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ZIKA VIRUS PURIFICATION

FIELD OF THE INVENTION

The disclosure relates to methods for the purification of Zika viruses for use in vaccines.

BACKGROUND OF THE INVENTION

Regulatory agencies such as the World Health Organization establish standards and guidelines for the production of pharmaceutical compositions administered to humans, such as vaccines, that limit quantity and components of the compositions. Meeting these standards is particularly challenging with regard to production of vaccines containing biological agents, such as viruses, which must be propagated on cell substrates. Such vaccine preparations must be sterile (*i.e.*, free from independently replicating organisms) and may contain no more than 10 ng of host cell DNA per human dose, among other requirements. These standards are in place in order to ensure safety of the composition for human administration, but may introduce challenges in the development of processes used to produce such compositions.

Protamine was originally isolated from the sperm of salmon and other species of fish but is now produced primarily through recombinant biotechnology. It is a highly cationic peptide that binds to negatively charged molecules such as nucleic acids to form a stable ion pair. Its use in removing host cell nucleic acid is well document.

SUMMARY

During the course of routine virus purification, it was observed that addition of protamine sulfate to a Zika virus harvest produced on a cell substrate removed not only contaminating DNA derived from host cells, as expected, but surprisingly also virtually eliminated immature and otherwise non-infectious virus particles from the preparation. This finding provides a streamlined, gentle and reproducible process for obtaining highly-purified infectious Zika virus particles for applications such as Zika vaccine preparation; furthermore, the process is not dependent on the charge of the Zika virus particle.

Disclosed herein are downstream processes for purifying Zika virus particles from a crude preparation. The downstream process can be applied to either a Zika virus which has not adapted for propagation on a particular cell substrate or for a partial / fully cell substrate adapted Zika virus particle.

Aspects of the invention provide processes for the purification of infectious Zika virus particles comprising the steps of (a) providing a crude harvest (a) comprising virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate; (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising a protamine salt, preferably a protamine sulphate, to obtain a virus preparation (b); and further purifying the Zika virus preparation (b) by method or methods selecting for size of the Zika virus particles, such as e.g. a sucrose density gradient centrifugation to obtain a Zika virus preparation (c) comprising the infectious Zika virus particles.

In some embodiments, the concentration of protamine sulphate in step (b) is about 1 to 10 mg/ml, more preferably about 1 to 5 mg/ml, more preferably about 1 to 2 mg/ml. In one embodiment, the concentration of protamine sulphate in step (b) is about 2 mg/mL. In one embodiment, the concentration of protamine sulphate is 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml. In a preferred embodiment, the concentration of protamine sulphate in step (b) is about 1.6 mg/ml or about 2 mg/ml.

In some embodiments, the residual host cell DNA of the virus preparation (e) is less than 1 µg/mL, especially less than 900, 800, 700, 600, 500, 400, 300 or 200 ng/mL, preferably less than 100 ng/mL. In a preferred embodiment, the residual host cell DNA of the virus preparation (c) is less than 10 ng/mL. In some embodiments, the residual host cell protein of the final virus preparation (c) is less than 10 µg/mL, especially less than 9, 8, 7, 6, 5, 4, 3 or 2 µg/mL, preferably less than 1 µg/mL. In a preferred embodiment, the residual host cell protein of the virus preparation (c) is less than 100 ng/mL. In some embodiments, the residual non-infectious virus particles of the final virus preparation (c) is less than 10 µg/mL, especially less than 9, 8, 7, 6, 5, 4, 3 or 2 µg/mL, preferably less than 1 µg/mL. In a preferred embodiment, the residual non-infectious virus particles of the virus preparation (c) is less than 100 ng/mL.

In some embodiments, the residual protamine is less than 1 µg/mL, especially less than 900, 800, 700, 600, 500, 400, 300 or 200 ng/mL, preferably less than 100 ng/mL, more preferably is below the detection limit of HPLC, in particular below the detection limit in the final drug substance. In some embodiments,

the PS content is tested by HPLC or size exclusion chromatography (SEC). For example, HPLC is validated for PS determination in JEV sucrose gradient pool samples as a routine release assay and is very sensitive (i.e., LOQ 3 µg/mL; LOD 1 µg/mL). In the current invention, PS content in Zika virus DS samples was <LOD. In one embodiment, the HPLC assessment of PS content can be performed on a Superdex Peptide 10/300GL column (GE: 17-5176-01) using 30% Acetonitrile, 0,1% Trifluoroacetic acid as solvent with a flow rate of 0,6 ml/min at 25°C and detection at 214 nm. A more sensitive method of measurement for residual protamine in a purified virus preparation is mass spectrometry (MS). In some embodiments, the residual PS levels in a Zika virus preparation are tested by MS or other such highly sensitive method, e.g., nuclear magnetic resonance (NMR). With this method, residual PS, as well as fragments and/or break-down products of PS, can be detected at trace amounts, such as levels as low as, for example, 10^6 , 10^7 or 10^8 molecules per typical sample load. In some embodiments, the PS levels are tested in the sucrose gradient pool. In some embodiments, the PS levels are tested in the drug product. In some embodiments, the PS levels are tested in the drug substance.

In some embodiments, the crude harvest (a) comprising the virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b). In some embodiments, the one or more pre-purification step(s) comprises digesting host cell genomic DNA in the crude harvest (a) comprising the virus particles and impurities by enzymatic treatment. In some embodiments, the one or more pre-purification step(s) comprises filtration, ultrafiltration, concentration, buffer exchange and/or diafiltration. In some embodiments, the one or more pre-purification steps is filtration using a filter having a pore size equal to or less than 1 µm. In some embodiments, the filter has a pore size equal to or less than 0.2 µm. In a preferred embodiment, the filter has a pore size of 0.2 µm. In some embodiments, the concentration and/or ultra/diafiltration and/or buffer exchange is performed by tangential flow filtration (TFF). In some embodiments, ultra/diafiltration of the crude harvest (a) comprising the virus particles and impurities is performed using a hollow fiber membrane having a cut-off of equal to or less than 300 kDa. In a preferred embodiment, the hollow fiber membrane has a cut-off of 100 kDa.

In some embodiments, the Zika virus particle is a live Zika virus, a chimeric virus, an attenuated live virus, a modified live virus, or a recombinant live virus. In a further step, the Zika virus particles of the invention may be optionally inactivated. In some embodiments, the Zika virus particle is an attenuated form of the virus particle. For example, the Zika virus may have reduced infectivity, virulence, and/or replication in a host, as compared to a wild-type Zika virus. In some embodiments, the Zika virus is a mutated or modified Zika virus, for example the nucleic acid of the Zika virus may contain at least one mutation relative to the wild-type Zika virus. In some embodiments, the Zika virus is a recombinant live

Zika virus, meaning a Zika virus that is generated recombinantly and may contain nucleic acid from different sources.

In some embodiments, the Zika virus particle is a live virus, an attenuated live virus, a modified live virus, or a recombinant live virus. In a most preferred embodiment, the Zika virus is a Zika virus from the Asian lineage.

In some embodiments, the relative reduction of impurity of the final Zika virus preparation relative to the liquid medium (a) comprising the Zika virus particles and impurities is in a range from 60 to 95%. In some embodiments, the residual impurity of the final Zika virus preparation is less than 1%. We observed a decrease in the HCP peaks and the non-infectious aggregate peaks in the HPLC-SEC or SDS-PAGE. An exact quantification is difficult but one can measure the density of the SDS-PAGE bands and other methods.

In some embodiments, the Zika virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line. In some embodiments, said cell line is a duck cell line. In some embodiments, said cell line is a diploid avian cell line. In some embodiments, said cell line is EB66 cell line. In a preferred embodiment, said cell line is a Vero cell line.

Aspects of the invention provide a use of any of the processes described herein for manufacturing a composition for immunization against a Zika viral infection. In a preferred embodiment, the composition is a vaccine. In one embodiment, the composition or vaccine is directed against a Zika virus of the Asian lineage.

Other aspects provide compositions comprising the Zika virus particles obtainable by any of the processes described herein for treating and/or preventing a Zika viral infection. In one embodiment, the Zika virus infection is caused by a Zika virus of the Asian lineage.

In some embodiments, the Zika virus is derived from the Asian lineage. In some embodiments, the Zika virus is a Zika virus as described partially or fully in Sequence section of this application, i.e. any of sequences SEQ ID Nos 2 to 69 or 72, in particular all partly or fully described Zika viruses of the Asian lineages or an immunogenic variant thereof. The immunogenic variants of the Zika virus or Zika virus of

the Asian lineages are herein defined as having at least 80% sequence identity to the nucleotide sequence of the sequences described in any of sequences SEQ ID Nos 2 to 69 or 72, especially at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% sequence identity.

In some embodiments, the process of the invention results in an enrichment of infectious Zika virus particles from the crude harvest comprising infectious Zika virus particles and non-infectious Zika virus particles and other Zika virus products such that the enrichment of the infectious Zika virus particles is at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, preferably at least 80%, especially 85% relative to the total virus particle content of the crude harvest (a) comprising the Zika virus particles and impurities.

In some embodiments, the residual impurity of the final Zika virus preparation with respect to all impurities in the crude harvest is less than 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, preferably less than 5% as determined by SEC-HPLC (Size Exclusion Chromatography – HPLC).

In some embodiments, the filtration step of the Zika virus preparation (b) after contact with the solid-phase matrix is performed using a filter having a pore size equal to or greater than 1 μm . In some embodiments, the filter has a pore size equal to or greater than 0.2 μm . In a preferred embodiment, the filter has a pore size of about 0.2 μm , such as 0.22 μm .

In some embodiments, the Zika virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line. In some embodiments, said cell line is a duck cell line. In some embodiments, said cell line is a diploid avian cell line. In some embodiments, said cell line is EB66 cell line. In a preferred embodiment, said cell line is a Vero cell line.

Aspects of the invention provide a use of any of the processes described herein for manufacturing a composition for immunization against a Zika virus infection. In a preferred embodiment, the composition is a vaccine. In preferred embodiments, the vaccine is administered to the subject once, twice or three or more times. In a preferred embodiment, the vaccine is administered once or twice. In a preferred embodiment, the vaccine is administered only once.

The herein disclosed *in vivo* data regarding immunogenicity of the inactivated Zika virus vaccine of the current invention indicates that the virus is surprisingly potently immunogenic and also highly cross-protective (very similar immunogenicity in African and Asian strains). Data indicate that immunogenicity was unexpectedly higher than the recently reported inactivated Zika virus vaccine candidate (Larocca, et. al, 2016, Nature doi:10.1038/nature18952.). Inactivated viruses are among the safest vaccines and especially preferred for delivery to populations where safety is especially concerning, such as pregnant women, children and immunocompromised individuals, which makes the herein disclosed inactivated Zika virus particularly suitable. Obtaining a high titer of inactivated virus is a challenge in the field. The herein disclosed process for purifying inactivated Zika virus results in not only a high yield, but also a very pure drug substance.

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings are not intended to be drawn to scale. The figures are illustrative only and are not required for enablement of the disclosure. For purposes of clarity, not every component may be labeled in every drawing, alignments were performed with the multi alignment package Jalview (Waterhouse et al., 2009, Bioinformatics 25 (9) 1189-1191). In the drawings:

Figure 1: Average distance tree (by % identity, nt), complete genomes.

Figure 2: Neighbor joining tree (by % identity, nt), complete genomes.

Figure 3: Pairwise alignment-Jalview (% identity, nt), complete genomes.

Figure 4: Average distance tree (by % identity, aa), E-protein.

Figure 5: Neighbor joining tree (by % identity, aa), E-protein.

Figure 6: Pairwise alignment-Jalview (% identity, aa), E-protein.

Figure 7: Alignment (shading: % identity, aa), E-protein.

Figure 8: An example of virus particle maturation in the host cell. As observed in flaviviruses, full maturation of the particles requires proteolytic cleavage of the precursor membrane glycoprotein (prM)

by the host protease furin. Not all prM molecules are cleaved, resulting in the release of mature, mosaic or immature-like conformations from the cells. Mosaic and immature forms are generally not infectious—only mature virions are infective and have hemagglutinin (HA) / TCID₅₀ activity. (Figure adapted from Plevka, et al., Maturation of flaviviruses starts from one or more icosahedrally independent nucleation centres, EMBO reports (2011) 12, 602–606).

Figure 9: An exemplary downstream Zika virus purification process from the crude harvest to formulation of the drug substance (vaccine), a preferred embodiment of the process of the invention (A). A flow-chart of an exemplary Zika virus inactivation process is shown in (B).

Figure 10: PS treatment results in selective removal of Zika virus aggregates and Vero HCP and LMW impurities (SEC-HPLC of 30x concentrated Zika Virus harvest day 5).

Figure 11: SEC-HPLC of individual 30x concentrated Zika harvest prior to PS treatment at different time points.

Figure 12: SEC-HPLC of individual 30x concentrated Zika harvest post PS treatment at different time points. The smaller graph indicates the observed cytopathic effect (CPE) over time.

Figure 13: Preparation of the sucrose gradient for Zika virus purification.

Figure 14: Representative SDS-PAGE from the sucrose gradient harvest of a Zika virus purification is shown.

Figure 15: Comparison of JEV and ZikaV harvest schedules/yields.

Figure 16: SEC-HPLC elution profile of ZikaV neutralized inactivated virus (NIV). Data were processed on Dionex Ultimate 3000 / Superose 6 Increase column. Both panels are from the same chromatogram. The upper graph is the complete elution profile; the lower graph is an enlargement of the ZikaV elution peak.

Figure 17: SEC-MALLS analysis of inactivated ZikaV.

Figure 18: Cumulative particle size distribution of Zika NIV.

Figure 19: Graphical representation of the neutralization of the Zika virus H/PF/2013 with pooled mouse sera. The number of plaques without serum was set to 100%. The EC50 was calculated using the 3-parameter method.

Figure 20: Graphical representation of the neutralization of the Zika virus MR766 with pooled mouse sera. The number of plaques without serum was set to 100%. The EC50 was calculated using the 3-parameter method.

Figure 21: Correlation between JEV antigen content in neutralized inactivated virus (NIV) analysed by ELISA and SEC-HPLC (Dionex Ultimate 3000, Superose 6 column).

DETAILED DESCRIPTION OF THE INVENTION

Disclosed herein are processes for the purification of infectious Zika virus particles, i.e., mature, functional Zika virus particles. The processes disclosed are characterized by the removal of undesired by-products of Zika virus production on host cells, such as non-infectious Zika virus particles and aggregated and immature Zika virus by-products. The processes provided herein allow the production of highly-purified Zika virus preparations comprising mostly infectious Zika virus particles. During the course of the invention, it was observed that protamine sulphate (PS), added to remove contaminating DNA during Zika virus purification, resulted not only in removal of contaminating DNA, but also in the loss of a high percentage of total Zika virus particles present in the preparation. Surprisingly, however, quantification of total infectious Zika virus particles by TCID50 before and after PS treatment revealed that the absolute number of infectious Zika virus particles did not change following this loss of total Zika virus particles. This observation clearly shows that treatment with PS can facilitate selective removal of non-infectious, aggregated and immature viral by-products, leaving behind the infectious Zika virus particles. Because by-products produced during Zika virus growth on host cells may have different (and undesirable) immunological properties or other unwanted side-effects or safety issues, a simple and robust way to remove these by-products is of high importance for the quality and safety of the final product.

Protamines are small arginine-rich nuclear proteins, present in high amounts in the sperm of fish, which have an important role in DNA packaging during spermatogenesis. Protamine sulfate (or “protamine” or “PS”) can form a stable ion pair with heparin and is thus commonly used during certain surgeries when

the anti-coagulation effect of heparin is no longer needed. In large doses, protamine sulfate administered alone can also have a weak anticoagulant effect ("Protamine sulfate". Wikipedia: The Free Encyclopedia. Wikimedia Foundation, Inc. 30 Sep 2015 Web. 26 Nov 2015 <https://en.wikipedia.org/wiki/Protamine_sulfate>). Protamine Sulphate is additionally routinely used in biotechnology applications such as DNA precipitation (e.g., removal of host cell DNA from cell culture processes), purification of DNA binding proteins and retroviral-mediated gene transfer.

Protamine is obtained from salmon sperm or produced recombinantly and is used as a sulphate salt. The four major peptides, which constitute almost the entire nitrogen-containing material in salmon protamine, have been fully characterized and found to be polypeptides of 30–32 amino acids in length, of which 21–22 residues are arginine. The average molecular mass is in the range of 4250 Da for the following sequence: PRRRRSSSRP VRRRRRPRVS RRRRRRGGRR RR (SEQ ID NO: 1). Herein, protamine is also referred to as protamine salt, or preferably protamine sulphate.

The present invention relates to the use of protamine sulphate (PS) in a process of purification of a live Zika virus, wherein the protamine sulphate facilitates the removal of impurities from a crude virus harvest, including non-infectious virus particles and aggregates. As seen in Fig. 8 using flaviviruses as an example, virus production in the host cell can result in the release of virus products which are not mature, and non-infectious particles, which can also be considered impurities according to the present invention. As such, the present invention also relates to the enrichment of infectious virus particles from a crude harvest containing a mixture of virus particles and other viral products in various stages of maturation.

The use of protamine sulphate can follow crude cell lysis or any further step after cell lysis (e.g. including after a pre-purification with filtration, chromatography etc) wherein the Zika virus particles are further enriched or concentrated and/or other impurities are removed and/or buffer components are exchanged. The further steps may comprise filtration or concentration of the crude cell lysate.

