro Tyr Gly 2590	Lys Val Ile 2595
Asp Leu Gly Cys Gly Arg 2600	Gly Gly Trp Ser Tyr Tyr 2605	Ala Ala Thr 2610
Ile Arg Lys Val Gln Glu 2615	Val Lys Gly Tyr Thr Lys 2620	Gly Gly Pro 2625
Gly His Glu Glu Pro Val 2630	Leu Val Gln Ser Tyr Gly 2635	Trp Asn Ile 2640
Val Arg Leu Lys Ser Gly 2645	Val Asp Val Phe His Met 2650	Ala Ala Glu 2655
Pro Cys Asp Thr Leu Leu 2660	Cys Asp Ile Gly Glu Ser 2665	Ser Ser Ser 2670
Pro Glu Val Glu Glu Ala 2675	Arg Thr Leu Arg Val Leu 2680	Ser Met Val 2685
Gly Asp Trp Leu Glu Lys 2690	Arg Pro Gly Ala Phe Cys 2695	Ile Lys Val 2700
Leu Cys Pro Tyr Thr Ser 2705	Thr Met Met Glu Thr Leu 2710	Glu Arg Leu 2715
Gln Arg Arg Tyr Gly Gly 2720	Gly Leu Val Arg Val Pro 2725	Leu Ser Arg 2730
Asn Ser Thr His Glu Met 2735	Tyr Trp Val Ser Gly Ala 2740	Lys Ser Asn 2745
Thr Ile Lys Ser Val Ser 2750	Thr Thr Ser Gln Leu Leu 2755	Leu Gly Arg 2760
Met Asp Gly Pro Arg Arg 2765	Pro Val Lys Tyr Glu Glu 2770	Asp Val Asn 2775
Leu Gly Ser Gly Thr Arg 2780	Ala Val Val Ser Cys Ala 2785	Glu Ala Pro 2790
Asn Met Lys Ile Ile Gly 2795	Asn Arg Ile Glu Arg Ile 2800	Arg Ser Glu 2805
His Ala Glu Thr Trp Phe 2810	Phe Asp Glu Asn His Pro 2815	Tyr Arg Thr 2820

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Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Cys	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			

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Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
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Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
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Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
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Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
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Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
 675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
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Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp

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Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His 725 730 735			
Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp 740 745 750			
Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn 755 760 765			
Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val 770 775 780			
Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val 785 790 795 800			
Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr 805 810 815			
Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser 820 825 830			
Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile 835 840 845			
Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser 850 855 860			
Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu 865 870 875 880			
Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln 885 890 895			
Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp 900 905 910			
Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val 915 920 925			
Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp 930 935 940			
Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser 945 950 955 960			
Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala 965 970 975			
Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu 980 985 990			
Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg 995 1000 1005			
Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His 1010 1015 1020			
Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro 1025 1030 1035			
Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly 1040 1045 1050			
Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu 1055 1060 1065			
Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu 1070 1075 1080			
Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser 1085 1090 1095			
Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro 1100 1105 1110			
Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu 1115 1120 1125			