The protamine sulphate may comprise the sequence PRRRRSSSRP VRRRRRPRVS RRRRRRGGRR RR (SEQ ID NO: 1) or a variant thereof wherein the amino acid sequence comprises from 28-35 amino acids, preferably 29-34, more preferably 30-33 amino acids, most preferably 31 or 32 amino acids. The protamine sulphate preferably comprises at least 19 arginine residues, more preferably at least 20 arginine residues, more preferably at least 21 arginine residues, even more preferably at least 22 residues, most preferably 20 or 21 arginine residues. Further, other protamine sulphate-like compounds or variants

thereof may be used. Therefore, the use of the term “protamine salt” herein shall serve to encompass natural variations on SEQ ID NO: 1, preferably, but not limited to, the protamine sulphate forms.

The process comprising the use of protamine sulphate of the invention can be applied to purification of Zika virus for use in pharmaceutical compositions, for example, for a pharmaceutical composition such as a vaccine where it is important that the Zika virus is in its infectious form. The Zika virus to be purified may be a live virus, a live attenuated virus or a live chimeric virus, preferably a live wild type Zika virus, such as a Zika virus of the Asian lineage. In one embodiment, the Zika virus particle is also be later inactivated. In a preferred embodiment, the Zika virus is inactivated with formaldehyde.

The process according to the current invention may also comprise the use of a sucrose gradient, preferably an optimized sucrose gradient. The sucrose gradient is preferably optimized for the removal of protamine sulfate, also for the removal of immature viral particles or other viral particles which are non-infectious or host cell proteins or nucleic acids (DNA, RNA, mRNA, etc) or other host cell debris. In the current invention the optimized sucrose gradient comprises at least two, at least three, at least four layers of sucrose solutions with different densities. In one embodiment, the virus preparation to be purified is provided in a sucrose solution which has a density of about 8%, about 9%, about 10%, about 11%, about 12% sucrose (w/w), preferably about 10%. In one embodiment, one sucrose solution in the gradient has a density of about 45%, about 46%, about 47%, about 48%, about 49%, about 50%, about 51%, about 52%, about 53%, about 54%, about 55% sucrose (w/w), preferably about 50%. In one embodiment, one sucrose solution in the gradient has a density of about 30%, about 31%, about 32%, about 33%, about 34%, about 35%, about 36%, about 37%, about 38%, about 39%, about 40% sucrose (w/w), preferably about 35%. In one embodiment, one sucrose solution in the gradient has a density of about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20% sucrose (w/w), preferably about 15% sucrose. In a preferred embodiment, the sucrose gradient comprises three layers of sucrose solutions of about 50%, about 35% and about 15% (w/w) sucrose and the virus composition to be purified is contained in about 10% (w/w) sucrose. Because the invention provided for means to not only test for host cell DNA but also immature viral particles, the skilled person in the art is able to more precisely optimize the sucrose gradient for most efficient purification and include additional tools such as PRNT assay to monitor purification success.

In a preferred embodiment, the produced Zika virus is derived from the Asian lineage (which includes the strains found in South America and all strains derived from any Asian lineage). In some other

embodiments, the produced Zika virus is a Zika virus as described in the Sequence section of this application (SEQ ID NO: 2 to 69). In a preferred embodiment, the Zika virus comprises the RNA corresponding to the DNA sequence provided by SEQ ID NO: 72 or variants thereof. In a preferred embodiment, the Zika virus encodes the entire polyprotein as provided by SEQ ID NO: 73.

Table 1. Overview of process buffers and stock solutions

Buffer	Composition	Final pH	Final conductivity [mS/cm]
A	0.5 M NaOH		n.a.
B	0.1 M NaOH		n.a.
C	25 mM Tris, 150 mM NaCl	7.4±0.2	16.5
D	1 M Tris	7.4±0.2	n.a.
E	4.5 M NaCl	n.a.	n.a.
F	1 M NaCl	n.a.	n.a.
G	1 % SDS	n.a.	n.a.
H	50 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.
I	35 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.
J	15 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.
K	10 x PBS	7.4±0.2	n.a.
L	50 mg/mL Protamine sulphate	7.4±0.2	n.a.
M	Drug substance formulation buffer (10mM Tris(hydroxymethyl)-aminomethan, 5 % Sucrose, 1% (10 mg/mL) rHSA)	7.4±0.2	1.3

Table 2. Abbreviations

°Bx	Degrees Brix = sugar content (w/w) of an aqueous solution
BSA	Bovine serum albumin
CC700	Capto™ Core 700
CPE	Cytopathic effect
EtOH	Ethanol
EU	Endotoxin units
DS	Drug Substance
DP	Drug Product
DSP	Downstream Process
HCP	Host cell protein
hcDNA	Host cell DNA
hpi	Hours post infection
HPLC	High Performance Liquid Chromatography
ID	Inner diameter
JEV	Japanese Encephalitis virus
LAL	Limulus amoebocyte lysate
LDS buffer	Lithium dodecyl sulfate sample loading buffer
LOD	Limit of detection
LOQ	Limit of quantitation
MALLS	Multiangle light scattering
mAU	Milli absorbance units

MS	Mass spectroscopy
NIV	Neutralized inactivated virus
PBS	Phosphate buffered saline
PD	Process development
PFU	Plaque forming units
p.i.	Post-infection
PS	Protamine sulphate or protamine sulfate
rcf	Relative centrifugal force
rHSA	Recombinant human serum albumin
Rms radius	Root mean square radius
rMSB	Research master seed bank
RSD	Relative standard deviation
SEC	Size exclusion chromatography
SGC	Sucrose gradient centrifugation
SGP	Sucrose gradient purified
SDS	Sodium dodecyl sulphate
TBS	Tris buffered saline
TFF	Tangential flow filtration
TCID ₅₀	Tissue culture infectious dose 50%
UF/DF	Ultrafiltration/diafiltration
WFI	Water for injection
ZikaV	Zika virus

Brix:

Degrees Brix (°Bx) is the sugar content of an aqueous solution. One degree Brix is 1 gram of sucrose in 100 grams of solution and represents the strength of the solution as percentage by mass. °Bx corresponds to the sucrose content in % (w/w), eg. 45 °Bx equals 45 % (w/w) sucrose.

Table A. Primers for Zika virus sequencing: lower case letters indicate bases not included in ZIKA but containing restriction sites for later cloning when needed (therefore, two Tms provided).

Primer Pair	Oligoname	Primer sequence (5'-3') restriction sites (lower case)	T _m (gene-specific)	T _m (entire primer)	Amplicon size [bp]
1	9320_Zika_PF_1F	SEQ ID NO: 74 ttaggatccGTTGTTGATCTGTGTGAAT	69.9	74.6	707
	9321_Zika_PF_1R	SEQ ID NO: 75 taactcgagCGTACACAACCCAAGTT	69.3	75.6	
2	9322_Zika_PF_2F	SEQ ID NO: 76 ttaggatccTCACTAGACGTGGGAGTG	70	73.9	704
	9323_Zika_PF_2R	SEQ ID NO: 77	69.8	73.7	

Primer Pair	Oligoname	Primer sequence (5'-3') restriction sites (lower case)	Tm (gene-specific)	Tm (entire primer)	Amplicon size [bp]
		taactcgagAAGCCATGTCYGATATTGAT			
3	9324_Zika_PF_3F	SEQ ID NO: 78 ttaggatccGCATACAGCATCAGGTG	72.3	74.5	712
	9325_Zika_PF_3R	SEQ ID NO: 79 taactcgagTGTGGAGTTCGGTGTCT	72	76.4	
4	9326_Zika_PF_4F	SEQ ID NO: 80 ttaggatccGAATAGAGCGAARGTTGAGATA	70.9	74	712
	9327_Zika_PF_4R	SEQ ID NO: 81 taactcgAGTGGTGGGTGATCTTCTTCT	70.5	73.7	
5	9328_Zika_PF_5F	SEQ ID NO: 82 ttaggatcCAGTCACAGTGGAGGTACAGTAC	70.3	75	704
	9329_Zika_PF_5R	SEQ ID NO: 83 taactcgagCRCAGATACCATCTTCCC	71.5	77.3	
6	9330_Zika_PF_6F	SEQ ID NO: 84 ttaggatCCCTTATGTGCTTGGCCTTAG	70.7	72.7	698
	9331_Zika_PF_6R	SEQ ID NO: 85 taactcgagTCTTCAGCCTCCATGTG	70.4	76.9	
7	9332_Zika_PF_7F	SEQ ID NO: 86 ttaggatccAATGCCCACTCAAACATAGA	71.9	75	716
	9333_Zika_PF_7R	SEQ ID NO: 87 taactcgagTCATTCTCTTTCAGCCCTT	71	74	
8	9334_Zika_PF_8F	SEQ ID NO: 88 ttaggatccAAGGGTGATCGAGGAAT	70.9	75.2	703
	9335_Zika_PF_8R	SEQ ID NO: 89 taactcgagTTCCCTTCAGAGAGAGGAGC	71.9	73.4	
9	9336_Zika_PF_9F	SEQ ID NO: 90 ttaggatccTCTTTGCAAACGCGATC	71.9	75	699

Primer Pair	Oligoname	Primer sequence (5'-3') restriction sites (lower case)	Tm (gene-specific)	Tm (entire primer)	Amplicon size [bp]
	9337_Zika_PF_9R	SEQ ID NO: 91 taactcgagTCCAGCTGCAAAGGGTAT	71	74.9	
10	9338_Zika_PF_10F	SEQ ID NO: 92 ttaggatccGTGTGGACATGTACATTGA	71.4	75.8	706
	9339_Zika_PF_10R	SEQ ID NO: 93 taactcgagCCCATTTGCCATAAAGTC	70.4	75.8	
11	9340_Zika_PF_11F	SEQ ID NO: 94 ttaggatccTCATACTGTGGTCCATGGA	71.6	78.1	692
	9341_Zika_PF_11R	SEQ ID NO: 95 taactcgagGCCCATCTCAACCCCTTG	74	78	
12	9342_Zika_PF_12F	SEQ ID NO: 96 ttaggatccTAGAGGGCTTCCAGTGC	70.9	74	707
	9343_Zika_PF_12R	SEQ ID NO: 97 taactcgAGATACTCATCTCCAGGTTTGTG	70.2	72.2	
13	9344_Zika_PF_13F	SEQ ID NO: 98 ttaggatccGAAAACAAAACATCAAGAGTG	70.6	75.4	726
	9345_Zika_PF_13R	SEQ ID NO: 99 taactcgagGAATCTCTGTGCATGTGCCT	71.9	75.6	
14	9346_Zika_PF_14F	SEQ ID NO: 100 ttaggatccTTGATGGCAGACCAAC	73.1	75.6	715
	9347_Zika_PF_14R	SEQ ID NO: 101 ttaggatccGTTGTTGATCTGTGTGAAT	70.8	77.9	
15	9348_Zika_PF_15F	SEQ ID NO: 102 taactcgagCAGGTCAATGTCCATTG	71.9	75.4	719
	9349_Zika_PF_15R	SEQ ID NO: 103 ttaggatccGTTGTGTTCTATTGCTGGT	73.9	77.2	
16	9350_Zika_PF_16F	SEQ ID NO: 104	72.3	75.4	703

Primer Pair	Oligoname	Primer sequence (5'-3') restriction sites (lower case)	Tm (gene-specific)	Tm (entire primer)	Amplicon size [bp]
		taactcgaGTGATCAGRCCCCAGC			
	9351_Zika_PF_16R	SEQ ID NO: 105 ttaggatccTGCTGCCCAGAAGAGAA	72	76.3	
17	9352_Zika_PF_17F	SEQ ID NO: 106 taactcgaGCACCAACAYGGGTCTT	73.6	76	705
	9353_Zika_PF_17R	SEQ ID NO: 107 ttaggatcCTCAAGGACGGTGTGGC	72	75.5	
18	9354_Zika_PF_18F	SEQ ID NO: 108 taactcgagCAATGATCTTCATGTTGGG	71.7	75.8	699
	9355_Zika_PF_18R	SEQ ID NO: 109 ttaggatccTATGGGGGAGGACTGGT	71	74.1	
19	9356_Zika_PF_19F	SEQ ID NO: 110 taactcGAGCCCAGAACCTTGGATC	73.3	75.5	711
	9357_Zika_PF_19R	SEQ ID NO: 111 ttaggatcCAGACCCCCAAGAAGGC	71.3	76.9	
20	9358_Zika_PF_20F	SEQ ID NO: 112 taactcgagCCCCTTGGTCTTGTCT	71.7	75	706
	9359_Zika_PF_20R	SEQ ID NO: 113 ttaggatccAGGAAGGATGTATGCAGATG	71.9	73.9	
21	9360_Zika_PF_21F	SEQ ID NO: 114 taactcgagACATTGCGCATATGATTTTG	70.4	75.7	709
	9361_Zika_PF_21R	SEQ ID NO: 115 ttaggatccAGGAAGGACACACAAGAGT	71.8	75	
22	9362_Zika_PF_22F	SEQ ID NO: 116 taactcgagACAGGCTGCACAGCTTT	70	79.1	581
	9363_Zika_PF_22R	SEQ ID NO: 117 ttaggatccTCTCTCATAGGGCACAGAC	74.8	81.1	

SEQUENCES

SEQ ID NO: 1

A typical form of protamine

PRRRSSSRP VRRRRRPRVS RRRRRRGRR RR

Provided below are examples of nucleic acid sequences of the genomes of Zika viruses that may be used in the methods, compositions, and/or vaccines described herein.

SEQ ID NO: 2

KU321639.1 Zika virus strain ZikaSPH2015, Brazil, complete genome

GTTGTTACTGTTGCTGACTCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTGGATT
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TAGCCCGTGTGAGCCCTTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTTG
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SEQ ID NO: 3

KU497555.1 Zika virus isolate Brazil-ZKV2015, Brazil, complete genome

CCAATCTGTGAATCAGACTGCGACAGTTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGGATTTGGA
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SEQ ID NO: 4

KU501215.1 Zika virus strain PRVABC59, Puerto Rico, complete genome

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KU509998.1 Zika virus strain Haiti/1225/2014, Haiti, complete genome

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SEQ ID NO: 6

KU527068.1 Zika virus strain Natal RGN, Brazil: Rio Grande do Norte, Natal, complete genome

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SEQ ID NO: 7

KU681081.3 Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14, Thailand, complete genome
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SEQ ID NO: 8

KU681082.3 Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740, Philippines, complete genome

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SEQ ID NO: 9

KU707826.1 Zika virus isolate SSABR1, Brazil, complete genome

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SEQ ID NO: 10

KU744693.1 Zika virus isolate VE_Ganxian, China, complete genome

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SEQ ID NO: 11

LC002520.1 Zika virus genomic RNA, strain: MR766-NIID, Uganda, complete genome

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SEQ ID NO: 12

AY632535.2 NC_012532.1 Zika virus strain MR 766, Uganda, complete genome

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GCGCCATCTGGTACATGTGTTGGGAGCCAGATTCTTGGAGTTTGAAGCCCTTGGATTCTTGAACGAGGACCATTGGATGGGA
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GGAGGAAAGATGTACGAGATGACACTGCTGGCTGGGACACCCGCATTAGTAAGTTTGATCTGGAGAATGAAGCTCTGATTA
CCAACCAAATGGAGGAAGGGCACAGAACTCTGGCGTTGGCCGTGATTAATAACATACCAAAACAAAGTGGTGAAGGTTCT
CAGACCAGCTGAAGGAGGAAAAACAGTTATGGACATCATTTCAAGACAAGACCAGAGAGGGAGTGGACAAGTTGTCACTTAT
GCTCTCAACACATTCACCAACTTGGTGGTGCAGCTTATCCGGAACATGGAAGCTGAGGAAGTGTAGAGATGCAAGACTTATG
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CTCAAGGATGGGAGATCCATTGTGGTCCCTTGGCGCCACCAAGATGAACTGATTGGCCGAGCTCGCGTCTCACCAGGGGCAG
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CGACTGATGGCTAATGCCATTTGCTCGGCTGTGCCAGTTGACTGGGTACCAACTGGGAGAACCACCTGGTCAATCCATGGAAA
GGGAGAATGGATGACCACTGAGGACATGCTCATGGTGTGGAATAGAGTGTGGATTGAGGAGAACGACCATATGGAGGACAA
GACTCCTGTAACAAAATGGACAGACATTCCCTATCTAGGAAAAAGGGAGGACTTATGGTGTGGATCCCTTATAGGGCACAGAC
CCCGCACCACTTGGGCTGAAAACATCAAAGACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAAAGTACATGGA
CTATCTATCCACCAAGTCCGCTACTTGGGTGAGGAAGGGTCCACACCCGAGTGTTGTAAGCACCAATTTAGTGTTGTGAGG
CCTGCTAGTCAGCCACAGTTTGGGGAAAGCTGTGCAGCCTGTAACCCCCCAGGAGAAGCTGGGAAACCAAGCTCATAGTCA
GGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACACTGAGTCAAAAAACCCACGCGCT

TGGAAGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCCTGAACTGGAGACTAGCTGTGAATC
TCCAGCAGAGGGGACTAGTGGTTAGAGGAGACCCCCGGAAAACGCAAAACAGCATATTGACGTGGGAAAAGACCAGAGACTC
CATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAACCTCGGCGGCCGGTGTGGGGAAATCCATGTTTTCT

SEQ ID NO: 13

KJ776791.1, Zika virus strain H/PF/2013 polyprotein gene, complete cds

AGTATCAACAGGTTTTATTTTGGATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGG
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TCAAGGTGGTCTGATGACCATCTGTGGCATGAACCAATAGCCATACCCTTTCAGCTGGAGCGTGGTACGTATACGTGAAG
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CAAGACTCCGTACTGTGATCTTAGCTCCAACCAAGGGTGTGCGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGT
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AGGCCTTACAAAGCCGCGGCGGCCCAATTGCCGAGACCCCTAGAGACCATTATGCTTTTGGGGTGTCTGGGAACAGTCTCGCT
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CTCATGTGGCTCTCGAAATTGAGCCAGCCAGAATTGCATGTGTCTCATTGTTGTGTTCTATTGCTGGTGGTGCTCATACCTG
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CAAGAGACGTGGGGGTGGAACAGGAGAGACCTGGGAGAGAAATGGAAGGCCGCTTGAACCAGATGTGCGCCCTGGAGT
TCTACTCTACAAAAAGTCAGGCATCACCGAGGTGTGCAGAGAAGAGGGCCCGCGCCCTCAAGGACGGTGTGGCAACGGG
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ACACATGAGATGTAAGTGGTCTCTGGAGCGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCCTCTTGGGGC
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GAACCAACCATATAGGACATGGGCTTACCATGGAAGCTATGAGGCCCCACACAAGGGTCAGCGTCTCTCTAATAAACGGGG
TTGTCAGGCTCTGTCAAAACCTGGGATGTGGTGAAGTGGAGTACAGGAATAGCCATGACCGACACCACACCGTATGGTCAG
CAAAGAGTTTTCAAGGAAAAAGTGGACACTAGGGTGCCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTC
CTGGTTGTGGAAAGAGCTAGGCAAAACACAAACGGCCACGAGTCTGTACCAAGAAGAGTTCATCAACAAGGTTCTAGCAAT
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CTAGTGGACAAGGAAAGAGAGCACCACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAAAG
AAACAAGGGGAATTTGGAAGGGCAAGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTTCTAGAGTTCGAAG
CCCTTGGATTCTTGAACGAGGATCACTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGAC
TCGGATATGTCCTAGAAGAGATGAGTCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCAT
CAGCAGGTTTGATCTGGAGAATGAAGCTCTAATCACCACCAAAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATC
AAGTACACATACCAAAACAAAGTGGTAAAGTCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTGAGAC
AAGACCAAGGGGGGAGCGGACAAGTTGTCACTTACGCTCTTAACACATTTACCAACCTAGTGGTGAACACTCATTTCGGAATATG
GAGGCTGAGGAAGTTCTAGAGATGCAAGACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAAC
GGATGGGATAGGCTCAAACGAATGGCAGTCACTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGCACATGCCC
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AATGTGGCAGCTCCTTTATTTCCACAGAAGGGACCTCCGACTGATGGCAATGCCATTTGTTCTGTGCCAGTTGACTGGGT
TCCAACCTGGGAGAACTACCTGGTCAATCCATGGAAGGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGA
GTGTGGATTGAGGAGAACGACCACATGGAAGACAAGACCCAGTTACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGG
AAGACTTGTGGTGTGGATCTCTCATAGGGCAGACCGCGCACCACTGGGCTGAGAACATTAAAAACACAGTCAACATGGT
GCGCAGGATCATAGGTGATGAAGAAAAAGTACATGGACTACCTATCCACCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACA
CCTGGAGTGTGTAAGCACCAATCTTAGTGTTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAGCTGTGCAGCCTGTGAC
CCCCCAGGAGAAGCTGGGAAACCAAGCCTATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGC
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TCAATCTGGGGCCTGAAGTGGAGATCAGCTGTGGATCTCCAGAAGAGGGGACTAGTGGTTAGAGGAG

In some embodiments, the Zika virus has a RNA genome corresponding to the DNA sequence provided by the nucleic acid sequence of any one of SEQ ID NOs: 2-13 or 72. In some embodiments, the Zika virus has a variant genome that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical to any one of SEQ ID NOs: 2-13 or 72.

Provided below are amino acid sequences of the E-proteins of Zika strains that may be used in the methods, compositions, and/or vaccines described herein.

SEQ ID NO: 14

isol-ARB15076.AHF49784.1.Central_African_Republic/291-788 Flavivirus envelope glycoprotein E.

IRICGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWNGCGLFGKGLVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDENRAKVEVTPNSPRA
EATLGGFGSLGLDCEPTGLDFSDLYLTMMNKHVWLHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGS
QEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGTDGPKVPAQM
AVDMQTLTPVGRILTANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLGDTAWDF
GSVGGVFNSLGKIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 15

isol-lbH_30656.AEN75265.1.Nigeria/291-788 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDENRAKVEVTPNSPRA
EATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPWHSGADTETPHWNNKEALVEFKDAHAKRQTVVVLGS
QEGAVHTALAGALEAEMDGAKGRLLSSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGRDGPCKVPAQM
AVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHRSIGKAFEATVRGAKRMAVLGDTAWDF
GSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 16

ArB1362.AHL43500.1.-/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDXXXXXXNRAEVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLFSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHRSIGTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 17

ArD128000.AHL43502.1.-/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMXXXXXGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHRLVRKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLFSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHLKGSSIGKAFEATVRGAKRMAVLG
TAWDFGSVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 18

ArD158095.AHL43505.1.-/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLFSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHRSIGTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 19

ArD158084.AHL43504.1.-/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLFSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHRSIGTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 20

isol-ARB13565.AHF49783.1.Central_African_Republic/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLFSGHLKCRKMDKLRKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCK

VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
DTAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 21

isol-ARB7701.AHF49785.1.Central_African_Republic/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGKRLFSGLKCRLLKMDKRLKGVSYSLCTAAFTFTKVPALHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
DTAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 22

isol-ArD_41519.AEN75266.1.Senegal/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGKRLFSGLKCRLLKMDKRLKGVSYSLCTAAFTFTKVPALHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
DTAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 23

MR766-NIID.BAP47441.1.Uganda/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMTVNDIGYETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGKRLFSGLKCRLLKMDKRLKGVSYSLCTAAFTFTKVPALHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 24

LC002520.1/326-829 Zika virus genomic RNA, strain: MR766-NIID, Uganda, Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMTVNDIGYETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGKRLFSGLKCRLLKMDKRLKGVSYSLCTAAFTFTKVPALHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 25

isol-MR_766.AEN75263.1.Uganda/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGYETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGKRLFSGLKCRLLKMDKRLKGVSYSLCTAAFTFTKVPALHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 26

ArD7117.AHL43501.1.-/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNCGFLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT

VVVLGSQEGAVHTALAGALEAEMDGAAGRLFSGHLKCRKMDKRLKGVSYSLCTAVCTAAKVP AETLHGTVTVEVQYAGTDGPC
KVPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVL
GDTAWDFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 27

AY632535.2/326-825 NC_012532.1 Zika virus strain MR 766, Uganda, Flavivirus envelope glycoprotein E.
IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGS LVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIGYETDEDRAKVEVTPNSPR
AEATLGGFGSLGLDCEPRTGLDFSDLYLT MNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNEALVEFKDAHAKRQTVVVL
GSQEGAVHTALAGALEAEMDGAAGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCKIPVQ
MAVDMQTLTPVGRITANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVLGDTAW
DFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 28

MR_766.AAV34151.1.Uganda/291-790 Flavivirus envelope glycoprotein E. |Q32ZE1|Q32ZE1_9FL
IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGS LVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIGYETDEDRAKVEVTPNSPR
AEATLGGFGSLGLDCEPRTGLDFSDLYLT MNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNEALVEFKDAHAKRQTVVVL
GSQEGAVHTALAGALEAEMDGAAGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCKIPVQ
MAVDMQTLTPVGRITANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVLGDTAW
DFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 29

MR_766.YP_009227198.1.Uganda/1-500 envelope protein E [Zika virus]
IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGS LVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIGYETDEDRAKVEVTPNSPR
AEATLGGFGSLGLDCEPRTGLDFSDLYLT MNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNNEALVEFKDAHAKRQTVVVL
GSQEGAVHTALAGALEAEMDGAAGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPAETLHGTVTVEVQYAGTDGPCKIPVQ
MAVDMQTLTPVGRITANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVLGDTAW
DFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

SEQ ID NO: 30

KU681081.3/308-811 Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14, Thailand, Flavivirus envelope
glycoprotein E.
IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGS LVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLT MNNKHVLVHKEWFHDIPLPWHTGADTGTPHWNNEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITEGTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVLG
DTAWDFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 31

isol-Zika_virus% H.sapiens-tc%THA%2014%SV0127-_14.AMD61710.1.Thailand/291-794 Flavivirus envelope
glycoprotein E.
IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGS LVTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLT MNNKHVLVHKEWFHDIPLPWHTGADTGTPHWNNEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITEGTENSKMMLELDPPFGDSYIVIGVGDKKITHHWHRSSTIGKA FEATVRGAKRMAVLG
DTAWDFGSGVGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 32

CK-ISL_2014.AIC06934.1.Cook_Islands/1-504 Flavivirus envelope glycoprotein E. (Fragment) OS=Zika virus GN=E PE=4 SV=1

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 33

Natal_RGN.AMB18850.1.Brazil:_Rio_Grande_do_Norte,_Natal/291-794 Flavivirus envelope glycoprotein E.]

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 34

isol-Si323.AMC37200.1.Colombia/1-504 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 35

KU707826.1/317-820 Zika virus isolate SSABR1, Brazil, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 36

KU509998.1/326-829 Zika virus strain Haiti/1225/2014, Haiti, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 37

isol-GDZ16001.AML82110.1.China/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 38

BeH819015.AMA12085.1.Brazil/291-794 Flavivirus envelope glycoprotein E.]

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 39

MRS_OPY_Martinique_PaRi_2015.AMC33116.1.Martinique/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 40

KU501215.1/308-811 Zika virus strain PRVABC59, Puerto Rico, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 41

Haiti%1225%2014.AMB37295.1.Haiti/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 42

KU527068.1/308-811 Zika virus strain Natal RGN, Brazil: Rio Grande do Norte, Natal, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 43

isol-Z1106027.ALX35662.1.Suriname/5-508 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTT VSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K

VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 44

isol-FLR.AMM39804.1.Colombia:_Barranquilla/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 45

PLCal_ZV_isol-From_Vero_E6_cells.AHL37808.1.Canada/254-757 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 46

BeH818995.AMA12084.1.Brazil/291-794 Flavivirus envelope glycoprotein E. [Zika virus].

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 47

H/PF/2013.AHZ13508.1.French_Polynesia/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 48

PRVABC59.AMC13911.1.Puerto_Rico/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 49

KU321639.1/326-829 Zika virus strain ZikaSPH2015, Brazil, Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHVLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHAKRQT

VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 50

ZikaSPH2015.ALU33341.1.Brazil/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 51

103344.AMC13912.1.Guatemala/291-794 polyprotein [Zika virus]. 103344.AMC13912.1.Guatemala Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEIRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 52

isol-Brazil-ZKV2015.AMD16557.1.Brazil/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGTQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 53

KU497555.1/308-811 Zika virus isolate Brazil-ZKV2015, Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGTQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 54

isol-ZJ03.AMM39806.1.China/291-794 Flavivirus envelope glycoprotein E.

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSSTIGKAFAEATVRGARRMAVLG
DTAWDFGSGGALNSLGKGIHQIFGAAGKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 55

isol-FSS13025.AFD30972.1.Cambodia/291-794 Flavivirus envelope glycoprotein E.

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 56

isol-Z1106032.ALX35660.1.Suriname/291-794 Flavivirus envelope glycoprotein E. [Zika virus]

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNNAKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 57

isol-Z1106033.ALX35659.1.Suriname/291-794 Flavivirus envelope glycoprotein E. [Zika virus]

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNNAKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 58

isol-BeH828305.AMK49165.1.Brazil/291-794 Flavivirus envelope glycoprotein E.

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 59

isol-GD01.AMK79468.1.China/291-794 Flavivirus envelope glycoprotein E.

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNGTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 60

isol-Z1106031.ALX35661.1.Suriname/291-794 Flavivirus envelope glycoprotein E.

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTTSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHTDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VLAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

SEQ ID NO: 61

ACD75819.1.Micronesia/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPAVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V L I F L S T A V S A

SEQ ID NO: 62

KU681082.3/308-811 Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740, Philippines, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V L I F L S T A V S A

SEQ ID NO: 63

isol-Zika_virus% H.sapiens-tc% PHL% 2012% CPC-0740.AMD61711.1.Philippines/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V L I F L S T A V S A

SEQ ID NO: 64

isol-BeH823339.AMK49164.2.Brazil/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEATISDIASDSRCPTQGEAYLDKQS
DTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D T G H E T D E N R A K V E I T P
N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
A V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S A

SEQ ID NO: 65

isol-P6-740.AEN75264.1.Malaysia/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D X G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T L H G T V T V E V Q Y A G T D G P C K
V P A Q M A V D M Q T L T P V G R L I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G D K K I T H H W X R S G S T I G K A F E A T V R G A K R M A V L G
D T A W D F G S V G G A L N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V L I F L S T A V S A

SEQ ID NO: 66

KU744693.1/326-829 Zika virus isolate VE_Ganxian, China, Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M L V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y Y L T M N N K H W L A H K E W F H D I P L P W H A G A A T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T V D G T V T V E G Q Y G G T D G P C K

VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPPFGDSYIVIGVGEKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGD
TAWDFG SVGGALNSLGKGIHQIIGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSG

SEQ ID NO: 67

isol-VE_Ganxian.AMK79469.1.China/291-794 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTAM AQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F A C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M L V N D T G H E T D E N R A K V E I T
P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y L T M N N K H W L A H K E W F H D I P L P W H A G A A T G T P H W N N K E A L V E F K D A H A K R Q T
V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L S S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K I P A E T V D G T V T V E G Q Y G G T D G P C K
V P A Q M A V D M Q T L T P V G R I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G E K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D
T A W D F G S V G G A L N S L G K G I H Q I I G A A F K S L F G G M S W F S Q I L I G T L L M W L G L N T K N G S I S L M C L A L G G V L I F L S T A V S G

SEQ ID NO: 68

ArD157995.AHL43503.1.-/291-794 Flavivirus envelope glycoprotein E.

ISCIGVSNRDLVEGMSGGTWVDV VLEHGGCVTEMAQDKPTVDIELVTMTVSNMAEVR SYCYEASLSDMASASRCPTQGEPSLDK
QSDTQSVCKRTLGD R G W G N G C G I F G K G S L V T C S K F T C C K K M P G K S I Q P E N L E Y R I M L P V H G S Q H S G M I V N D I G H E T D E N R A K V E V
T P N S P R A E A T L G G F G S L G L D C E P R T G L D F S D L Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q
T V V V L G S Q E G A V H T A L A G A L E A E M D G A K G R L F S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K V P A E T L H G T V T V E V Q S A G T D G P C
K V P A Q M A V D M Q T L T P V G R I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G D K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L
G D T A W D F G S V G G V F N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V M I F L S T A V S A

SEQ ID NO: 69

MR_766.ABI54475.1.Uganda/291-788 Flavivirus envelope glycoprotein E.