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Val Thr	Ala Gly	Ser Thr	Asp	His Met	Asp His	Phe	Ser Leu	Gly		
1145			1150			1155				
Val Leu	Val Ile	Leu Leu	Met	Val Gln	Glu Gly	Leu	Lys Lys	Arg		
1160			1165			1170				
Met Thr	Thr Lys	Ile Ile	Ile	Ser Thr	Ser Met	Ala	Val Leu	Val		
1175			1180			1185				
Ala Met	Ile Leu	Gly Gly	Phe	Ser Met	Ser Asp	Leu	Ala Lys	Leu		
1190			1195			1200				
Ala Ile	Leu Met	Gly Ala	Thr	Phe Ala	Glu Met	Asn	Thr Gly	Gly		
1205			1210			1215				
Asp Val	Ala His	Leu Ala	Leu	Ile Ala	Ala Phe	Lys	Val Arg	Pro		
1220			1225			1230				
Ala Leu	Leu Val	Ser Phe	Ile	Phe Arg	Ala Asn	Trp	Thr Pro	Arg		
1235			1240			1245				
Glu Ser	Met Leu	Leu Ala	Leu	Ala Ser	Cys Leu	Leu	Gln Thr	Ala		
1250			1255			1260				
Ile Ser	Ala Leu	Glu Gly	Asp	Leu Met	Val Leu	Ile	Asn Gly	Phe		
1265			1270			1275				
Ala Leu	Ala Trp	Leu Ala	Ile	Arg Ala	Met Val	Val	Pro Arg	Thr		
1280			1285			1290				
Asp Asn	Ile Thr	Leu Ala	Ile	Leu Ala	Ala Leu	Thr	Pro Leu	Ala		
1295			1300			1305				
Arg Gly	Thr Leu	Leu Val	Ala	Trp Arg	Ala Gly	Leu	Ala Thr	Cys		
1310			1315			1320				
Gly Gly	Phe Met	Leu Leu	Ser	Leu Lys	Gly Lys	Gly	Ser Val	Lys		
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Lys Asn	Leu Pro	Phe Val	Met	Ala Leu	Gly Leu	Thr	Ala Val	Arg		
1340			1345			1350				
Leu Val	Asp Pro	Ile Asn	Val	Val Gly	Leu Leu	Leu	Leu Thr	Arg		
1355			1360			1365				
Ser Gly	Lys Arg	Ser Trp	Pro	Pro Ser	Glu Val	Leu	Thr Ala	Val		
1370			1375			1380				
Gly Leu	Ile Cys	Ala Leu	Ala	Gly Gly	Phe Ala	Lys	Ala Asp	Ile		
1385			1390			1395				
Glu Met	Ala Gly	Pro Met	Ala	Ala Val	Gly Leu	Leu	Ile Val	Ser		
1400			1405			1410				
Tyr Val	Val Ser	Gly Lys	Ser	Val Asp	Met Tyr	Ile	Glu Arg	Ala		
1415			1420			1425				
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1430			1435			1440				
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1460			1465			1470				
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1475			1480			1485				
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His Thr 1550	Met Trp His Val 1555	Thr 1555	Lys Gly Ser Ala Leu 1560	Arg Ser Gly
Glu Gly 1565	Arg Leu Asp Pro 1570	Tyr 1570	Trp Gly Asp Val Lys 1575	Gln Asp Leu
Val Ser 1580	Tyr Cys Gly Pro 1585	Trp 1585	Lys Leu Asp Ala Ala 1590	Trp Asp Gly
His Ser 1595	Glu Val Gln Leu 1600	Leu 1600	Ala Val Pro Pro Gly 1605	Glu Arg Ala
Arg Asn 1610	Ile Gln Thr Leu 1615	Pro 1615	Gly Ile Phe Lys Thr 1620	Lys Asp Gly
Asp Ile 1625	Gly Ala Val Ala 1630	Leu 1630	Asp Tyr Pro Ala Gly 1635	Thr Ser Gly
Ser Pro 1640	Ile Leu Asp Lys 1645	Cys 1645	Gly Arg Val Ile Gly 1650	Leu Tyr Gly
Asn Gly 1655	Val Val Ile Lys 1660	Asn 1660	Gly Ser Tyr Val Ser 1665	Ala Ile Thr
Gln Gly 1670	Arg Arg Glu Glu 1675	Glu 1675	Thr Pro Val Glu Cys 1680	Phe Glu Pro
Ser Met 1685	Leu Lys Lys Lys 1690	Gln 1690	Leu Thr Val Leu Asp 1695	Leu His Pro
Gly Ala 1700	Gly Lys Thr Arg 1705	Arg 1705	Val Leu Pro Glu Ile 1710	Val Arg Glu
Ala Ile 1715	Lys Thr Arg Leu 1720	Arg 1720	Thr Val Ile Leu Ala 1725	Pro Thr Arg
Val Val 1730	Ala Ala Glu Met 1735	Glu 1735	Glu Ala Leu Arg Gly 1740	Leu Pro Val
Arg Tyr 1745	Met Thr Thr Ala 1750	Val 1750	Asn Val Thr His Ser 1755	Gly Thr Glu
Ile Val 1760	Asp Leu Met Cys 1765	His 1765	Ala Thr Phe Thr Ser 1770	Arg Leu Leu
Gln Pro 1775	Ile Arg Val Pro 1780	Asn 1780	Tyr Asn Leu Tyr Ile 1785	Met Asp Glu
Ala His 1790	Phe Thr Asp Pro 1795	Ser 1795	Ser Ile Ala Ala Arg 1800	Gly Tyr Ile
Ser Thr 1805	Arg Val Glu Met 1810	Gly 1810	Glu Ala Ala Ala Ile 1815	Phe Met Thr
Ala Thr 1820	Pro Pro Gly Thr 1825	Arg 1825	Asp Ala Phe Pro Asp 1830	Ser Asn Ser
Pro Ile 1835	Met Asp Thr Glu 1840	Val 1840	Glu Val Pro Glu Arg 1845	Ala Trp Ser
Ser Gly 1850	Phe Asp Trp Val 1855	Thr 1855	Asp His Ser Gly Lys 1860	Thr Val Trp
Phe Val 1865	Pro Ser Val Arg 1870	Asn 1870	Gly Asn Glu Ile Ala 1875	Ala Cys Leu
Thr Lys 1880	Ala Gly Lys Arg 1885	Val 1885	Ile Gln Leu Ser Arg 1890	Lys Thr Phe
Glu Thr 1895	Glu Phe Gln Lys 1900	Thr 1900	Lys His Gln Glu Trp 1905	Asp Phe Val
Val Thr	Thr Asp Ile Ser 1905	Glu	Met Gly Ala Asn Phe 1910	Lys Ala Asp

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2330						2335					2340			
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Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
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Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
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Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
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Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
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Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
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Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
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Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
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2600						2605					2610			
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2615						2620					2625			
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2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			

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Leu Cys 2705	Pro Tyr Thr Ser Thr	Met Met Glu Thr Leu	Glu Arg Leu	2710	2715
Gln Arg 2720	Arg Tyr Gly Gly Gly	Leu Val Arg Val Pro	Leu Ser Arg	2725	2730
Asn Ser 2735	Thr His Glu Met Tyr	Trp Val Ser Gly Ala	Lys Ser Asn	2740	2745
Thr Ile 2750	Lys Ser Val Ser Thr	Thr Ser Gln Leu Leu	Leu Gly Arg	2755	2760
Met Asp 2765	Gly Pro Arg Arg Pro	Val Lys Tyr Glu Glu	Asp Val Asn	2770	2775
Leu Gly 2780	Ser Gly Thr Arg Ala	Val Val Ser Cys Ala	Glu Ala Pro	2785	2790
Asn Met 2795	Lys Ile Ile Gly Asn	Arg Ile Glu Arg Ile	Arg Ser Glu	2800	2805
His Ala 2810	Glu Thr Trp Phe Phe	Asp Glu Asn His Pro	Tyr Arg Thr	2815	2820
Trp Ala 2825	Tyr His Gly Ser Tyr	Glu Ala Pro Thr Gln	Gly Ser Ala	2830	2835
Ser Ser 2840	Leu Ile Asn Gly Val	Val Arg Leu Leu Ser	Lys Pro Trp	2845	2850
Asp Val 2855	Val Thr Gly Val Thr	Gly Ile Ala Met Thr	Asp Thr Thr	2860	2865
Pro Tyr 2870	Gly Gln Gln Arg Val	Phe Lys Glu Lys Val	Asp Thr Arg	2875	2880
Val Pro 2885	Asp Pro Gln Glu Gly	Thr Arg Gln Val Met	Ser Met Val	2890	2895
Ser Ser 2900	Trp Leu Trp Lys Glu	Leu Gly Lys His Lys	Arg Pro Arg	2905	2910
Val Cys 2915	Thr Lys Glu Glu Phe	Ile Asn Lys Val Arg	Ser Asn Ala	2920	2925
Ala Leu 2930	Gly Ala Ile Phe Glu	Glu Glu Lys Glu Trp	Lys Thr Ala	2935	2940
Val Glu 2945	Ala Val Asn Asp Pro	Arg Phe Trp Ala Leu	Val Asp Lys	2950	2955
Glu Arg 2960	Glu His His Leu Arg	Gly Glu Cys Gln Ser	Cys Val Tyr	2965	2970
Asn Met 2975	Met Gly Lys Arg Glu	Lys Lys Gln Gly Glu	Phe Gly Lys	2980	2985
Ala Lys 2990	Gly Ser Arg Ala Ile	Trp Tyr Met Trp Leu	Gly Ala Arg	2995	3000
Phe Leu 3005	Glu Phe Glu Ala Leu	Gly Phe Leu Asn Glu	Asp His Trp	3010	3015
Met Gly 3020	Arg Glu Asn Ser Gly	Gly Gly Val Glu Gly	Leu Gly Leu	3025	3030
Gln Arg 3035	Leu Gly Tyr Val Leu	Glu Glu Met Ser Arg	Ile Pro Gly	3040	3045
Gly Arg 3050	Met Tyr Ala Asp Asp	Thr Ala Gly Trp Asp	Thr Arg Ile	3055	3060
Ser Arg 3065	Phe Asp Leu Glu Asn	Glu Ala Leu Ile Thr	Asn Gln Met	3070	3075
Glu Lys 3080	Gly His Arg Ala Leu	Ala Leu Ala Ile Ile	Lys Tyr Thr	3085	3090
Tyr Gln	Asn Lys Val Val Lys	Val Leu Arg Pro Ala	Glu Lys Gly		

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Gly Gln Val Val Thr Tyr Ala Leu Asn Thr Phe Thr Asn Leu Val 3125 3130 3135		
Val Gln Leu Ile Arg Asn Met Glu Ala Glu Glu Val Leu Glu Met 3140 3145 3150		
Gln Asp Leu Trp Leu Leu Arg Arg Ser Glu Lys Val Thr Asn Trp 3155 3160 3165		
Leu Gln Ser Asn Gly Trp Asp Arg Leu Lys Arg Met Ala Val Ser 3170 3175 3180		
Gly Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala His 3185 3190 3195		
Ala Leu Arg Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Thr 3200 3205 3210		
Gln Glu Trp Lys Pro Ser Thr Gly Trp Asp Asn Trp Glu Glu Val 3215 3220 3225		
Pro Phe Cys Ser His His Phe Asn Lys Leu His Leu Lys Asp Gly 3230 3235 3240		
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly 3245 3250 3255		
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Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser 3290 3295 3300		
Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser 3305 3310 3315		
Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val 3320 3325 3330		
Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp 3335 3340 3345		
Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys 3350 3355 3360		
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<210> SEQ ID NO 18

<211> LENGTH: 3433

<212> TYPE: PRT

<213> ORGANISM: West Nile virus

<400> SEQUENCE: 18

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Ala Met Leu Ser Leu Ile Asp Gly Lys Gly Pro Ile Arg Phe Val Leu
          35           40           45
Ala Leu Leu Ala Phe Phe Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala
          50           55           60
Val Leu Asp Arg Trp Arg Gly Val Asn Lys Gln Thr Ala Met Lys His
65           70           75           80
Leu Leu Ser Phe Lys Lys Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn
          85           90           95
Arg Arg Ser Ser Lys Gln Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala
          100          105          110
Val Met Ile Gly Leu Ile Ala Ser Val Gly Ala Val Thr Leu Ser Asn
          115          120          125
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp

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Ala	Met	Asp	Val	Gly	Tyr	Met	Cys	Asp	Asp	Thr	Ile	Thr	Tyr	Glu	Cys
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Pro	Val	Leu	Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys
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Tyr	Ala	Leu	Val	Ala	Ala	Val	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Thr
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Met	Gln	Arg	Val	Val	Phe	Val	Val	Leu	Leu	Leu	Leu	Val	Ala	Pro	Ala
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Val	Thr	Ile	Met	Ser	Lys	Asp	Lys	Pro	Thr	Ile	Asp	Val	Lys	Met	Met
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Val	Gly	Ala	Thr	Gln	Ala	Gly	Arg	Phe	Ser	Ile	Thr	Pro	Ala	Ala	Pro
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Ser	Tyr	Thr	Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys
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Glu	Pro	Arg	Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val
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Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly
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Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr
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Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr
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Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser
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Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His
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Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly
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Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
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Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe
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Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln
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Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp
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Leu Ser Val Asn Val His Ala Asp Thr Gly Cys Ala Ile Asp Ile Ser
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Arg Gln Glu Leu Arg Cys Gly Ser Gly Val Phe Ile His Asn Asp Val
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Glu Ala Trp Met Asp Arg Tyr Lys Tyr Tyr Pro Glu Thr Pro Gln Gly
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Gly Ser Ser Glu Arg Val 1445	Asp Val Arg Leu Asp 1450	Asp Asp Gly Asn 1455
Phe Gln Leu Met Asn Asp 1460	Pro Gly Ala Pro Trp 1465	Lys Ile Trp Met 1470
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Glu Asp Arg Leu Cys Tyr 1580	Gly Gly Pro Trp Lys 1585	Leu Gln His Lys 1590
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Pro Glu Gly Glu Ile Gly 1625	Ala Val Thr Leu Asp 1630	Phe Pro Thr Gly 1635
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Phe Glu Pro Glu Met Leu 1685	Arg Lys Lys Gln Ile 1690	Thr Val Leu Asp 1695
Leu His Pro Gly Ala Gly 1700	Lys Thr Arg Arg Ile 1705	Leu Pro Gln Ile 1710
Ile Lys Glu Ala Ile Asn 1715	Arg Arg Leu Arg Thr 1720	Ala Val Leu Ala 1725
Pro Thr Arg Val Val Ala 1730	Ala Glu Met Ala Glu 1735	Ala Leu Arg Gly 1740
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Ala Trp 2315	Ser Leu Tyr Ala Val 2320	Thr Thr Ala Val Leu 2325	Thr Pro Leu
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<211> LENGTH: 3725