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD R G W G N G C G L F G K G S L V T C A K F T C S K K M T G K S I Q P E N L E Y R I M L S V H G S Q H S G M I V N D E N R A K V E V T P N S P R A
E A T L G G F G S L G L D C E P R T G L D F S D L Y L T M N N K H W L V H K E W F H D I P L P W H A G A D T G T P H W N N K E A L V E F K D A H A K R Q T V V V L G S
Q E G A V H T A L A G A L E A E M D G A K G R L F S G H L K C R L K M D K L R L K G V S Y S L C T A A F T F T K V P A E T L H G T V T V E V Q Y A G T D G P C K V P A Q M
A V D M Q T L T P V G R I T A N P V I T E S T E N S K M M L E L D P P F G D S Y I V I G V G D K K I T H H W H R S G S T I G K A F E A T V R G A K R M A V L G D T A W D F
G S V G G V F N S L G K G I H Q I F G A A F K S L F G G M S W F S Q I L I G T L L V W L G L N T K N G S I S L T C L A L G G V M I F L S T A V S A

SEQ ID NO: 70

5'-(dIdC)₁₃-3'

dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC dIdC

SEQ ID NO: 71

KLK peptide

KLKLLLLKLK

SEQ ID NO: 72

ZIKV Sequence H/PF/2013 as sequenced

CAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTTGGATTGGAAACGAGAGTTTCT
GGTCATGAAAAACCCAAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGGAGTAGCCCGTGTGAGCCCC
TTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTATGGGCCATCAGGATGGTCTTGGCGATTCTAGCCTTTTT
GAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAAAGAGGCTATGGAAATAATA
AAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGAGGCGCAGATACT
AGTGTGCGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTGCATACTATATGTA
GGACAGAAACGACGCTGGGGAGGCCATATCTTTTCCAACCACATTGGGGATGAATAAGTGTTATATACAGATCATGGATCTTG
GACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGAACACAGATGACGTCGATTGTTGGTG
CAACACGACGTCAACTGGGTTGTGTACGGAACCTGCCATCAGAAAAAGGTGAAGCACGGAGATCTAGAAGAGCTGTGACG
CTCCCCTCCATTCCACTAGGAAGCTGCAACCGGTCGCAACCTGGTTGGAATCAAGAGAATACACAAAGCACTTGATTAG
AGTCGAAAAATTGGATATTCAGGAACCCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTGGGAAGCTCAACGAGCC
AAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATCAGGTGCATAGGAGTCAGCAATAGGGACTTT
GTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGAACATGGAGGTTGTGTACCGTAATGGCACAGGACAAAC

CGACTGTCGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCTATGAGGCATCAATATCG
GACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAAG
AACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTTGGCAAAGGGAGCCTGGTGACATGCGCTAAGTTTGCATGC
TCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTGAGTTTATGGCTCCCAGCACA
GTGGGATGATCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAACGCCCAATTCACCAAGAGC
CGAAGCCACCCTGGGGGGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTTTTCAGATTTGTATTACT
TGACTATGAATAACAAGCACTGGTTGGTTACAAGGAGTGGTTCCACGACATTCATTACCTTGGCAGCGTGGGGCAGACACC
GGAATCCACACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAAACTGTCGTGGTTCTAG
GGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGTGCAAAGGGAAGGCTGTCCT
CTGGCCACTTGAATGTGCGCTGAAAATGGATAAATCTAGATTGAAGGGCGTGTCTACTCCTTGTGTACCGCAGCGTTCACAT
TCACCAAGATCCCGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAGATGGACCTTGCAAGGT
TCCAGCTCAGATGGCGTGGACATGCAAACTCTGACCCCACTTGGGAGGTTGATAACCGCTAACCCGTAATCACTGAAAGCA
CTGAGAACTCTAAGATGATGCTGGAATTTGATCCACCATTTGGGGACTTTACATTGTCTAGGAGTGGGGGAGAAGAAGATC
ACCCACCACTGGCAGAGGAGTGGCAGCACCATTGGAAGAGCATTGGAAGCCACTGTGAGAGGTGCCAAGAGAATGGCAGTCT
TGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCCATCAAAATTTTGGAGCA
GCTTTCAAATCATTGTTTGGAGGAATGTCCTGGTTCTCAAAATTTCTATTGGAACGTTGCTGATGTGGTTGGGTCTGAACACA
AAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTATCCACAGCTGTCTCTGCTGATGTGGGG
TGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTCTGCTATAACGACGTTGAAGCCTGGAGGGACA
GGTACAAGTACCATCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATGGTATCTGTGGGATCTCC
TCTGTTTCAAGAATGGAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAAGAGAATGGAGTTCAAC
TGACGGTCGTTGTGGGATCTGTAAAAAACCCATGTGGAGAGGTCCACAGAGATTGCCCCGTGCTGTGAACGAGCTGCCCCAC
GGCTGGAAGGCTTGGGGGAAATCGTACTTCGTGAGCAGCAGCAAGACAAATAACAGCTTTGCTGTGGATGGTGACACACTGA
AGGAATGCCCACTCAAACATAGAGCATGGAACAGCTTTCTGTGGAGGATCATGGGTTGGGGTATTTCACTAGTGTCTGG
CTCAAGGTTAGAGAAGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGAAAGGAGGCTGTACACA
GTGATCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCATCTGATCGAGATGAAAACAT
GTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGTGATCATACCAAGTCTTTAGCTGGGCCA
CTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCAGTGAAGAGCTTGAAATTCGGTTTG
AGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGAGATCAACCACTGCAAGCGG
AAGGGTGATCGAGGAATGGTGTGTCAGGGAGTGCACAATGCCCCACTGTCGTTCCGGGCTAAAGATGGCTGTTGGTATGGA
ATGGAGATAAAGGCCAGGAAAGAACAGAAAGTAAGTGAAGGTCAATGGTGACTGCAGGATCACTGATCAGATGGATC
ACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCACAAAGATCATCATAAGC
ACATCGATGGCAGTGTGGTAGCTATGATCCTGGGAGGATTTCAATGAGTGACCTGGCTAAGCTTGCAATTTTATGGGTGC
CACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAAAGTCAGACCAGCGTTGCTG
GTATCTTTTATCTTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGTGTCTTTTGCAAACTGCGATCT
CCGCTTGGAAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGCGATGGTTGTTCCACGCA
CTGATAACATCACTTGGCAATCCTGGCTGCTGACACCACTGGCCCGGGGCACACTGCTTGTGGCGTGGAGAGCAGGCCTT
GCTACTTGGGGGGGTTTATGCTCCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTACCATTGTCTATGGCCCTGGG
ACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGTGGGAAGCGGAGCTGGCCC
CCTAGCGAAGTACTACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCGCCAAGGCAGATATAGAGATGGCTGGGC
CCATGGCCGCGGTGCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACATTGAAAGAGCAGGTGA
CATCAGATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGAGAGTGGTGATTTCTCC
CTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTGGCATGAACCCAATAGC
CATACCTTTGCACTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGCTCTATGGGATGTGCTGCTCCCA
AGGAAGTAAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGTAGGTTCAACACAAGTTGGAG
TGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGAAGCGGTGAAGGGAGAC
TTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGATGCCGCTGGGACGGGCA
CAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCGGAATATTTAAGACAAAG
GATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAGACAAGTGTGGGAGAGTGA
TAGGACTTTATGGCAATGGGGTCGTGATCAAAAATGGGAGTTATGTTAGTGCCATCACCCAAGGGAGGAGGGAGGAAGAGA
CTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAAGTGTCTTAGACTTGATCTGGAGCTGGGAAAACC
AGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTAAGTGTGATCTTAGCTCAACCAAGGTTGTGCT
GCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTACCCACTCTGGAACAGAAAT
CGTCGACTTAATGTGCCATGCCACCTTCACTTACGTCTACTACAGCCAATCAGAGTCCCCAACTATAATCTGTATATTATGGAT

GAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGATGGGCGAGGCGGCTGCCA
TCTTCATGACCGCCACGCCACAGGAACCCGTGACGCATTTCCGACTCCAACCTACCAATTATGGACACCGAAGTGGAAGTCC
CAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGAAAAACAGTTTGGTTTGTTCAGCGTGAGGAA
CGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGAAAAACGGGTCATACAGCTCAGCAGAAAAGACTTTTGAGACAGAGTTT
CAGAAAAACAAACATCAAGAGTGAGGACTTTGTCTGACAACTGACATTTACAGAGATGGGCGCCAACCTTAAAGCTGACCGTGT
CATAGATTCCAGGAGATGCCTAAAGCCGGTCATACTTGATGGCGAGAGAGTCACTTGGCTGGACCATGCCTGTACACATG
CCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATCTGTATGGAGGTGGGTGCG
CAGAGACTGACGAAGACCATGCACACTGGCTGAAGCAAGAATGCTCCTTGACAATATTTACCTCCAAGATGGCCTCATAGCC
TCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGAGCAAAGGAAGACCTTTG
TGAAACTCATGAAAAGAGGAGATCTTCTGTTTGGCTGGCTATCAGGTTGCATCTGCCGGAATAACCTACACAGATAGAAGA
TGGTGCTTTGATGGCAGGACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGACCAGACACGGAGAGAAA
AGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATTCAAGGAGTTTGGCGCTG
GGAAAAGAGGAGCGGCTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAGAGATTCCAGGAAGCCA
TTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCTTACAAAGCCGCGGCGGCCCAATTGCCGGAGACCT
AGAGACCATTATGCTTTTGGGGTGTCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGATGAGGAACAAGGGCATAGGGA
AGATGGGCTTTGGAATGGTGACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGCCAGCCAGAATTGCATGT
GTCCTCATTGTTGTGTTCTATTGCTGGTGGTGTCTACCTGAGCCAGAAAAGCAAAGATCTCCCCAGGACAACCAATGGCA
ATCATCATCATGGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCAATGAAGTCGGATGGTTGGAGAGAACAAAGAGTGACCT
AAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACCTGCGGCCAGCCTCAGCTTGG
GCCATCTATGCTGCCTTGACAACTTTCATTACCCAGCCGTCCAACATGCAGTGACCACTTCATACAACAACTACTCCTAATGG
CGATGGCCACGCAAGCTGGAGTGTTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGACTTTGGAGTCCCCTGTCTA
ATGATAGGTTGCTACTCACAATTAACACCCCTGACCCTAATAGTGGCCATCATTTTCTCGTGCGCACTACATGTACTTGATCC
CAGGGCTGCAGGCAGCAGCTGCGCGTGCTGCCAGAAAGAGAACGGCAGCTGGCATCATGAAGAACCCTGTTGTGGATGGAA
TAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGGAGAAAAAGATGGGACAGGTGCTACTCATAGCAGTAGC
CGTCTCCAGCGCCATACTGTCGCGGACCGCTGGGGTGGGGGAGGCTGGGGCCCTGATCACAGCGGCAACTTCACTTTG
TGGAAGGCTCTCCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACATTTTTAGGGGAAGTTACTTGGCTGGA
GCTTCTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGGAGAGACCCTGGGAGAG
AAATGGAAGGCCCGCTTGAACAGATGTCGGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATCACCGAGGTGTGCAGAG
AAGAGGCCCGCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCGAGGAAGTGAAAGCTGAGATGGT
TGGTGAGCGGGGATACCTGCAGCCCTATGGAAGGTCATTGATCTTGGATGTGGCAGAGGGGGCTGGAGTTACTACGCCG
CACCATCCGCAAAGTTCAAGAAGTGAAAGGATACAAAAAGGAGGCCCTGGTCATGAAGAACCCTGTTGGTGCAAAGCTAT
GGGTGGAACATAGTCCGTCTAAGAGTGGGGTGGACGTCTTTCATATGGCGGCTGAGCCGTGTGACACGTTGCTGTGTGACA
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AAGACCAGGAGCCTTTGTATAAAAGTGTGTGCCATACACCAGCACTATGATGGAACCTGGAGCGACTGCAGCGTAGGT
ATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACATGAGATGTACTGGTCTCTGGAGCGAAAAGCAACAC
CATAAAAGTGTGTCCACCACGAGCCAGCTCCTCTTGGGCGCATGGACGGGCCAGGAGGCCAGTGAATATGAGGAGGAT
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GATCCGCAGTGAGCACGCGGAAACGTGGTTCTTGGACGAGAACCACCATATAGGACATGGGCTTACCATGGAAGCTATGAG
GCCCCACACAAGGGTCAGCGTCTCTCTAATAAACGGGTTGTGAGGCTCCTGTCAAACCTGGGATGTGGTGACTGGAGT
CACAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAGAGTTTTCAAGGAAAAAGTGGACACTAGGGTGCCAGAC
CCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGAAAGAGCTAGGCAACACAAACGGCCACGAG
TCTGTACCAAGAAGAGTTTCATCAACAAGGTTCTAGCAATGCAGTCTTAGGGGCAATATTTGAAGAGGAAAAAGAGTGGAA
GACTGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGACACCCTGAGAGGAGAGTG
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ACACATTTACCAACCTAGTGGTGCAACTATTGGAATATGGAGGCTGAGGAAGTTCTAGAGATGCAAGACTTGTGGCTGTG
CGGAGGTGAGAGAAAGTGACCAACTGGTTGAGAGCAACGGATGGGATAGGCTCAAACGAATGGCAGTCAGTGGAGATGAT
TGCGTTGTGAAGCCAATTGATGATAGGTTTGCATGCCCCTCAGGTTCTGAATGATATGGGAAAAAGTTAGGAAGGACACACA
AGAGTGGAAACCTCACTGGATGGGACAACCTGGGAAGAAGTTCCGTTTTGCTCCCACTTCAACAAGCTCCATCTCAAGG

ACGGGAGGTCCATTGTGGTTCCTGCCGCCACCAAGATGAACTGATTGGCCGGGCGCGTCTCTCCAGGGGCGGGATGGAG
 CATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAAGGGACCTCCGACTGAT
 GGCCAATGCCATTTGTTTCATCTGTGCCAGTTGACTGGGTTCCTGAGGAGAACTACCTGGTCAATCCATGGAAAGGGAGAAT
 GGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGGAAGACAAGACCCAG
 TTACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATAGGGCACAGACCGCGCACC
 ACCTGGGCTGAGAACATTAACACAGTCAACATGGTGCAGGATCATAGGTGATGAAGAAAAGTACATGGACTACCTAT
 CCACCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGTGTAAGCACCACATCTAGTGTGTGAGGCCTGCTA
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 AACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCTCAGAGGACACTGAGTCAAAAAACCCACGCGCTTGGAGGC
 GCAGGATGGGAAAAAGAGGTGGCGACCTTCCCCACCTTCAATCTGGGCTGAACTGGAGATCAGCTGTGGATCTCCAGAA
 GAGGGACTAGTGGTTAGAGGAGACCCCCGAAAAACGCAAAACAGCATATTGACGCTGGGAAAGACCAGAGACTCCATGAG
 TTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGCGCGCGGTGTGGGG

SEQ ID NO: 73

AHZ13508.1, Zika virus polyprotein from Polynesian outbreak (H/PF/2013)

MKNPKKSGGFRIVNMLKRGVARVSPFGGLKRLPAGLLGHGPIRMVLAFLRFTAIPSLGLINRWGSGVKKEAMEIHKFKKDLA
 AMLRIINARKEKKRRGADTSVGIVGLLLTAMAAEVTRRGSAYMYLDRNDAGEAISFPTTLGMNKCQIYQIMDLGHMCDATMSYEC
 PMLDEGVEPDDVDCWCNTTSTWVVYGTCHHKKEARRSRRAVTLPSHSTRKLQTRSQTWLESREYTKHLIRVENWIFRNPGFALA
 AAIAWLLGSSTSQKVIYLMILLIAPAYSIRCIQVSNRDFVEGMSGGTWVDVVLHGGCVTVMAQDKPTVDIELVTTTNSMAEVR
 SYCYEASISDMASDSRCPTQGEAYLDKQSDTQYVCKRTLVDRGWNGCGFLGKGLVTCAKFACSKKMTGKSIQENLEYRIMLSV
 HGSQHSQMIVNDTGHETDENRAKVEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNKHVLVHKEWFHDIPLPWA
 GADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGAVHTALAGALEAEMDGAAGRLSSGHLKRLKMDKRLKGVSYSLCTAAF
 TFTKIPAEHLHGTVTVEVQYAGTDGPKVPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHH
 WHRSGSTIGKAFETVRGAKRMAVLGDTAWDFGSGVGGALNSLKGHIFGAFAKSLFGGMSWFSQILIGTLLMWLGLNTKNGSI
 SLMCLALGGVLIFLSTAVSADVGSVDFSKKETRCGTGVFVYNDVEAWRDYKYHPDSPRRLAAAVKQAWEDGICGSSVSRMENI
 MWRSEVELNAILLENGVQLTVVGSVKNPMWRGPQRLPVPVNLPHGWKAWGKSYFVRAAKTNSFVVDGDTLKECPLKHRA
 WNSFLVEDHGFVFTSVWLKVREDYSLECDPAVIGTAVKGKEAVHSDLGWIESEKNDTWRLKRAHLEIMKTCEWPKSHTLWTD
 GIEESDLIPKSLAGPLSHHNTREGYRTQMKGPWHSEELIRFEPCGTKVHVEETCGTRGPSLRSTTASGRVIEEWCCRECTMPPLSF
 RAKDGCWYGMIEPRKEPESNLVRSMTAGSTDHMDHFSGLVLVILLMVQEGLLKRMTHKIIISTMAVLVAMILGGFMSDLAKL
 AILMGATFAEMNTGGDVLAHALIAAFKVRPALLVSIFIRANWTPRESMLLALASCLLQTAISALEGDLMLVINGFALAWLAIRAMVV
 PRTDNITLAILAALTPLARGTLLVAWRAGLATCGGFMLLSLKGKGSVKKNLFPVMAVGTLAVRLVDPINVVGLLLTRSGKRSWPPSE
 VLTAVGLICALAGGFAKADIEMAGPMAAVGLLIVSYVVSQSVDMYIERAGDITWEKDAEVTGNSPRLDVALDESGDFSLVEDDGP
 MREILKVVLMTCGMNPIAIPFAAGAWYVYVKTGKRSALWDVPAPEVKKGETTDGVYRVMTRRLLGSTQVGVGMQEGVFH
 TMWHVTKGSALRSGEGRDPYWGDKQDLVSYCGPWKLDAAWDGHSVEQLLAVPPGERARNIQLPGIFKTKDGDIGAVALDYP
 AGTSGSPILDKCGRVIGLYGNGVVIKNGSYVSAITQGRREEETPVECFEPMKLLKQLTVLDLHPGAGKTRRLPEIVREAIKTRLRVIL
 APTRVVAAEMEEALRGLPVRYMTTAVNVTHSGTEIVDLMCHATFTSRLLQPIRVPNYNLYIMDEAHFTDPSSIAARGYISTRVEMGE
 AAIFMTATPPGTRDAFPDSNPMDETEVEPERAWSSGFDWVTDHSGKTVWFVPSVRNGNEIAACLTAKAGKRVQLSRKTFETEF
 QKTKHQEWDFVTTDISEMGANFKADRVISRRCLKPVILDGERVILAGMPVTHASAAQRRGRIGRNPKNKPGDELYGGGCAETD
 EDHAHWLEARMILLDNIYLDGLIASLYRPEADKVAIEGEFKLRTQKTFVELMKRGDLPVWLAYQVAGITYTDRRWCFDGT
 NNTIMEDSVPAEVWTRHGEKRVLPKRWMDARVCSHAALKSFKEFAAGKRGAAFGVMEALGTLPGHMTERFQEAIDNLAVLMR
 AETGSRPYKAAAQPLPETLETIMLLGLLGTVSLGIFFVLMRNKGIGKMGFMVTLGASAWLMWLSEIEPARIACVLIVFLLVLIPE
 PEKQSRPQDNQMAIIIMVAVGLLGLITANELGWLERTKSDLSHLMGRREEGATIGFSMDIDLRPASAWAIYAALTTFITPAVQHAVT
 TSYNNYSLMAMATQAGVLFMGKGMPPFYAWDFGVPLLMIGCYSQTLPLTLIVAIILLVAHYMYLIPGLQAAAARAAQKRTAAGIM
 KNPVVDGIVVTDIDTMTIDPQVEKKMGQVLLIYAVVSSAISRATWGWGEAGALITAATSTLWEGSPNKYWNSSATSLCNIFRGSY
 LAGASLIYTVTRNAGLVKRRGGGTGETLGEKWKARLNQMSALEFYSYKSGITEVCREARRALKDGVATGGHAVSRGSAKLRLV
 ERGYLQPYGKVIDLGCGRGWSYAAATIRKVQEVKGYTKGGPGHEEPMLVQSYGWNIVRLKSGVDVFHMAAEPDCTLLCDIGESS
 SPEVEEARLRLVSMVGDWLEKRPAGAFKVLCPYTSTMMETLERLQRRYGGGLVRVPLSRNSTHEMYWVSGAKSNTIKSVSTTSQ
 LLGRMDGPRRPVKYEEVDNLGSGTRAVVSCAEPNMKIIGNRIERIRSEHAETWFFDENHPYRTWAYHGSYEAPTQGSASSLINGV
 VRLSKPWVVDVGTGAMTDTTPYGGQQRVFKEKVDTRVPDPQEGTRQVMSMVSSWLWKELGKHKRPRVCTKEEFINKVRSNAA
 LGAIFEEKEWKTAVEAVNDPRFWALVDKEREHLRGECQSCVYNMMGKREKKQGEFGKAKGSRAIYWMWLGARFLEFEALGFL
 NEDHWMGRENSGGGVEGLGLQRLGYVLEEMSRIPGGRMYYADDTAGWDTRISRFLENEALITNQMEKGHRALALAIKYTYQNK
 VVKVLRPAEKGTVMIDISRDQRGSGQVVTYALNTFTNLVVQLIRNMEAEVLEMQDLWLLRSEKVTNWVQSNQWDRKLRMA
 VSGDDCVVKPIDDRFAHALRFLNDMGKVRKDTQEWKPGTWDNWEVFPFCSHHFNKLHLKDGSRIVVPCRHQDELIGRARVSPG