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 20

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35          40          45
Met Lys Tyr Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile
50          55          60
Thr Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn
65          70          75          80
Leu Cys Val Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu
85          90          95
Ser Ala Ala Phe Met Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln
100         105         110
Asp Ile Ala Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp
115        120        125
Asp Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala
130        135        140
Asp Ile Thr Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys
145        150        155        160
Phe Tyr Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met
165        170        175
Thr Asp Asn Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys
180        185        190
Gln Gly Ile Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp
195        200        205

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 Val Pro Arg Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr
 225 230 235 240
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 245 250 255
 His Ala Ile Ala Ser Gly Ser Ala Leu Pro Gly Ser Gly Ala Thr Asn
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 Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
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 Met Ser Lys Lys Pro Gly Gly Pro Gly Lys Ser Arg Ala Val Asn Met
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 Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
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 610 615 620

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Glu	Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	645	650	655	
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Arg	Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	675	680	685	
Lys	Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	690	695	700	
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Pro	Leu	Pro	Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	805	810	815	
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Phe	Gly	Asp	Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Glu	Lys	Lys	Ile	Thr	965	970	975	
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Gly Ser 1100	Gly Val Phe Ile His 1105	Asn Asp Val Glu Ala Trp Met Asp 1110
Arg Tyr 1115	Lys Tyr Tyr Pro Glu 1120	Thr Pro Gln Gly Leu Ala Lys Ile 1125
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Ala Thr 1190	Thr Glu Lys Leu Glu 1195	Ile Gly Trp Lys Ala Trp Gly Lys 1200
Ser Ile 1205	Leu Phe Ala Pro Glu 1210	Leu Ala Asn Asn Thr Phe Val Val 1215
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Asn Ser 1235	Leu Glu Val Glu Asp 1240	Phe Gly Phe Gly Leu Thr Ser Thr 1245
Arg Met 1250	Phe Leu Lys Val Arg 1255	Glu Ser Asn Thr Thr Glu Cys Asp 1260
Ser Lys 1265	Ile Ile Gly Thr Ala 1270	Val Lys Asn Asn Leu Ala Ile His 1275
Ser Asp 1280	Leu Ser Tyr Trp Ile 1285	Glu Ser Arg Leu Asn Asp Thr Trp 1290
Lys Leu 1295	Glu Arg Ala Val Leu 1300	Gly Glu Val Lys Ser Cys Thr Trp 1305
Pro Glu 1310	Thr His Thr Leu Trp 1315	Gly Asp Gly Ile Leu Glu Ser Asp 1320
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Thr Thr 1385	Glu Ser Gly Lys Leu 1390	Ile Thr Asp Trp Cys Cys Arg Ser 1395
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1505						1510					1515			
Lys	Ile	Gln	Pro	Val	Phe	Met	Val	Ala	Ser	Phe	Leu	Lys	Ala	Arg
1520						1525					1530			
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1535						1540					1545			
Phe	Gln	Met	Ala	Tyr	Tyr	Asp	Ala	Arg	Gln	Ile	Leu	Leu	Trp	Glu
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1580						1585					1590			
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1610						1615					1620			
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1760						1765					1770			
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Lys 1910	Pro	Gly	Val	Phe	Lys	Thr 1915	Pro	Glu	Gly	Glu	Ile 1920	Gly	Ala	Val
Thr 1925	Leu	Asp	Phe	Pro	Thr	Gly 1930	Thr	Ser	Gly	Ser	Pro 1935	Ile	Val	Asp
Lys 1940	Asn	Gly	Asp	Val	Ile	Gly 1945	Leu	Tyr	Gly	Asn	Gly 1950	Val	Ile	Met
Pro 1955	Asn	Gly	Ser	Tyr	Ile	Ser 1960	Ala	Ile	Val	Gln	Gly 1965	Glu	Arg	Met
Asp 1970	Glu	Pro	Ile	Pro	Ala	Gly 1975	Phe	Glu	Pro	Glu	Met 1980	Leu	Arg	Lys
Lys 1985	Gln	Ile	Thr	Val	Leu	Asp 1990	Leu	His	Pro	Gly	Ala 1995	Gly	Lys	Thr
Arg 2000	Arg	Ile	Leu	Pro	Gln	Ile 2005	Ile	Lys	Glu	Ala	Ile 2010	Asn	Arg	Arg
Leu 2015	Arg	Thr	Ala	Val	Leu	Ala 2020	Pro	Thr	Arg	Val	Val 2025	Ala	Ala	Glu
Met 2030	Ala	Glu	Ala	Leu	Arg	Gly 2035	Leu	Pro	Ile	Arg	Tyr 2040	Gln	Thr	Ser
Ala 2045	Val	Pro	Arg	Glu	His	Asn 2050	Gly	Asn	Glu	Ile	Val 2055	Asp	Val	Met
Cys 2060	His	Ala	Thr	Leu	Thr	His 2065	Arg	Leu	Met	Ser	Pro 2070	His	Arg	Val
Pro 2075	Asn	Tyr	Asn	Leu	Phe	Val 2080	Met	Asp	Glu	Ala	His 2085	Phe	Thr	Asp
Pro 2090	Ala	Ser	Ile	Ala	Ala	Arg 2095	Gly	Tyr	Ile	Ser	Thr 2100	Lys	Val	Glu
Leu 2105	Gly	Glu	Ala	Ala	Ala	Ile 2110	Phe	Met	Thr	Ala	Thr 2115	Pro	Pro	Gly
Thr 2120	Ser	Asp	Pro	Phe	Pro	Glu 2125	Ser	Asn	Ser	Pro	Ile 2130	Ser	Asp	Leu
Gln 2135	Thr	Glu	Ile	Pro	Asp	Arg 2140	Ala	Trp	Asn	Ser	Gly 2145	Tyr	Glu	Trp
Ile 2150	Thr	Glu	Tyr	Thr	Gly	Lys 2155	Thr	Val	Trp	Phe	Val 2160	Pro	Ser	Val
Lys 2165	Met	Gly	Asn	Glu	Ile	Ala 2170	Leu	Cys	Leu	Gln	Arg 2175	Ala	Gly	Lys
Lys 2180	Val	Val	Gln	Leu	Asn	Arg 2185	Lys	Ser	Tyr	Glu	Thr 2190	Glu	Tyr	Pro
Lys 2195	Cys	Lys	Asn	Asp	Asp	Trp 2200	Asp	Phe	Val	Ile	Thr 2205	Thr	Asp	Ile
Ser 2210	Glu	Met	Gly	Ala	Asn	Phe 2215	Lys	Ala	Ser	Arg	Val 2220	Ile	Asp	Ser
Arg 2225	Lys	Ser	Val	Lys	Pro	Thr 2230	Ile	Ile	Thr	Glu	Gly 2235	Glu	Gly	Arg

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Tyr 2630	Ile	Asn	Thr	Ser	Leu	Thr 2635	Ser	Ile	Asn	Val	Gln 2640	Ala	Ser	Ala
Leu 2645	Phe	Thr	Leu	Ala	Arg	Gly 2650	Phe	Pro	Phe	Val	Asp 2655	Val	Gly	Val
Ser 2660	Ala	Leu	Leu	Leu	Ala	Ala 2665	Gly	Cys	Trp	Gly	Gln 2670	Val	Thr	Leu
Thr 2675	Val	Thr	Val	Thr	Ala	Ala 2680	Thr	Leu	Leu	Phe	Cys 2685	His	Tyr	Ala
Tyr 2690	Met	Val	Pro	Gly	Trp	Gln 2695	Ala	Glu	Ala	Met	Arg 2700	Ser	Ala	Gln
Arg 2705	Arg	Thr	Ala	Ala	Gly	Ile 2710	Met	Lys	Asn	Ala	Val 2715	Val	Asp	Gly
Ile 2720	Val	Ala	Thr	Asp	Val	Pro 2725	Glu	Leu	Glu	Arg	Thr 2730	Thr	Pro	Ile
Met 2735	Gln	Lys	Lys	Val	Gly	Gln 2740	Ile	Met	Leu	Ile	Leu 2745	Val	Ser	Leu
Ala 2750	Ala	Val	Val	Val	Asn	Pro 2755	Ser	Val	Lys	Thr	Val 2760	Arg	Glu	Ala
Gly 2765	Ile	Leu	Ile	Thr	Ala	Ala 2770	Ala	Val	Thr	Leu	Trp 2775	Glu	Asn	Gly
Ala 2780	Ser	Ser	Val	Trp	Asn	Ala 2785	Thr	Thr	Ala	Ile	Gly 2790	Leu	Cys	His
Ile 2795	Met	Arg	Gly	Gly	Trp	Leu 2800	Ser	Cys	Leu	Ser	Ile 2805	Thr	Trp	Thr
Leu 2810	Ile	Lys	Asn	Met	Glu	Lys 2815	Pro	Gly	Leu	Lys	Arg 2820	Gly	Gly	Ala
Lys 2825	Gly	Arg	Thr	Leu	Gly	Glu 2830	Val	Trp	Lys	Glu	Arg 2835	Leu	Asn	Gln
Met 2840	Thr	Lys	Glu	Glu	Phe	Thr 2845	Arg	Tyr	Arg	Lys	Glu 2850	Ala	Ile	Ile
Glu 2855	Val	Asp	Arg	Ser	Ala	Ala 2860	Lys	His	Ala	Arg	Lys 2865	Glu	Gly	Asn
Val 2870	Thr	Gly	Gly	His	Pro	Val 2875	Ser	Arg	Gly	Thr	Ala 2880	Lys	Leu	Arg
Trp 2885	Leu	Val	Glu	Arg	Arg	Phe 2890	Leu	Glu	Pro	Val	Gly 2895	Lys	Val	Ile
Asp 2900	Leu	Gly	Cys	Gly	Arg	Gly 2905	Gly	Trp	Cys	Tyr	Tyr 2910	Met	Ala	Thr
Gln 2915	Lys	Arg	Val	Gln	Glu	Val 2920	Arg	Gly	Tyr	Thr	Lys 2925	Gly	Gly	Pro
Gly 2930	His	Glu	Glu	Pro	Gln	Leu 2935	Val	Gln	Ser	Tyr	Gly 2940	Trp	Asn	Ile
Val 2945	Thr	Met	Lys	Ser	Gly	Val 2950	Asp	Val	Phe	Tyr	Arg 2955	Pro	Ser	Glu
Cys 2960	Cys	Asp	Thr	Leu	Leu	Cys 2965	Asp	Ile	Gly	Glu	Ser 2970	Ser	Ser	Ser
Ala 2975	Glu	Val	Glu	Glu	His	Arg 2980	Thr	Ile	Arg	Val	Leu 2985	Glu	Met	Val
Glu 2990	Asp	Trp	Leu	His	Arg	Gly 2995	Pro	Arg	Glu	Phe	Cys 3000	Val	Lys	Val
Leu 3005	Cys	Pro	Tyr	Met	Pro	Lys 3010	Val	Ile	Glu	Lys	Met 3015	Glu	Leu	Leu