AGWSIRETACLAKSYAQMWQLLYFHRRDLRLMANAICSSVPVDWVPTGRTTWSIHGKGEWMTTEDMLVVWNRVWIEENDHM
EDKTPVTKWTDIPYLGKREDLWCGSLIGHRPRTTWAENIKNTVNMVRRIGDEEKYMDYLSTQVRYLGEEGSTPGVL

SEQ ID NO: 74
9320_Zika_PF_1F
ttaggatccGTTGTTGATCTGTGTGAAT

SEQ ID NO: 75
9321_Zika_PF_1R
taactcgagCGTACACAACCCAAGTT

SEQ ID NO: 76
9322_Zika_PF_2F
ttaggatccTCACTAGACGTGGGAGTG

SEQ ID NO: 77
9323_Zika_PF_2R
taactcgagAAGCCATGTCYGATATTGAT

SEQ ID NO: 78
9324_Zika_PF_3F
ttaggatccGCATACAGCATCAGGTG

SEQ ID NO: 79
9325_Zika_PF_3R
taactcgagTGTGGAGTCCGGTGTCT

SEQ ID NO: 80
9326_Zika_PF_4F
ttaggatccGAATAGAGCGAARGTTGAGATA

SEQ ID NO: 81
9327_Zika_PF_4R
taactcgAGTGGTGGGTGATCTTCTTCT

SEQ ID NO: 82
9328_Zika_PF_5F
ttaggatcCAGTCACAGTGGAGGTACAGTAC

SEQ ID NO: 83
9329_Zika_PF_5R
taactcgagCRCAGATACCATCTTCCC

SEQ ID NO: 84
9330_Zika_PF_6F
ttaggatCCCTTATGTGCTTGGCCTTAG

SEQ ID NO: 85
9331_Zika_PF_6R
taactcgagTCTTCAGCCTCCATGTG

SEQ ID NO: 86

9332_Zika_PF_7F
ttaggatccAATGCCCACTCAAACATAGA

SEQ ID NO: 87
9333_Zika_PF_7R
taactcgagTCATTCTCTTCTCAGCCCTT

SEQ ID NO: 88
9334_Zika_PF_8F
ttaggatccAAGGGTGATCGAGGAAT

SEQ ID NO: 89
9335_Zika_PF_8R
taactcgagTTCCCTTCAGAGAGAGGAGC

SEQ ID NO: 90
9336_Zika_PF_9F
ttaggatccTCTTTGCAAACGCGATC

SEQ ID NO: 91
9337_Zika_PF_9R
taactcgagTCCAGCTGCAAAGGGTAT

SEQ ID NO: 92
9338_Zika_PF_10F
ttaggatccGTGTGGACATGTACATTGA

SEQ ID NO: 93
9339_Zika_PF_10R
taactcgagCCCATTGCCATAAAGTC

SEQ ID NO: 94
9340_Zika_PF_11F
ttaggatccTCATACTGTGGTCCATGGA

SEQ ID NO: 95
9341_Zika_PF_11R
taactcgagGCCCATCTCAACCCTTG

SEQ ID NO: 96
9342_Zika_PF_12F
ttaggatccTAGAGGGCTTCCAGTGC

SEQ ID NO: 97
9343_Zika_PF_12R
taactcgAGATACTCATCTCCAGGTTTGTTG

SEQ ID NO: 98
9344_Zika_PF_13F
ttaggatccGAAAACAAAACATCAAGAGTG

SEQ ID NO: 99
9345_Zika_PF_13R

taactcgagGAATCTCTCTGTCATGTGTCCT

SEQ ID NO: 100

9346_Zika_PF_14F

ttaggatccTTGATGGCACGACCAAC

SEQ ID NO: 101

9347_Zika_PF_14R

ttaggatccGTTGTTGATCTGTGTGAAT

SEQ ID NO: 102

9348_Zika_PF_15F

taactcgagCAGGTCAATGTCCATTG

SEQ ID NO: 103

9349_Zika_PF_15R

ttaggatccTGTGTGTTCTATTGCTGGT

SEQ ID NO: 104

9350_Zika_PF_16F

taactcgaGTGATCAGRGCCCCAGC

SEQ ID NO: 105

9351_Zika_PF_16R

ttaggatccTGCTGCCCAGAAGAGAA

SEQ ID NO: 106

9352_Zika_PF_17F

taactcgaGCACCAACAYGGGTCTT

SEQ ID NO: 107

9353_Zika_PF_17R

ttaggatcCTCAAGGACGGTGTGGC

SEQ ID NO: 108

9354_Zika_PF_18F

taactcgagCAATGATCTTCATGTTGGG

SEQ ID NO: 109

9355_Zika_PF_18R

ttaggatccTATGGGGGAGGACTGGT

SEQ ID NO: 110

9356_Zika_PF_19F

taactcGAGCCCAGAACCTTGGATC

SEQ ID NO: 111

9357_Zika_PF_19R

ttaggatcCAGACCCCAAGAAGGC

SEQ ID NO: 112

9358_Zika_PF_20F

taactcgagCCCCTTGGTCTTGCT

SEQ ID NO: 113
9359_Zika_PF_20R
ttaggatccAGGAAGGATGTATGCAGATG

SEQ ID NO: 114
9360_Zika_PF_21F
taactcgagACATTGCGCATATGATTTTG

SEQ ID NO: 115
9361_Zika_PF_21R
ttaggatccAGGAAGGACACACAAGAGT

SEQ ID NO: 116
9362_Zika_PF_22F
taactcgagACAGGCTGCACAGCTTT

SEQ ID NO: 117
9363_Zika_PF_22R
ttaggatccTCTCTCATAGGGCACAGAC

In some embodiments, the Zika virus has a polyprotein, including an envelope (E) protein, with an amino acid sequence provided by any one of SEQ ID NO: 14-69. In some embodiments, the polyprotein or E protein sequence is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical to any one of SEQ ID NOs: 2-69 or 72.

The terms "identical" or percent "identity" in the context of two or more nucleic acids or amino acid sequences refer to two or more sequences or subsequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (*e.g.*, at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length. In some embodiments, the identity exists over the length of a protein, such as the E protein.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. Methods of alignment of sequences for comparison are well known in the art. See, *e.g.*, by the local homology algorithm of Smith and Waterman (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48:443, 1970, by the search for

similarity method of Pearson and Lipman. Proc. Natl. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, Jalview and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group. 575 Science Dr., Madison. WI), by multi sequence alignment implementation using e.g. CLUSTALW (Larkin et al., (2007). Bioinformatics, 23, 2947-2948.) or MAFFT (Kato & Toh 2008 Briefings in Bioinformatics 9:286-298), or by manual alignment and visual inspection (see. *e.g.*, Brent et al., Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (Ringbou ed., 2003)). Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., Nuc. Acids Res. 25:3389-3402, 1997 and Altschul et al., J. Mol. Biol. 215:403-410, 1990, respectively.

EXAMPLES

Example 1: Production of a Zika drug substance suitable for application as a vaccine in humans and animals

Materials and Methods:

For the production of ZikaV the JEV process platform (Srivastava et al., Vaccine 19 (2001) 4557-4565; US 6,309,650B1) was used as a basis. Small changes of certain process steps were adapted to ZikaV properties and to improve purity. A short summary of the process steps is outlined below (see also Figure 9A and B). Briefly, the unexpected and novel purification properties of protamine sulphate (PS) were evaluated in purification processes for Zika Virus. As shown in Figure 10, non-infectious virus particle aggregates, HCP and other LMW impurities were removed by PS precipitation as shown by removal of aggregate shoulder in SEC-HPLC and no loss of infectious virus titer by PS treatment. Further optimization of the Zika purification protocol is provided below.

Upstream:

- Roller Bottle based Vero cell expansion (25x850cm² CellBind):
- 5% CO₂, 35°C, MEM+2mM L-Glutamine + 10% FBS
- Infection with ZikaV research Master Seed Bank (rMSB) at MOI 0.01
- Virus Production without serum
- 5% CO₂, 35°C, MEM+2mM L-Glutamine
- Multiple harvests (days 2, 3, 5 and 7) with re-feed
- Sterile filtration of harvests and storage at 2-8°C until further processing

Downstream:

- Pooling of harvests and concentration by ultrafiltration (100kDa)
- Stabilization of concentrated harvest (Tris/10% sucrose) for storage if required (-80°C)
- Removal of hcDNA by Protamine Sulphate (2 mg/mL)
- Sucrose Gradient Purification (optimized three layered gradient)
- Formaldehyde Inactivation (0.02%, 22°C, 10 days), neutralization with Na-metabisulfite
- Dilution to DS antigen target content and formulation with Aluminium hydroxide (0.5mg Al/mL)

Zika Virus Strain H/PF/2013 was originally isolated from a 51-year-old woman (accession number KJ776791.1, also SEQ ID NO: 13 herein) from French Polynesia. A sample was obtained from the European Virus Archive (EVAg; Ref-SKU: 001v-EVA1545). Based on this material, a research master

seed bank (rMSB) was prepared on Vero cells as the cell substrate and the genomic sequence was checked by sequencing. Because the genomic sequence at the 5' and 3' flanking sequences of Zika virus strain H/PF/2013 was unknown, primers for sequencing were designed in those regions based on other Zika virus strains whereas the internal primers were designed from the published sequence (SEQ ID NOs: 74 to 117, see also Table A). The sequence obtained from the rMSB by use of these primers is provided by SEQ ID NO: 72. There was 100% overlap of the sequence with the published sequence of Zika Virus Strain H/PF/2013 (SEQ ID NO: 13). However, we sequenced additional regions 5' (an additional 40 bp) and 3' (an additional 160 bp) represented in SEQ ID NO: 72. In a preferred embodiment, the Zika virus of the invention comprises SEQ ID NO: 72. The genomic RNA is somewhat longer than the sequence according to SEQ ID NO: 72 (perhaps an additional 200 bp). Additionally, a Zika virus adapted to a host cell such as e.g. Vero cells may be expected to contain one or more mutations. For these reasons, the Zika virus of the current invention comprises the sequence of SEQ ID NO: 72 or, preferably, a sequence with at least 95%, 96%, 97%, 98%, or at least 99% sequence identity to the sequence provided by SEQ ID NO: 72. Furthermore, because the viral genome is likely to contain even further flanking regions to SEQ ID NO: 72; in one embodiment, the Zika virus of the invention contains the sequence of SEQ ID NO: 72 and optionally further comprises extensions at the 5' and/or 3' ends of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 110, at least 120 or at least 130 nucleotides. In a preferred embodiment, the Zika virus comprises at least the coding sequence for the entire polyprotein of Zika Virus Strain H/PF/2013 of the invention i.e. the amino acid sequence of SEQ ID NO: 73 or a polyprotein with at least 95%, 96%, 97%, 98%, or at least 99% sequence identity to the sequence provided by SEQ ID NO: 73. Furthermore, the Zika virus comprises at least the coding sequence for the E-protein of Zika Virus Strain H/PF/2013 of the invention SEQ ID NO: 47 or an E-protein thereof with at least 95%, 96%, 97%, 98%, or at least 99% sequence identity to the sequence provided by SEQ ID NO: 47.

Virus growth on Vero Cells

Vero cells were grown in Eagle's minimal essential medium (EMEM) containing 10% fetal bovine serum (FBS). Roller bottle cultures of Vero cell monolayers were infected with Zika Virus Strain H/PF/2013 at a multiplicity of infection (moi) of 0.01 plaque forming units (pfu) per cell. After 2 hours of virus adsorption, the cultures were washed 3 times with PBS and fed with EMEM without FBS and incubated at +35°C with 5% CO₂. Infected Vero cell cultures were incubated until the virus titer reaches a desired level.

The culture medium was harvested at days 2, 3, 5 and 7 and were pooled from those harvest days and then centrifuged in a standard centrifuge. The supernatants were then filtered. Virus culture supernatants were concentrated by TFF ultrafiltration to remove cell culture media components and to reduce batch volume.

Evaluation of harvest Procedure

The current JEV harvest process has scheduled harvests on days 3, 5, 7 and 9 post infection. To mimic the JEV process roller bottles were infected with ZIKV bank P4-FBS at an MOI of 0.01 in infection medium (MEM with 2% FBS + 2mM L-glutamine) for 2 hours. After removing the inoculum the cells were washed twice with PBS and 200 mL production medium (MEM+ 2mM L-glutamine) was added.

After taking a sample on day 2 the first virus harvest was conducted on day 3 after infection. At this point significantly higher CPE could be observed compared to cells where virus was removed on day 2. Plaque assay analysis showed that the viral titers on day 2 were in the same range as for the standard harvesting schedule. However, starting with the day 3 harvest, the observed titers were significantly lower correlating with the increased CPE observed compared to the standard harvest schedule. On day 5 post infection no more living cells could be observed at all and the experiment was terminated with a final day 5 harvest.

Table 3: The calculated titers per plaque assay are summarized in the list below.

	Log 10 PFU/mL
sample day2	7.02
harvest day 3	6.66
harvest day 5	6.26

This finding led to an optimized harvest schedule to better control of CPE and allow additional harvest day 5 and 7, see Figure 15. For both harvest days the optimized ZikaV protocol yield significant higher virus titers compared to the modified protocol showing that the time of the first harvest is crucial for production yields. Additionally first harvesting at day 3 results in maximum 2 harvest points whereas first harvesting at day 2 allows for 4 harvest points further increasing the yield gain.

Downstream Purification of Zika virus

The purification process was carried out at room temperature (18-22°C) unless stated otherwise. Virus purification started with concentration of filtered combined harvest using 100 kDa cut-off TFF ultrafiltration modules to remove cell culture media components and reduce batch volume. After

concentration, the pooled filtered harvest material was adjusted to a final concentration of 25 mM Tris pH 7.5 and 10% sucrose (w/w) using stock solution of both components (see Figure 11 for SEC-HPLC of different harvests prior to PS treatment). This allowed for freezing the concentrated harvest at $<-65^{\circ}\text{C}$ if required.

Host cell DNA and protein reduction as well reduction of non-infectious virus aggregates in the concentrated material was achieved by precipitation with protamine sulphate (2 mg/mL) followed by sucrose density centrifugation ($2-8^{\circ}\text{C}$) as final polishing step (see Figure 20 for SEC-HPLC of different harvests post PS treatment). The purification process was designed to be completed within 2 working days with SGC starting on end of day 1 followed by fractionation and SDS-PAGE analysis on day 2. The sucrose gradient fractions were stored at $2-8^{\circ}\text{C}$ during the SDS-PAGE analysis (Silver staining) to identify the pure fractions containing ZikaV (see Figure 21). After pooling the relevant fractions, the pool was diluted and inactivated by Formalin. After pooling the relevant fractions of sucrose gradient centrifugation, the pool was diluted 1:3 in PBS and inactivated by Formalin (0.02% v/v, 200ppm). Fractions were subjected to analysis by SDS-PAGE.

Effect of PS treatment on virus recovery

Samples of individual 30x concentrated harvests days 2, 3, 5 and 7 were analysed before (Figure 11) and after PS (Figure 12) treatment by SEC-HPLC and plaque assay. SEC-HPLC was used for determination of relative total ZikaV content (active + inactive) expressed as peak area, whereas the rel. ZikaV peak purity is given as relative content of virus monomer population to total virus peak. Plaque assay states the content of total active virus particles in each sample. Experimental results are summarized in Table 4. The virus peak recovery by SEC-HPLC was only between 12 to 36% with peak purity after PS treatment in the range of $>90\%$ (no virus aggregates detected). The recovery of active virus particles by plaque assay was all $> 100\%$ (130-700%, range within the variability of the assay) showing that no active virus particles were lost during PS treatment. These results show that during PS treatment only non-infective (immature and/or aggregated virus) particles were removed.

Table 4: ZikaV recovery by SEC-HPLC and plaque assay before and after PS treatment.

SEC-HPLC

	Peak area mAU*min			
Harvest day	30x conc	30x + PS	SEC Recovery (%)	rel. virus monomer

				content after PS (%)
Day 2	101.36	18.63	18	89%
Day 3	144.51	17.48	12	90%
Day 5	19.97	5.92	30	96%
Day 7	68.80	24.43	36	99%

Plaque Assay

	PFU/mL		
Harvest day	30x conc	30x + PS	Plaque Recovery (%)
Day 2	3E+08	5E+08	179
Day 3	2E+08	4E+08	193
Day 5	1E+08	9E+08	700
Day 7	3E+08	4E+08	132

Sucrose gradient centrifugation

The PS treated harvest was split in two parts and loaded on two centrifuge bottles. Sucrose density gradient centrifugation (SGC) was used for final concentration and polishing of the ZikaV material. The ZikaV PS treated concentrated harvest was loaded on top of a solution consisting of three layers of sucrose with different densities. The three sucrose layers were selected based on a preliminary study which showed the formation of a linear sucrose gradient and complete separation of the virus particles from residual contaminants as demonstrated for ChikV (Fig. 15D). The optimal volumes of the sucrose solutions were determined empirically. The volumes of individual layers for a centrifugation in 100 mL bottle scale are shown in Table 5.

Table 5: Individual layers/volumes for a centrifugation in bottle.

Solution	Volume (mL)
PS treated harvest in 10% sucrose (L)	40

15% sucrose (J)	15
35% sucrose (I)	15
50% sucrose (H)	20
Total volume	90

The sucrose gradient bottles were prepared by stratifying the individual sucrose layers. A plastic tube was attached to peristaltic pump tubing. The plastic tube was mounted on a laboratory stand using a clamp and placed into the centrifuge bottle. The nozzle of the plastic tube was touching the bottom of the bottle. Using a peristaltic pump the ZikaV material and the sucrose solutions were pumped into the cylinder. A measuring cylinder was used as feed vessel. The first solution pumped was the ZikaV material as it represented the solution of lowest density (10 % sucrose (w/w)). After the ZikaV material the sucrose solutions were pumped in ascending order starting with the 15 % (w/w) solution J, followed by 35 % sucrose solution I and finishing with the highest density sucrose solution H (50 % (w/w)). The described setup is shown in Figure 14. After all sucrose solutions were transferred the plastic tubing was carefully removed in order not to disturb the layers.

Prior to centrifugation the centrifuge was pre-cooled to 4°C. The prepared SG bottles were carefully transferred into the pre-cooled rotor. (Note: Sudden movement of the bottles during transfer to the rotor must be avoided in order not to disturb the sucrose layers.) The bottles were centrifuged at ~11.000 RCF max at 4 °C for at least 20 hours, no brake/deceleration activated. In case a different centrifuge system with a different rotor is used the necessary speed and centrifugation times need to be calculated based on the k-factor in order to achieve comparable centrifugation efficiency.

Harvesting of the sucrose gradient was done manually using a peristaltic pump. A plastic tube attached to peristaltic pump tubing was used for harvesting the sucrose gradient. The bottle containing the gradient was mounted onto a laboratory stand in a tilted position (~12°) using a clamp. The plastic tubing was then placed into the bottle touching the bottom edge of the bottle and was fastened in position using a clamp. This resulted in a small gap of 1-2 mm between the tubing inlet and the bottom of the bottle (see Figure 14).

Using a peristaltic pump set to a flow rate of 30 mL per minute the gradient was harvested and manually split into 2 mL fractions. A total number of 32 fractions per bottle were harvested (~ 64 mL) and the remaining volume was discarded. The fractions were immediately tested by SDS-PAGE / silver stain to

identify the virus containing fractions with sufficient high purity. Representative SDS-PAGE is shown in Figure 14. Fraction 10-14 were pooled and further processed.

The purified viral solution was inactivated by incubation with 0.02% formaldehyde over a period of ten days in a 22°C controlled-temperature incubator. The formaldehyde is neutralized by addition of sodium metabisulphite on the tenth day.

The sucrose gradient pool (~17mL after sampling) was further diluted 3-fold with PBS to a final volume of 51 mL in a PETG container. A volume of 1% formaldehyde (10,000 ppm) solution equivalent to 1/50 of the final volume of the pre-formaldehyde pool was added to this pool resulting in an effective concentration of 200 ppm. The formaldehyde-treated solution was mixed on a magnetic stirrer for 10 minutes. After sampling, the formaldehyde-treated viral solution was placed within a cooled incubator at 22°C ± 2°C. On Day 5 post addition of formaldehyde, the formaldehyde-treated viral solution was filtered through a 0.2 µm filter and then placed in the incubator at 22°C ± 2°C again. On Day 10, after removing the 10-Day inactivation final sample, a volume of 1 % (of the weight of the final formaldehyde-treated viral solution) of 200 mM-sodium metabisulphite solution (2mM final concentration) was aseptically transferred into the PETG container containing the formaldehyde-treated viral solution. After mixing for 5 minutes on a magnetic stirrer, the neutralized inactivated viral solution is held at room temperature (20 to 25°C) for a minimum of 30 minutes. After sampling, the neutralized inactivated viral solution is stored at 5°C ± 3°C until further processing.

Inactivation by formaldehyde

Critical parameters for this step are final formalin concentration, temperature, mixing and transfer into a new container. A preliminary acceptance criterion for maximum pfu/mL (determined by plaque assay) has been set on the diluted pool pre formaldehyde treatment.

The quality of the neutralized inactivated viral solution was monitored by the following parameters: Plaque assay on Day 10, SEC-HPLC, SDS-PAGE/Western Blot.

Interestingly, SEC-HPLC analysis of samples taken during the inactivation period followed by neutralization with bisulfite showed more or less constant peak area throughout the inactivation period. This is in contrast to JEV where losses of viral particles up to 60% are observed using the process disclosed by Srivastava et al. Vaccine 19 (2001) 4557-4565. In a scale-down model the viral losses were even much higher due to surface/area ratio at smaller scale and high losses due to unspecific adsorption. Differences of the ZikaV inactivation experiment and JEV inactivation were noticed as follows:

A) Much higher purity of ZikaV SGP pool with regard to residual PS ($<2\mu\text{g/mL}$) compared to JEV. The 3-fold ZikaV inactivated sample contained therefore $<<1\mu\text{g/mL}$ of residual PS. Commercial JEV SGP pool contains on average $\sim 120\mu\text{g/mL}$ (up to $152\mu\text{g/mL}$ possible). The average dilution to inactivation solution of ~ 14 -fold results in a residual PS content up to $\sim 11\mu\text{g/mL}$. It may be that higher amount of residual PS could cause virus precipitation due to cross-linking / reaction with formalin.

B) ZikaV inactivation sample contained $\sim 10\%$ sucrose (3-fold dilution of SGP pool containing ~ 30 - 35% sucrose). Sucrose might have stabilizing effect of viral ZikaV particles during treatment with formalin.

Dilution to DS and Formulation with Aluminium hydroxide (DP)

For preparation of ZikaV drug substance used in mouse potency assay an antigen content (expressed as total viral particles or SEC peak area) of 5 times higher compared to Ixiaro was targeted. The basis for determination of antigen content was SEC-HPLC. Briefly, a Superose 6 10/300 Increase column (GE Healthcare) equilibrated with PBS + 250 mM NaCl, pH 7.4 at 1 ml/min and 25°C , was used to detect ZikaV at 214 nm detection wavelength in harvest samples and throughout the downstream process. In the current JEV process the antigen content in NIV is determined by a specific ELISA. A good correlation was observed between antigen content determined by ELISA and SEC-HPLC. On average, the antigen content in commercial NIV samples is in the range of 33 AU/mL corresponding to $\sim 5.2\text{mAU}$ JEV peak area, see Figure 21.

ZikaV NIV day10 (Zika peak $\sim 36\text{ mAU}$, analysed on Waters HPLC/Superose6 Increase column) was diluted with PBS to a target of 6.3 ($\sim 5.7\text{x}$ dilution). Aluminium hydroxide was added to a final concentration of 0.5 mg/mL Aluminium (1/20 v/v Alum 2% stock solution added) to prepare ZikaV Drug Product (DP). The DP was gently mixed for 5 min. An aliquot of the DP was removed, Alum sedimented by centrifugation and the clear supernatant analysed by SEC-HPLC. No ZikaV peak was detected in the supernatant indicating complete adsorption (estimated as $>95\%$) of viral particles on the mineral adjuvant. Formulated ZikaV DP was stored at 2 - 8°C .

The impurity profile of the inactivated Zika virus DS is comparable to the profile of JEV DS with the exception of a lower PS content (Table 6).

Table 6: Determination of impurity profile in Zika and JEV DS samples:

	Specification (JEV DS)	JEV	Zika
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HCP (ng/mL)	<100 LOQ 12 ng/mL	<LOQ	<LOQ
DNA (pg/mL)	<200 LOQ 40 pg/mL	<40	<40
Aggregates by SEC-MALLS (%)	Not specified, part of characterization LOQ 5%	<LOQ	<LOQ
PS (μg/mL)	Specification only at SGP pool to demonstrate consistent process performance (19-152 μg/mL), *PS content in DS calculated based on PS content in SGP pool (~100 μg/mL) and average dilution factor (~28x) to DS; LOQ 2 μg/mL	~4*	<<LOQ

*Typical PS impurity in a JEV sample produced in accordance with protocol disclosed in Srivastava et al. Vaccine 19 (2001) 4557-4565.

SEC-MALLS Results

A representative SEC-HPLC elution profile of ZikaV NIV at 214 nm detection wave length is shown in Figure 16. Note that BSA (50 μg/mL) was added to the sample to minimize losses in HPLC glass vial due to unspecific surface adsorption. ZikaV monomer content was estimated as ~98% with a multimer content of ~2%.

SEC-MALLS analysis (Figure 17) of the sample confirmed the radius R_z of the monomer ZikaV population peak 1 as 21.6 nm and ~49 nm for the multimer peak 2. Cumulative particle size distribution showed that 89% of all viral particles are within a radius range between 18 to 25 nm (Figure 18).

Results confirm purity and homogeneity of ZikaV NIV.

Viral titer by plaque assay

Table 7: Active ZikaV pfus were quantified by plaque assay throughout the process.

Sample	Pfu/mL
Harvest day 2 (filtered)	6.4×10^7
Harvest day 3 (filtered)	1.0×10^8
Harvest day 5 (filtered)	1.5×10^8
Harvest day 7 (filtered)	1.1×10^8
PS treated harvest 300x concentrate (=SGP load)	9.0×10^8
SGP pool	8.9×10^8
Inactivation start (SGP pool 1:3 diluted)	3.4×10^8
Inactivation day 5	<LOD
Inactivation day 10	<LOD

Comparison of PS and Benzonase on process performance

A direct comparison of DNA removal method of concentrated ZikaV harvest pool was done. One aliquot was treated with PS (2 mg/mL, 15min at room temperature), the other aliquot was treated with Benzonase (50 U/mL, 2 mM MgCl₂, 4h RT, 48h 2-8°C). Both samples were further purified by sucrose gradient as described in this report. Interestingly, the Benzonase treated samples did not yield any pure fractions after sucrose gradient centrifugation of the treated ZikaV harvest. In those fractions where the specific virus bands were detected, a high amount of host cell protein was detected throughout the collected fractions. The PS treated material resulted in pure ZikaV containing fractions as expected. This finding may suggest that PS is not only effective for DNA removal by precipitation; in addition it improves the recovery of virus particles in the gradient by disrupting interaction of DNA (fragments) and virus particles. Benzonase treatment does not remove DNA, it only results in its fragmentation. Residual DNA fragments might still interact with virus particles and residual HCPs resulting in cross-contamination and co-purification in the sucrose gradient. Pooled SGP fractions were also analysed by SEC-HPLC. Although a large peak was detected, SDS-PAGE confirmed that this sample was highly contaminated with HCPs. A large peak might be detected at UV214 and 280nm after SEC-HPLC analysis due to possible interaction of HCPs with large virus particles, changing the UV absorbance.

Immunogenicity of Vero grown Zika virus*Immunization of mice*

Prior to immunization, groups of ten 6-week-old female CD1 mice were bled via vena facialis and pre-immune sera were prepared. One intraperitoneal immunizations of 200 µL were administered. A dose titration (12 µg, 3 µg, 1 µg, 0.33 µg, 0.11 µg, 0.037 µg and 0.012 µg, equivalent to the protein amount in IXIARO) of inactivated Zika virus formulated with aluminium hydroxide (Al(OH)₃) at a final concentration of 0.7%. Three weeks after immunization, blood was collected and immune sera were prepared. All animal experiments were conducted in accordance with Austrian law (BGB1 Nr. 501/1989) and approved by “Magistratsabteilung 58”.

Plaque reduction neutralization test (PRNT)

Twelve well plates were used for PRNT. Each well was seeded with 1 mL medium containing 4×10^5 Vero cells and incubated 35°C with 5% CO₂ overnight. Pools of heat inactivated sera from each dose group were tested in triplicate. The target viruses (H/PF/2013 (SEQ ID NO: 13) or MR766 (SEQ ID NO: 11)) were diluted to 100 pfu/165 µL. Equal volumes of target virus and serum dilution were incubated at 35°C with 5% CO₂ for 1 hour. The cell culture medium was aspirated from the Vero cells and 330 µL of the mixture target virus/serum dilution were added to each well and the plates were rocked back and forth 5 times before incubating for 2 hours at 35°C with 5% CO₂. To each well 1 mL of a 2% methylcellulose solution containing EMEM and nutrients was added, the plates were then incubated for 5 days at 35°C with 5% CO₂ before staining the cells for 1 hour with crystal violet/5% formaldehyde and subsequently washed 3 times with deionized water. The plates were air dried and the numbers of plaques in each well were manually counted.

Results

Neutralization was observed with serum pools from mice immunized with inactivated Zika virus vaccine (H/PF/2013) down to 37 ng (dosing equivalent to the amount protein in IXIARO®) against Zika viruses of both the Asian (H/PF/2013) and African (MR766) lineages (Figures 19 and 20, respectively). Complete inhibition was seen at the 1:20 serum dilution with an immunization dose down to 110 ng (dosing equivalent to the amount protein in IXIARO®). The neutralization of both the Asian (H/PF/2013) and African (MR766) lineages of the Zika virus was equivalent, which indicates high cross-neutralization between different Zika virus strains of the inactivated Zika virus vaccine (H/PF/2013).

Another neutralization assay was performed using the microneutralization assay as described by Larocca, et al. (2016, Nature doi:10.1038/nature18952). It was found that the inactivated Zika virus of the current invention had an MN50 (microneutralization) titer of 90 at 1 µg of inactivated purified virus.

Further methods: The immunogenicity of inactivated Zika virus preparations is assessed using a mouse model of Zika infection. Groups of adult mice are immunized subcutaneously (s.c.) with 500, 50, or 5 ng of inactivated Zika virus with adjuvant (*e.g.* aluminium hydroxide with or without IC31®), or without adjuvant. An additional group of mice receive PBS as a negative control. Each group is administered the indicated inoculum at t=0 and in some cases also at three to four weeks later (t=3/4). Beginning approximately three weeks after administration of the last immunization, serum samples are obtained from each of the mice at regular intervals. The serum samples are tested for the presence of neutralizing antibodies using PRNT.

The *in vivo* protective efficacy of the inactivated Zika virus preparations is also assessed using a mouse model of Zika infection, *i.e.* IFN-alpha/beta receptor knock-out mice (A129) (see *e.g.* Dowall et al., 4. March 2016, <http://dx.doi.org/10.1101/042358>) or blocking of the IFN-alpha/beta receptor by administration of anti-IFN-alpha/beta receptor monoclonal antibodies to C57BL/6 or BALB/c mice (see *e.g.* Pinto et al., 7. December 2011, DOI: 10.1371/journal.ppat.1002407). For protection assays, groups of 10 three- to eight-weeks-old A129, C57BL/6 or BALB/c mice are inoculated subcutaneously in the hindquarters with inactivated Zika virus with adjuvant (aluminium hydroxide) or without adjuvant at t=0. Age-matched controls are inoculated with PBS or non-specific antigens in alum. Mice are optionally boosted with a second administration of the indicated inoculation three to four weeks later. The mice are then challenged subcutaneously at three to eight weeks post immunization by inoculation with a deadly dose of live Zika virus. One day prior to challenge of C57BL/6 and BALB/c mice, they are passively administered (intraperitoneally) anti-IFN-alpha/beta receptor monoclonal antibodies. Challenged mice are monitored daily for morbidity and mortality for up to twenty-one days. Another alternative is to challenge intracranially adult vaccinated/non-vaccinated adult mice and observe protection.

It is expected that the Zika virus produced by the process of the invention will provide very similar functional read-outs in *in vitro*, *in vivo* and finally human trials as the currently licensed JEV vaccine in the EU and US and elsewhere, IXIARO®. The dosage may alter but due to the very similar impurity profile and almost identical manufacture, a very similar efficacy and safety result will be expected as was determined for the currently licensed JEV vaccine (licensed in the EU and US and elsewhere).