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Gln Arg	Arg Tyr Gly Gly	Gly	Leu Val Arg Asn Pro	Leu Ser Arg
3020		3025	3030	
Asn Ser	Thr His Glu Met	Tyr	Trp Val Ser Arg Ala	Ser Gly Asn
3035		3040	3045	
Val Val	His Ser Val Asn	Met	Thr Ser Gln Val Leu	Leu Gly Arg
3050		3055	3060	
Met Glu	Lys Arg Thr Trp	Lys	Gly Pro Gln Tyr Glu	Glu Asp Val
3065		3070	3075	
Asn Leu	Gly Ser Gly Thr	Arg	Ala Val Gly Lys Pro	Leu Leu Asn
3080		3085	3090	
Ser Asp	Thr Ser Lys Ile	Lys	Asn Arg Ile Glu Arg	Leu Arg Arg
3095		3100	3105	
Glu Tyr	Ser Ser Thr Trp	His	His Asp Glu Asn His	Pro Tyr Arg
3110		3115	3120	
Thr Trp	Asn Tyr His Gly	Ser	Tyr Asp Val Lys Pro	Thr Gly Ser
3125		3130	3135	
Ala Ser	Ser Leu Val Asn	Gly	Val Val Arg Leu Leu	Ser Lys Pro
3140		3145	3150	
Trp Asp	Thr Ile Thr Asn	Val	Thr Thr Met Ala Met	Thr Asp Thr
3155		3160	3165	
Thr Pro	Phe Gly Gln Gln	Arg	Val Phe Lys Glu Lys	Val Asp Thr
3170		3175	3180	
Lys Ala	Pro Glu Pro Pro	Glu	Gly Val Lys Tyr Val	Leu Asn Glu
3185		3190	3195	
Thr Thr	Asn Trp Leu Trp	Ala	Phe Leu Ala Arg Glu	Lys Arg Pro
3200		3205	3210	
Arg Met	Cys Ser Arg Glu	Glu	Phe Ile Arg Lys Val	Asn Ser Asn
3215		3220	3225	
Ala Ala	Leu Gly Ala Met	Phe	Glu Glu Gln Asn Gln	Trp Arg Ser
3230		3235	3240	
Ala Arg	Glu Ala Val Glu	Asp	Pro Lys Phe Trp Glu	Met Val Asp
3245		3250	3255	
Glu Glu	Arg Glu Ala His	Leu	Arg Gly Glu Cys His	Thr Cys Ile
3260		3265	3270	
Tyr Asn	Met Met Gly Lys	Arg	Glu Lys Lys Pro Gly	Glu Phe Gly
3275		3280	3285	
Lys Ala	Lys Gly Ser Arg	Ala	Ile Trp Phe Met Trp	Leu Gly Ala
3290		3295	3300	
Arg Phe	Leu Glu Phe Glu	Ala	Leu Gly Phe Leu Asn	Glu Asp His
3305		3310	3315	
Trp Leu	Gly Arg Lys Asn	Ser	Gly Gly Gly Val Glu	Gly Leu Gly
3320		3325	3330	
Leu Gln	Lys Leu Gly Tyr	Ile	Leu Arg Glu Val Gly	Thr Arg Pro
3335		3340	3345	
Gly Gly	Lys Ile Tyr Ala	Asp	Asp Thr Ala Gly Trp	Asp Thr Arg
3350		3355	3360	
Ile Thr	Arg Ala Asp Leu	Glu	Asn Glu Ala Lys Val	Leu Glu Leu
3365		3370	3375	
Leu Asp	Gly Glu His Arg	Arg	Leu Ala Arg Ala Ile	Ile Glu Leu
3380		3385	3390	
Thr Tyr	Arg His Lys Val	Val	Lys Val Met Arg Pro	Ala Ala Asp
3395		3400	3405	
Gly Arg	Thr Val Met Asp	Val	Ile Ser Arg Glu Asp	Gln Arg Gly

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3410	3415	3420
Ser Gly Gln Val Val Thr Tyr Ala Leu Asn Thr Phe Thr Asn Leu 3425 3430 3435		
Ala Val Gln Leu Val Arg Met Met Glu Gly Glu Gly Val Ile Gly 3440 3445 3450		
Pro Asp Asp Val Glu Lys Leu Thr Lys Gly Lys Gly Pro Lys Val 3455 3460 3465		
Arg Thr Trp Leu Phe Glu Asn Gly Glu Glu Arg Leu Ser Arg Met 3470 3475 3480		
Ala Val Ser Gly Asp Asp Cys Val Val Lys Pro Leu Asp Asp Arg 3485 3490 3495		
Phe Ala Thr Ser Leu His Phe Leu Asn Ala Met Ser Lys Val Arg 3500 3505 3510		
Lys Asp Ile Gln Glu Trp Lys Pro Ser Thr Gly Trp Tyr Asp Trp 3515 3520 3525		
Gln Gln Val Pro Phe Cys Ser Asn His Phe Thr Glu Leu Ile Met 3530 3535 3540		
Lys Asp Gly Arg Thr Leu Val Val Pro Cys Arg Gly Gln Asp Glu 3545 3550 3555		
Leu Val Gly Arg Ala Arg Ile Ser Pro Gly Ala Gly Trp Asn Val 3560 3565 3570		
Arg Asp Thr Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Leu 3575 3580 3585		
Leu Leu Tyr Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala 3590 3595 3600		
Ile Cys Ser Ala Val Pro Val Asn Trp Val Pro Thr Gly Arg Thr 3605 3610 3615		
Thr Trp Ser Ile His Ala Gly Gly Glu Trp Met Thr Thr Glu Asp 3620 3625 3630		
Met Leu Glu Val Trp Asn Arg Val Trp Ile Glu Glu Asn Glu Trp 3635 3640 3645		
Met Glu Asp Lys Thr Pro Val Glu Lys Trp Ser Asp Val Pro Tyr 3650 3655 3660		
Ser Gly Lys Arg Glu Asp Ile Trp Cys Gly Ser Leu Ile Gly Thr 3665 3670 3675		
Arg Ala Arg Ala Thr Trp Ala Glu Asn Ile Gln Val Ala Ile Asn 3680 3685 3690		
Gln Val Arg Ala Ile Ile Gly Asp Glu Lys Tyr Val Asp Tyr Met 3695 3700 3705		
Ser Ser Leu Lys Arg Tyr Glu Asp Thr Thr Leu Val Glu Asp Thr 3710 3715 3720		
Val Leu 3725		

The invention claimed is:

1. A nucleic acid chimera comprising:

a first nucleic acid molecule comprising a 5' non-coding region, a nucleic acid encoding a capsid (C) protein and non-structural proteins, and a 3' non-coding region, each from a West Nile virus genome, wherein the C protein comprises a portion of a premembrane (prM) signal sequence from the West Nile virus genome and a portion of a prM signal sequence from a Zika virus genome; and

a second nucleic acid molecule operably linked to the first nucleic acid molecule, encoding a prM protein and an envelope (E) protein from the Zika virus genome.

2. The nucleic acid chimera of claim 1, wherein:

(i) the portion of the prM signal sequence from the West Nile virus genome comprises the first 15 amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome comprises the last three amino acids of the Zika virus prM signal sequence;

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- (ii) the portion of the prM signal sequence from the West Nile virus genome comprises the first 13 amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome comprises the last five amino acids of the Zika virus prM signal sequence; or
- (iii) the portion of the prM signal sequence from the West Nile virus genome comprises the first three amino acids of the West Nile virus prM signal sequence and the portion of the prM signal sequence from the Zika virus genome comprises the last 15 amino acids of the Zika virus prM signal sequence.
3. The nucleic acid chimera of claim 2(i), wherein: the first 15 amino acids of the West Nile virus prM signal sequence comprises amino acids 106-120 of SEQ ID NO: 2 or SEQ ID NO: 4; the last three amino acids of the Zika virus prM signal sequence comprises AMA; or the first 15 amino acids of the West Nile virus prM signal sequence comprises amino acids 106-120 of SEQ ID NO: 2 or SEQ ID NO: 4, and the last three amino acids of the Zika virus prM signal sequence comprises AMA.
4. The nucleic acid chimera of claim 2(ii), wherein: the first 13 amino acids of the West Nile virus prM signal sequence comprises amino acids 106-118 of SEQ ID NO: 6; the last five amino acids of the Zika virus prM signal sequence comprises amino acids 119-123 of SEQ ID NO: 6; or the first 13 amino acids of the West Nile virus prM signal sequence comprises amino acids 106-118 of SEQ ID NO: 6 and the last five amino acids of the Zika virus prM signal sequence comprises amino acids 119-123 of SEQ ID NO: 6.
5. The nucleic acid chimera of claim 2(iii), wherein: the first three amino acids of the West Nile virus prM signal sequence comprises amino acids 106-108 of SEQ ID NO: 8; the last 15 amino acids of the Zika virus prM signal sequence comprises amino acids 109-123 of SEQ ID NO: 8; or the first three amino acids of the West Nile virus prM signal sequence comprises amino acids 106-108 of SEQ ID NO: 8 and the last 15 amino acids of the Zika virus prM signal sequence comprises amino acids 109-123 of SEQ ID NO: 8.
6. The nucleic acid chimera of claim 1, wherein the West Nile virus is strain NY99.
7. The nucleic acid chimera of claim 1, wherein the Zika virus is strain SPH2015, PRVABC59 or R103451.
8. The nucleic acid chimera of claim 1, comprising a nucleic acid sequence at least 95% identical to SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7.
9. The nucleic acid chimera of claim 8, comprising the nucleic acid sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7.
10. The nucleic acid chimera of claim 1, wherein the nucleic acid chimera encodes an amino acid sequence at least 95% identical to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8.
11. The nucleic acid chimera of claim 10, wherein the nucleic acid chimera encodes the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 or SEQ ID NO: 8.
12. An immunogenic composition comprising an inactivated virus comprising the nucleic acid chimera of claim 1 and a pharmaceutically acceptable carrier.

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13. The immunogenic composition of claim 12, wherein the inactivated virus is inactivated by one or more of chemical treatment, physical treatment and irradiation.
14. A method of eliciting an immune response against Zika virus in a subject, comprising administering to the subject the immunogenic composition of claim 12.
15. A method, comprising inactivating a virus comprising a nucleic acid chimera of claim 1.
16. The method of claim 15, wherein inactivating the virus comprises treating the virus with a chemical inactivation agent, high pressure, ultraviolet irradiation, gamma irradiation, or any combination thereof.
17. The method of claim 15, further comprising administering the inactivated virus to a subject.
18. The nucleic acid chimera of claim 1, further comprising a reporter gene.
19. The nucleic acid chimera of claim 18, wherein the reporter gene encodes a fluorescent protein or a bioluminescent protein.
20. The nucleic acid chimera of claim 18, wherein the reporter gene is human codon optimized.
21. The nucleic acid chimera of claim 18, comprising a nucleic acid sequence at least 95% identical to SEQ ID NO: 9, SEQ ID NO: 11 or SEQ ID NO: 19.
22. The nucleic acid chimera of claim 21, comprising the nucleic acid sequence of SEQ ID NO: 9, SEQ ID NO: 11 or SEQ ID NO: 19.
23. A chimeric virus, comprising the nucleic acid chimera of claim 18.
24. A method of detecting Zika virus-specific antibodies in a sample, comprising: contacting the sample with the chimeric virus of claim 23 under conditions sufficient to form virus-antibody complexes if Zika virus antibodies are present in the sample; and detecting the virus-antibody complexes, thereby detecting Zika virus-specific antibodies in the sample.
25. A method of detecting Zika virus-specific antibodies in a sample, comprising: contacting the sample with the chimeric virus of claim 23 to form a virus-sample mixture, wherein virus-antibody complexes are formed in the virus-sample mixture if Zika virus-specific antibodies are present in the sample; inoculating a cell culture with the virus-sample mixture under conditions sufficient to allow plaque formation or micro-focus formation in the cell culture; and detecting a decrease in plaque formation or micro-focus formation in the cell culture as compared to a control cell culture, thereby detecting a Zika virus-specific antibody in the sample.
26. A method of detecting Zika virus-specific antibodies in a sample, comprising: providing the chimeric virus of claim 23 bound to a solid support; contacting the chimeric virus-bound solid support with the sample under conditions sufficient to form virus-antibody complexes if Zika virus-specific antibodies are present in the sample; contacting the virus-antibody complexes with a secondary antibody; and detecting binding of the secondary antibody to the virus-antibody complexes, thereby detecting Zika virus-specific antibodies in the sample.
27. A method of detecting Zika virus-specific antibodies in a sample, comprising:

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providing a secondary antibody bound to a solid support; contacting the secondary antibody-bound solid support with the sample under conditions sufficient to allow binding of the secondary antibody to any Zika virus-specific antibodies present in the sample, thereby forming antibody-antibody complexes;

contacting the antibody-antibody complexes with the chimeric virus of claim 23 under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibodies, thereby forming immune complexes; and

detecting the presence of the immune complexes, thereby detecting Zika virus-specific antibodies in the sample.