Discussion & Conclusion

The existing manufacturing platform for production of inactivated JEV vaccine IXIARO® was used as a basis for a manufacturing feasibility study of inactivated ZikaV vaccine candidate (Asian strain H/PF/2013). The virus was produced on Vero cells cultivated in roller bottles. The virus was purified by PS treatment followed by an optimized sucrose gradient. Inactivation was done by formalin treat (0.02 %, 10 days at 22 °C). For exploratory immunization studies in mice, a DP formulated with Alum was prepared with an estimated 5-fold higher virus particle content compared to IXIARO®, the commercial JEV Vaccine. The impurity profile of the DS met all criteria as defined in the specification for IXIARO®, the commercial JEV vaccine. The neutralization of both the Asian (H/PF/2013) and African (MR766) lineages of the Zika virus was equivalent, which indicates high cross-neutralization between different Zika virus strains of the inactivated Zika virus vaccine (H/PF/2013).

The in vivo data regarding immunogenicity of the inactivated Zika virus vaccine of the current invention indicates that the virus is surprisingly potently immunogenic and also highly cross-protective (very similar immunogenicity in African and Asian strains). Data indicate that immunogenicity was higher than the recently reported inactivated Zika virus vaccine candidate (Larocca, et. al, 2016, supra.). Inactivated viruses are among the safest vaccines and especially preferred for deliver to populations where safety is especially concerning, such as pregnant women, children and immunocompromised individuals, which makes the herein disclosed inactivated Zika virus particularly suitable. Obtaining a high titer of inactivated virus is a challenge in the field. The herein disclosed process for purifying inactivated Zika virus results in not only a high yield, but also a very pure drug substance.

Further more detailed aspects of the invention:

A1. A Zika virus vaccine comprising an optimally inactivated Zika virus particle, wherein the Zika virus particle is able to seroconvert a subject that is administered the Zika virus vaccine with at least a 70% probability.

A2. The Zika virus vaccine of A1, wherein the Zika virus particle is able to seroconvert the subject that is administered the Zika virus vaccine with at least a 80%, 85%, 90%, or 95% probability.

A3. The vaccine of A1 or A2, wherein the Zika virus particle has a RNA genome corresponding to the DNA sequence provided by any one of the nucleic acid sequences of SEQ ID NOs: 2-13 or 72, or a variant nucleic acid sequence that is at least 88% identical to any one of SEQ ID NOs: 2-13 or 72 and able to pack a virulent Zika virus.

A4. The vaccine of any one of A1-A3, wherein the Zika virus particle has an E protein selected from the amino acid sequences provided by any one of SEQ ID NOs: 14-69, or a variant amino acid sequence that is at least 95% identical to any one of SEQ ID NOs: 14-69 and able to pack a virulent Zika virus.

A5. The vaccine of any one of A1-A4, wherein the Zika virus is inactivated by chemical inactivation, thermal inactivation, pH inactivation, or UV inactivation.

A6. The vaccine of A5, wherein the chemical inactivation comprises contacting the Zika virus with a chemical inactivation agent to completely inactivate the Zika virus as measured by plaque assay.

A7. The vaccine of A6, wherein the chemical inactivation comprises contacting the Zika virus with formaldehyde.

A8. The vaccine of A7, wherein the formaldehyde inactivation comprises contacting the Zika virus with formaldehyde for between 2-10 days.

A9. The vaccine of any one of A5-A8, wherein the chemical activation is performed at about +4°C or about +22°C.

A10. The vaccine of any one of A1-A9, further comprising an adjuvant.

A11. The vaccine of A10, wherein the adjuvant is an aluminum salt adjuvant.

A12. The vaccine of A11, wherein the aluminum salt adjuvant is aluminium hydroxide or aluminium phosphate salt.

A13. The vaccine of any one of A10-A12, wherein the vaccine comprises or further comprises an adjuvant comprising a peptide and a deoxyinosine-containing immunostimulatory oligodeoxynucleic acid molecule (I-ODN).

A14. The vaccine of A13, wherein the peptide comprises the sequence KLKL5KLK (SEQ ID NO: 71) and the I-ODN comprises oligo-d(IC)13 (SEQ ID NO: 70).

A15. The vaccine of any one of A1-A14, further comprising one or more pharmaceutically acceptable excipient.

B1. A kit comprising a Zika virus vaccine of any one of A1-A15.

B2. The kit of B1, further comprising a second vaccine.

B3. The kit of B2, wherein the second vaccine is a West Nile virus vaccine, a Japanese Encephalitis virus vaccine, a yellow fever virus vaccine, a Dengue virus vaccine or a Chikungunya virus vaccine.

- C1. A method, comprising administering a first dose of a therapeutically effective amount of the Zika virus vaccine of any one of A1-A15 to a subject in need thereof.
- C2. The method of C1, further comprising administering a second dose of a therapeutically effective amount of the Zika virus vaccine.
- C3. The method of C1 or C2, wherein the second dose of the Zika virus vaccine is administered about 7 days after the first dose of the Zika virus vaccine.
- C4. The method of C1 or C2, wherein the second dose of the Zika virus vaccine is administered about 14 days after the first dose of the Zika virus vaccine.
- C5. The method of C1 or C2, wherein the second dose of the Zika virus vaccine is administered about 28 days after the first dose of the Zika virus vaccine.
- C6. The method of any one of C1-C5, wherein the administering results in production of Zika virus neutralizing antibodies.
- D1. A method of producing a Zika virus vaccine, comprising
- (i) passaging a Zika virus on Vero cells, thereby producing a culture supernatant comprising the Zika virus;
 - (ii) harvesting the culture medium of (i);
 - (iii) precipitating the harvested culture medium of (ii), thereby producing a Zika virus supernatant; and
 - (iv) optimally inactivating the Zika virus in the Zika virus supernatant of (iii) thereby producing an inactivated Zika virus.
- D2. The method of D1, further comprising concentrating the culture medium of (ii) prior to step (iii).
- D3. The method of D1 or D2, wherein the precipitating of (iii) comprises contacting the culture medium of (ii) with protamine sulfate or benzonase.

D4. The method of any one of D1-D3, further comprising (v) dialyzing the inactivated Zika virus of (iv), thereby producing a dialyzed Zika virus.

D5. The method of D4, further comprising (vi) filtering the dialyzed Zika virus of (v).

D6. The method of any one of D1-D5, wherein the inactivating is by chemical inactivation, thermal inactivation, pH inactivation, or UV inactivation.

D7. The method of D6, wherein the chemical inactivation comprises contacting the Zika virus with a chemical inactivation agent for at least 4 days.

D8. The method of D6 or D7, wherein the chemical inactivation agent comprises formaldehyde.

D9. The method of any one of D6-D8, wherein the chemical activation is performed at about +4°C or about +22°C.

D10. The method of D8 or D9, further comprising neutralizing the formaldehyde.

D11. The method of D10, wherein the neutralizing is performed with sodium metabisulfite.

E1. The use of the optimally inactivated Zika virus vaccine of any one of A1-A15 for the treatment and prevention of a Zika virus infection.

E2. The use of E1, wherein the inactivated Zika virus vaccine is administered in a first dose of a therapeutically effective amount to a subject in need thereof.

E3. The use of E2, wherein the inactivated Zika virus vaccine is administered in a second dose of a therapeutically effective amount to the subject.

E4. The use of E3, wherein the second dose of the inactivated Zika virus vaccine is administered about 7 days after the first dose of the Zika virus vaccine.

E5. The use of E3, wherein the second dose of the Zika virus vaccine is administered about 14 days after the first dose of the Zika virus vaccine.

E6. The use of E3, wherein the second dose of the Zika virus vaccine is administered about 28 days after the first dose of the Zika virus vaccine.

E7. The use of any one of E1-E6, wherein the vaccine administration results in production of Zika virus neutralizing antibodies.

F1. A pharmaceutical composition for use in the treatment and prevention of a Zika virus infection, wherein said pharmaceutical composition comprises the optimally inactivated Zika virus vaccine of any one of A1-A15.

F2. The pharmaceutical composition of F1, wherein the inactivated Zika virus vaccine is administered in a first dose of a therapeutically effective amount to a subject in need thereof.

F3. The use of F2, wherein the inactivated Zika virus vaccine is administered in a second dose of a therapeutically effective amount to the subject.

F4. The use of F3, wherein the second dose of the inactivated Zika virus vaccine is administered about 7 days after the first dose of the Zika virus vaccine.

F5. The use of F3, wherein the second dose of the Zika virus vaccine is administered about 14 days after the first dose of the Zika virus vaccine.

F6. The use of F3, wherein the second dose of the Zika virus vaccine is administered about 28 days after the first dose of the Zika virus vaccine.

F7. The use of any one of F1-F6, wherein the vaccine administration results in production of Zika virus neutralizing antibodies.

- G1. A Zika virus vaccine comprising an inactivated Zika virus particle, wherein the Zika virus vaccine is able to confer seroprotection on at least 70% of subjects that are administered the Zika virus vaccine.
- G2. The Zika virus vaccine of G1, wherein the Zika virus particle is able to confer seroprotection on at least 75%, 80%, 90%, 95%, 96%, 97%, 98%, or at least 99% of vaccinated subjects that are administered the Zika virus vaccine, preferably on at least 80% of subjects.
- G3. The vaccine of G1 or G2, wherein the Zika virus particle has a RNA genome corresponding to the DNA sequence provided by any one of the nucleic acid sequences of SEQ ID NOs: 2-13 or 72, or a variant nucleic acid sequence that is at least 88% identical to any one of SEQ ID NOs: 2-13 or 72 and able to pack a virulent Zika virus.
- G4. The vaccine of any one of G1 to G3, wherein the Zika virus particle has an E protein selected from the amino acid sequences provided by any one of SEQ ID NOs: 14-69, or a variant amino acid sequence that is at least 95% identical to any one of SEQ ID NOs: 14-69 and able to pack a virulent Zika virus.
- G5. The vaccine of any one of G1 to G4, wherein the Zika virus is inactivated by chemical inactivation, thermal inactivation, pH inactivation, or UV inactivation.
- G6. The vaccine of G5, wherein the chemical inactivation comprises contacting the Zika virus with a chemical inactivation agent for longer than is required to completely inactivate the Zika virus as measured by plaque assay.
- G7. The vaccine of G6, wherein the chemical inactivation comprises contacting the Zika virus with formaldehyde.
- G8. The vaccine of G7, wherein the formaldehyde inactivation comprises contacting the Zika virus with formaldehyde for between 2-10 days.
- G9. The vaccine of any one of G5 to G8, wherein the chemical activation is performed at about +4°C or about +22°C.

- G10. The vaccine of any one of G1 to G9, further comprising an adjuvant.
- G11. The vaccine of G10, wherein the adjuvant is an aluminum salt adjuvant.
- G12. The vaccine of G11, wherein the aluminum salt adjuvant is aluminium hydroxide or aluminium phosphate salt.
- G13. The vaccine of any one of G10 to G12, wherein the vaccine comprises or further comprises an adjuvant comprising a peptide and a deoxyinosine-containing immunostimulatory oligodeoxynucleic acid molecule (I-ODN).
- G14. The vaccine of G13, wherein the peptide comprises the sequence KLKL5KLK (SEQ ID NO: 71) and the I-ODN comprises oligo-d(IC)13 (SEQ ID NO: 70).
- G15. The vaccine of any one of G1 to G14, further comprising one or more pharmaceutically acceptable excipients.
- G16. The vaccine of any one of G1 to G15, wherein the vaccine contains protamine sulphate or fragments or break-down products of PS at amounts too low to detect by HPLC, i.e., below 1 µg/mL, especially below 100 ng/mL.
- G17. The vaccine of G16, wherein said protamine sulphate or fragments or break-down products of PS can be detected by mass spectroscopy or another sensitive method.
- Q1. A process of purification of infectious Zika virus particles, comprising the steps of:
- (a) providing a crude harvest (a) comprising Zika virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate;
 - (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a virus preparation (b);
 - (c) further purifying the virus preparation (b) by an optimized sucrose density gradient centrifugation, wherein the optimized sucrose gradient is provided such that the protamine can be completely or almost completely separated from the virus fraction; and wherein the

protamine concentration is reduced by this step to the extent that the protamine concentration in the final drug substance is below 1 µg/ml, preferably below 0.5 µg/mL, more preferably below 0.1 µg/mL, most preferably below 0.05µg/mL.

Q2. The process of Q2, wherein the virus particles are from Zika virus.

Q3. The process of Q1 or Q2, additionally comprising the step of:

(d) a solid-phase matrix packed in a column comprising a ligand-activated core and an inactive shell comprising pores, wherein the molecular weight cut off of the pores excludes the virus particles from entering the ligand-activated core, and wherein a molecule smaller than the molecular weight cutoff of the pores can enter the ligand-activated core and collecting the virus particles.

Q4. The process of any of Q1 to 3, wherein the residual host cell DNA of the Zika virus preparation (c) is less than 10 ng/mL and the residual host cell protein of the final Zika virus preparation (c) is less than 100 ng/mL.

Q5. The process of any of Q1 to 4, wherein the crude harvest (a) comprising Zika virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b).

Q6. The process of Q5, wherein the one or more pre-purification step(s) comprises

- (a) filtration using a filter having a pore size equal to or less than 0.2 µm; and/or
- (b) digestion of host cell genomic DNA by enzymatic treatment; and/or
- (c) ultra/diafiltration using a hollow fiber membrane having a pore size equal to or greater than 300 kDa, preferably equal to or greater than 100 kDa.

Q7. The process of any one of Q1 to 6, wherein the concentration of protamine sulphate is 0.5 to 3 mg/ml, more preferably 1 to 2 mg/ml, more preferably 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml, most preferably 1.6 mg/ml or 2 mg/ml.

Q8. The process of any one of Q1 to 7, wherein the enrichment of infectious Zika virus particles in the virus preparation (c) or any final virus preparation relative to total Zika virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.

Q9. The process of any one of Q5 to 8, wherein the one or more pre-purification step(s) prior to step (b) of any of Q5 to 8 is performed using a filter having a pore size equal to or less than 1 μm , preferably 0.2 μm .

Q10. The process of any one of Q1 to 9, wherein the residual impurity of the Zika virus preparation (c) is less than 10%.

Q11. The process of any one of Q1 to 10, wherein the Zika virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line.

Q12. The process of Q11, wherein said cell line is a Vero cell line.

Q13. The process of any one of Q1 to 12, wherein the infectious Zika virus particle is a live virus, an attenuated live virus, a chimeric virus, a modified live virus, or a recombinant live virus.

Q14. The process of any one of Q1 to 13, wherein the Zika virus is a Zika virus strain of the Asian lineage or an immunogenic variant thereof.

Q15. The process of any one of Q1 to 14, wherein said process resulting in final Zika virus preparation (c) or (d) is followed by an inactivation step, wherein the virus is inactivated preferably by formaldehyde.

Q16. Use of the process according to any one of Q1 to 15 for manufacturing a composition for immunization against a Zika virus infection.

Q17. The use according to Q16, wherein the composition for immunization against a virus infection is an infection caused by Zika virus.

Q18. A composition comprising the Zika virus particles obtainable or obtained by the process of any one of Q1 to 17 for treating and/or preventing an infection, such as e.g. a Zika virus infection.

Q19. A Zika virus vaccine comprising an inactivated Zika virus particle grown on vero cells, wherein the Zika virus particle is able to seroconvert a subject that is administered the Zika virus vaccine with at least a 70% probability and comprises minor amounts of protamine sulphate, preferably below the detection limit.

Q20. The Zika virus vaccine of Q19, wherein the Zika virus particle is able to seroconvert the subject that is administered the Zika virus vaccine with at least a 80%, 85%, 90%, or 95% probability, preferably a 80% probability.

Q21. The vaccine of Q19 or 20, wherein the Zika virus particle has a RNA genome corresponding to the DNA sequence provided by any one of the nucleic acid sequences of SEQ ID NOs: 2-13 or 72, or a variant nucleic acid sequence that is at least 88% identical to any one of SEQ ID NOs: 2-13 or 72 and able to pack a virulent Zika virus.

Q22. The vaccine of any one of Q19, 20 and 21, wherein the Zika virus particle has an E protein selected from the amino acid sequences provided by any one of SEQ ID NOs: 14-69, or a variant amino acid sequence that is at least 95% identical to any one of SEQ ID NOs: 14-69 and able to pack a virulent Zika virus.

Q23. The vaccine of any one of Q19, 20 to 22, wherein the Zika virus obtained by culturing on Vero cells is purified by protamine sulfate precipitation and sucrose gradient centrifugation.

Q24. The vaccine of Q23, wherein the sucrose gradient centrifugation is an optimized sucrose gradient centrifugation.

Q25. The vaccine of Q24, wherein the optimized sucrose gradient centrifugation comprises a virus comprising fraction in a 10% (w/w) sucrose solution and three layers of sucrose with different densities, i.e. a first sucrose solution with 15% (w/w) sucrose solution, a second sucrose solution with 35% (w/w) sucrose solution, and a third sucrose solution with a 50% (w/w) sucrose solution.

Q26. The vaccine of any one of Q19, 20 to 25, wherein the Zika virus is inactivated by chemical inactivation, thermal inactivation, pH inactivation, or UV inactivation.

Q27. The vaccine of Q26, wherein the chemical inactivation comprises contacting the Zika virus with a chemical inactivation agent for longer than is required to completely inactivate the Zika virus as measured by plaque assay.

Q28. The vaccine of Q27, wherein the chemical inactivation comprises contacting the Zika virus with formaldehyde.