28. The method of claim 27, wherein detecting the presence of the immune complexes comprises contacting the immune complexes with an antibody that specifically binds the chimeric virus and comprises a detectable label.

29. A method of detecting Zika virus-specific antibodies in a sample, comprising:

providing a Zika virus-specific antibody bound to a solid support;

contacting the antibody-bound solid support with the chimeric virus of claim 23 under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibody to form antibody-virus complexes;

contacting the antibody-virus complexes with the sample to allow binding of any Zika virus-specific antibodies present in the sample to the chimeric virus, thereby forming immune complexes;

contacting the immune complexes with a secondary antibody; and

detecting binding of the secondary antibody to the immune complexes, thereby detecting Zika virus-specific antibodies present in the sample.

30. The method of claim 26, wherein the secondary antibody comprises an anti-IgM antibody or an anti-IgG antibody.

31. The method of claim 24, wherein the sample comprises a biological fluid sample.

32. The method of claim 31, wherein the biological fluid sample comprises serum, blood or plasma.

33. A chimeric virus, comprising the nucleic acid chimera of claim 1.

34. A method of detecting Zika virus-specific antibodies in a sample, comprising:

contacting the sample with the chimeric virus of claim 33 under conditions sufficient to form virus-antibody complexes if Zika virus antibodies are present in the sample; and

detecting the virus-antibody complexes, thereby detecting Zika virus-specific antibodies in the sample.

35. A method of detecting Zika virus-specific antibodies in a sample, comprising:

contacting the sample with the chimeric virus of claim 33 to form a virus-sample mixture, wherein virus-antibody complexes are formed in the virus-sample mixture if Zika virus-specific antibodies are present in the sample;

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inoculating a cell culture with the virus-sample mixture under conditions sufficient to allow plaque formation or micro-focus formation in the cell culture; and detecting a decrease in plaque formation or micro-focus formation in the cell culture as compared to a control cell culture, thereby detecting a Zika virus-specific antibody in the sample.

36. A method of detecting Zika virus-specific antibodies in a sample, comprising:

providing the chimeric virus of claim 33 bound to a solid support;

contacting the chimeric virus-bound solid support with the sample under conditions sufficient to form virus-antibody complexes if Zika virus-specific antibodies are present in the sample;

contacting the virus-antibody complexes with a secondary antibody; and

detecting binding of the secondary antibody to the virus-antibody complexes, thereby detecting Zika virus-specific antibodies in the sample.

37. A method of detecting Zika virus-specific antibodies in a sample, comprising:

providing a secondary antibody bound to a solid support; contacting the secondary antibody-bound solid support with the sample under conditions sufficient to allow binding of the secondary antibody to any Zika virus-specific antibodies present in the sample, thereby forming antibody-antibody complexes;

contacting the antibody-antibody complexes with the chimeric virus of claim 33 under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibodies, thereby forming immune complexes; and

detecting the presence of the immune complexes, thereby detecting Zika virus-specific antibodies in the sample.

38. The method of claim 37, wherein detecting the presence of the immune complexes comprises contacting the immune complexes with an antibody that specifically binds the chimeric virus and comprises a detectable label.

39. A method of detecting Zika virus-specific antibodies in a sample, comprising:

providing a Zika virus-specific antibody bound to a solid support;

contacting the antibody-bound solid support with the chimeric virus of claim 33 under conditions sufficient for the chimeric virus to bind the Zika virus-specific antibody to form antibody-virus complexes;

contacting the antibody-virus complexes with the sample to allow binding of any Zika virus-specific antibodies present in the sample to the chimeric virus, thereby forming immune complexes;

contacting the immune complexes with a secondary antibody; and

detecting binding of the secondary antibody to the immune complexes, thereby detecting Zika virus-specific antibodies present in the sample.

* * * * *

专利名称(译)	嵌合西尼罗河/寨卡病毒及其使用方法		
公开(公告)号	US10632185	公开(公告)日	2020-04-28
申请号	US16/315897	申请日	2017-07-06
[标]申请(专利权)人(译)	美国卫生及公共服务部		
申请(专利权)人(译)	THE U.S.A. , 为代表局局长, 卫生与公众服务		
当前申请(专利权)人(译)	美利坚合众国为代表局局长, 卫生与公众服务		
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IPC分类号	A61K39/12 A61K39/00 C07K14/005 G01N33/533 A61K39/295 C12N7/00		
CPC分类号	C12N7/00 G01N33/533 A61K39/12 C07K14/005 Y02A50/392 A61K2039/525 A61K2039/53 A61K2039/5252 Y02A50/394 C12N2770/24141 A61K2039/5254 C12N2770/24134 C12N2770/24122 C12N2770/24144		
优先权	62/359807 2016-07-08 US		
其他公开文献	US20190298818A1		
外部链接	Espacenet		

摘要(译)

嵌合黄病毒，包括非编码区，非结构蛋白，衣壳蛋白（C）和来自西尼罗河病毒（WNV）的一部分前膜（prM）信号序列，以及一部分prM信号序列，prM描述了寨卡病毒（ZIKV）的蛋白和E蛋白。还描述了在受试者中引起免疫应答，例如针对ZIKV的免疫应答的组合物和方法。进一步描述了利用嵌合西尼罗河病毒/寨卡病毒的诊断检测方法。