Q29. The vaccine of Q28, wherein the formaldehyde inactivation comprises contacting the Zika virus with formaldehyde for between 2-10 days.

Q30. The vaccine of any one of Q27-29, wherein the chemical activation is performed at about +4°C or about +22°C.

Q31. The vaccine of any one of Q19 to 30, further comprising an adjuvant.

Q32. The vaccine of Q31, wherein the adjuvant is an aluminum salt adjuvant.

Q33. The vaccine of Q32, wherein the aluminum salt adjuvant is aluminium hydroxide or aluminium phosphate salt.

Q34. The vaccine of Q32, wherein the aluminum salt adjuvant is aluminium hydroxide with less than 1.25 ppb Cu based on the final pharmaceutical composition comprising the Zika virus, preferably the inactivated Zika virus.

Q35. The vaccine of any one of Q19 to 34, further comprising one or more pharmaceutically acceptable excipient(s).

R1. Use of protamine, preferably a protamine salt, to separate infectious and non-infectious Zika virus particles, host cell proteins and/or undefined low molecular weight materials.

R2. A process of purification of infectious Zika virus particles, comprising the steps of:

- (a) providing a crude harvest (a) comprising Zika virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate;
- (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a virus preparation (b), wherein the enrichment of infectious virus particles in the virus preparation (b) relative to total virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.

R3. The use of R1 or the process of R2, wherein the virus particles are from Zika virus.

R4. A process of purification of infectious Zika virus particles, comprising the steps of:

- (a) providing a crude harvest (a) comprising Zika virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate;
- (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a virus preparation (b);

- (c) further purifying the virus preparation (b) by one or more size exclusion methods such as (i) a sucrose density gradient centrifugation, (ii) a solid-phase matrix packed in a column comprising a ligand-activated core and an inactive shell comprising pores, wherein the molecular weight cut off of the pores excludes the virus particles from entering the ligand-activated core, and wherein a molecule smaller than the molecular weight cutoff of the pores can enter the ligand-activated core and collecting the virus particles, and/or (iii) size exclusion chromatography to obtain a virus preparation (c) comprising the infectious virus particles, wherein the residual host cell DNA of the virus preparation (c) is less than 100 ng/mL and the residual host cell protein and the residual aggregates of infectious virus particles of the final virus preparation (c) is less than 1 µg/mL.

R5. The process of R4, wherein the residual host cell DNA of the Zika virus preparation (c) is less than 10 ng/mL and the residual host cell protein of the final virus preparation (c) is less than 100 ng/mL.

R6. The process of any of R2 to 5, wherein the crude harvest (a) comprising virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b).

R7. The process of R6, wherein the one or more pre-purification step(s) comprises

- (a) filtration using a filter having a pore size equal to or less than 0.2 µm; and/or
- (b) digestion of host cell genomic DNA by enzymatic treatment; and/or
- (c) ultra/diafiltration using a hollow fiber membrane having a pore size equal to or greater than 300 kDa, preferably equal to or greater than 100 kDa.

R8. The process of any one of R2 to 7, wherein the concentration of protamine sulphate is 0.5 to 3 mg/ml, more preferably 1 to 2 mg/ml, more preferably 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml, most preferably 1.6 mg/ml.

R9. The process of any one of R2 to 8, wherein the enrichment of infectious virus particles in the virus preparation (c) or any final virus preparation relative to total virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.

R10. The process of any one of R6 to 9, wherein the one or more pre-purification step(s) prior to step (b) of any of R6 to 9 is performed using a filter having a pore size equal to or less than 1 μm , preferably 0.2 μm .

R11. The process of any one of R2 to 10, wherein the residual impurity of the Zika virus preparation (c) is less than 10%.

R12. The process of any one of R2 to 11, wherein the Zika virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line.

R13. The process of R12, wherein said cell line is a Vero cell line.

R14. The process of any one of R2 to 13, wherein the Zika virus is a live virus, an attenuated live virus, a chimeric virus, a modified live virus, or a recombinant live virus.

R15. The process of any one of R2 to 14, wherein the Zika virus is a Zika virus strain of the Asian lineage or an immunogenic variant thereof.

R16. The process of any one of R2 to 15, wherein said process resulting in final virus preparation (c) is followed by an inactivation step, wherein the virus is inactivated preferably by formaldehyde.

R17. Use of the process according to any one of R1 to 16 for manufacturing a composition for immunization against a virus infection.

R18. The use according to R17, wherein the composition for immunization against a virus infection is an infection caused by a Zika virus.

R19. A composition comprising the virus particles obtainable or obtained by the process of any one of R2 to 16 for treating and/or preventing an infection.

CLAIMS

What is claimed is:

1. Use of protamine, preferably a protamine salt, to separate infectious Zika virus particles from non-infectious Zika virus particles.
2. The use according to claim 1, wherein the protamine salt also facilitates the separation of infectious Zika virus particles from host cell proteins and/or low molecular weight materials.
3. A process of purification of infectious Zika virus particles, comprising the steps of:
 - a) providing a crude harvest (a) comprising Zika virus particles and impurities, wherein the impurities are generated from growing said Zika virus particles on a cell substrate;
 - b) reducing impurities from said crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a Zika virus preparation (b), wherein the enrichment of infectious Zika virus particles in the Zika virus preparation (b) relative to total Zika virus products in the crude harvest (a) is in the range of at least 50% to 95%, preferably at least 80%.
4. A process of purification of infectious Zika virus particles, comprising the steps of:
 - a) providing a crude harvest (a) comprising Zika virus particles and impurities, wherein the impurities are generated from growing said Zika virus particles on a cell substrate;
 - b) reducing impurities from said crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a Zika virus preparation (b);
 - c) further purifying said Zika virus preparation (b) by one or more size exclusion methods such as (i) a sucrose density gradient centrifugation, (ii) a solid-phase matrix packed in a column comprising a ligand-activated core and an inactive shell comprising pores, wherein the molecular weight cut off of the pores excludes the Zika virus particles from entering the ligand-activated core, and wherein a molecule smaller than the molecular weight cutoff of the pores can enter the ligand-activated core and collecting the virus particles, and/or (iii) size exclusion chromatography to obtain a virus preparation (c) comprising the infectious Zika virus particles, wherein the residual host cell DNA of the virus preparation (c) is less

than 100 ng/mL and the residual host cell protein and the residual aggregates of infectious virus particles of the final virus preparation (c) is less than 1 µg/mL.

5. The process of claim 4, wherein the residual host cell DNA of the Zika virus preparation (c) is less than 10 ng/mL and the residual host cell protein of the final virus preparation (c) is less than 100 ng/mL.
6. The process of any of claims 3 to 5, wherein the crude harvest (a) comprising Zika virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b).
7. The process of claim 6, wherein the one or more pre-purification step(s) comprises
 - a) filtration using a filter having a pore size equal to or less than 0.2 µm; and/or
 - b) digestion of host cell genomic DNA by enzymatic treatment; and/or
 - c) ultra/diafiltration using a hollow fiber membrane having a pore size equal to or greater than 300 kDa, preferably equal to or greater than 100 kDa.
8. The process of any one of claims 3 to 7, wherein the concentration of protamine sulphate is 0.5 to 3 mg/ml, more preferably 1 to 2 mg/ml, more preferably 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml, most preferably 2.0 mg/ml.
9. The process of any one of claims 3 to 8, wherein the enrichment of infectious Zika virus particles in the Zika virus preparation (c) or any final Zika virus preparation relative to total Zika virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.
10. The process of any one of claims 6 to 9, wherein the one or more pre-purification step(s) prior to step (b) of any of claims 6 to 9 is performed using a filter having a pore size equal to or less than 1 µm, preferably 0.2 µm.
11. The process of any one of claims 3 to 10, wherein the residual impurity of the Zika virus preparation (c) is less than 10%.
12. The process of any one of claims 3 to 11, wherein the Zika virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero-αHis cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell

line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line.

13. The process of claim 12, wherein said cell line is a Vero cell line.
14. The process of any one of claims 3 to 13, wherein said Zika virus is a live virus, an attenuated live virus, a chimeric virus, a modified live virus, or a recombinant live virus.
15. The process of any one of claims 3 to 14, wherein said Zika virus is preferably a Zika virus strain of the Asian lineage or an immunogenic variant thereof.
16. The process of any one of claims 3 to 15, wherein said process resulting in final Zika virus preparation (c) is followed by an inactivation step, wherein the Zika virus is inactivated preferably by formaldehyde.
17. A composition comprising the Zika virus particles obtainable or obtained by the process of any one of claims 3 to 16, wherein the composition contains protamine at levels below detection in size exclusion chromatography.
18. The composition according to claim 17, wherein the composition contains trace amounts of protamine or fragments thereof detectable by mass spectroscopy or other sensitive methods.
19. The composition according to claim 17 or 18 for treating and/or protecting from a Zika virus infection.
20. Use of the process according to any one of claims 3 to 16 for manufacturing a composition for immunization against a Zika virus infection.

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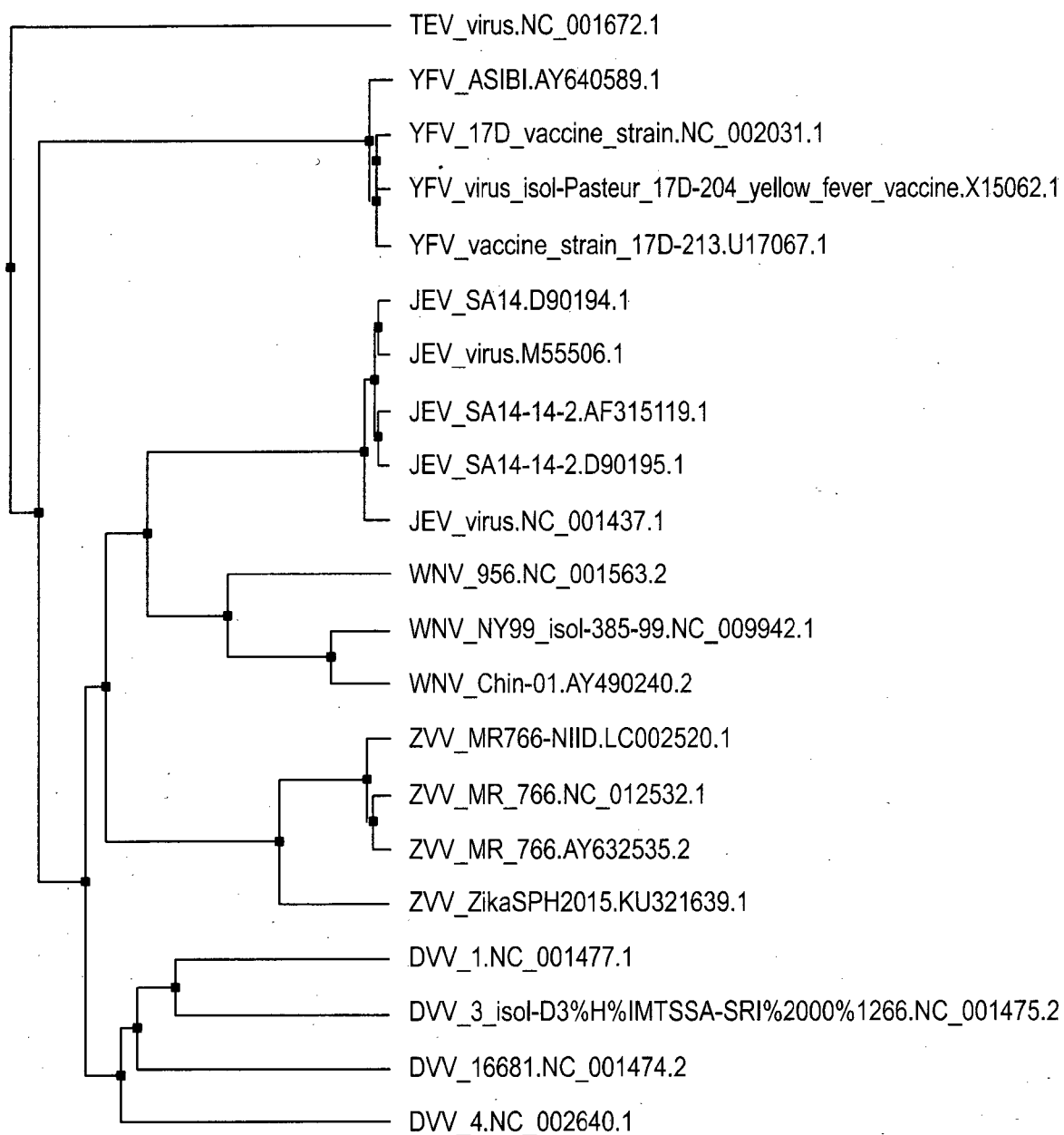


Figure 1

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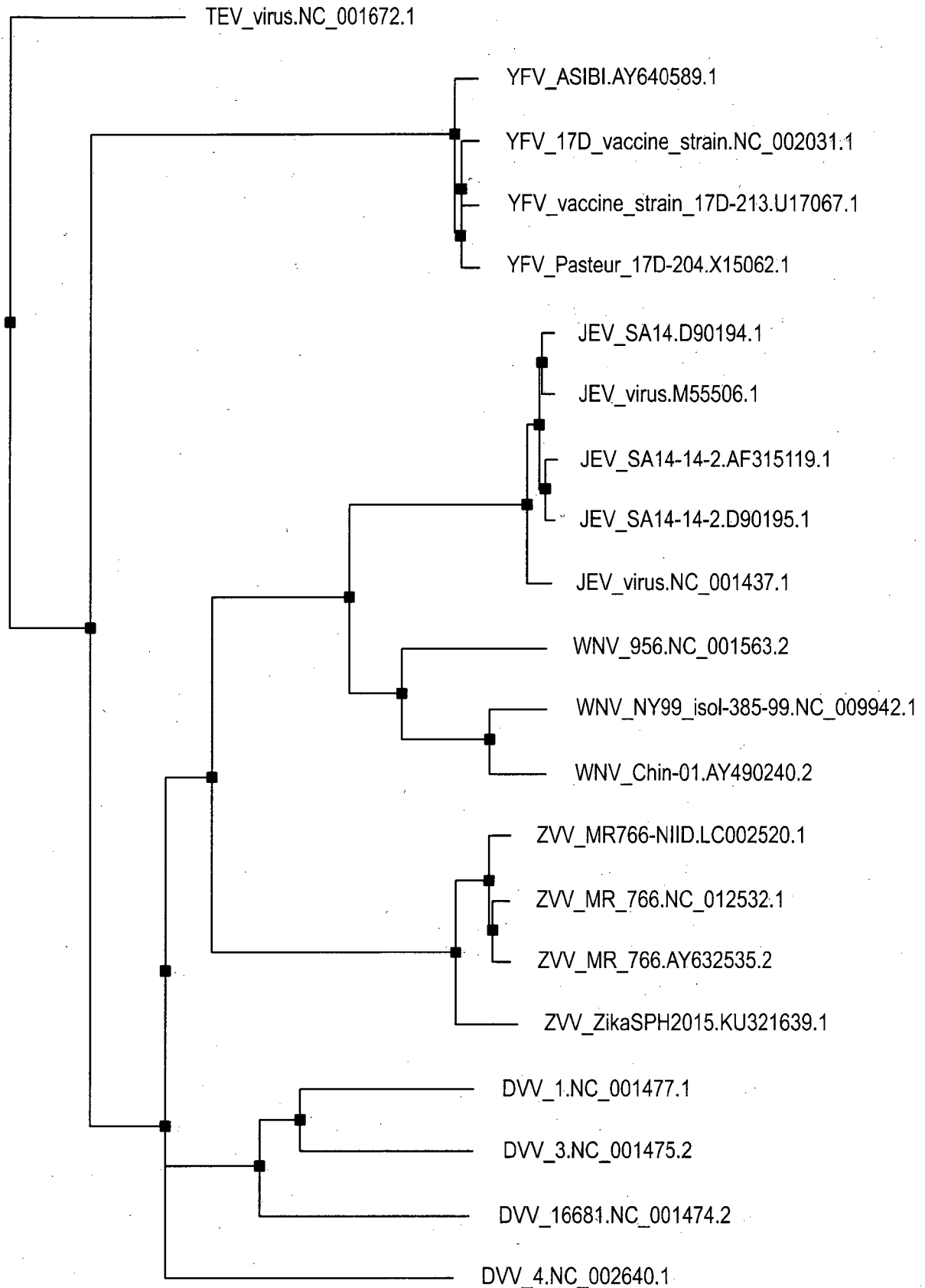


Figure 2

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
DWV 1.NC 001477.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
DWV 1681.NC 001474.2	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
DWV 3.NC 001475.2	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
DWV 4.NC 002640.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
JEV SA14-14-2.AF315119.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
JEV SA14-14-2.D90195.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
JEV SA14.D90194.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
JEV virus.M55506.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
JEV virus.NC 001437.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
TEV virus.NC 001672.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
WNV 956.NC 001563.2	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
WNV Chin-01.AY490240.2	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
WNV NY99 isol-385-99.NC 009942.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
YFV 17D vaccine strain.NC 002031.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
YFV ASIB.AY640589.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
YFV Pasteur 17D-204.X15062.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
YFV vaccine strain 17D-213.U17067.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
ZWV MR766-NIID.LC002520.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
ZWV MR 766.AY632535.2	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
ZWV MR 766.NC 012532.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
ZWV ZikaSPH2015.KU321639.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0

 % Identity and higher
 % Identity and higher
 % Identity and higher

Figure 3

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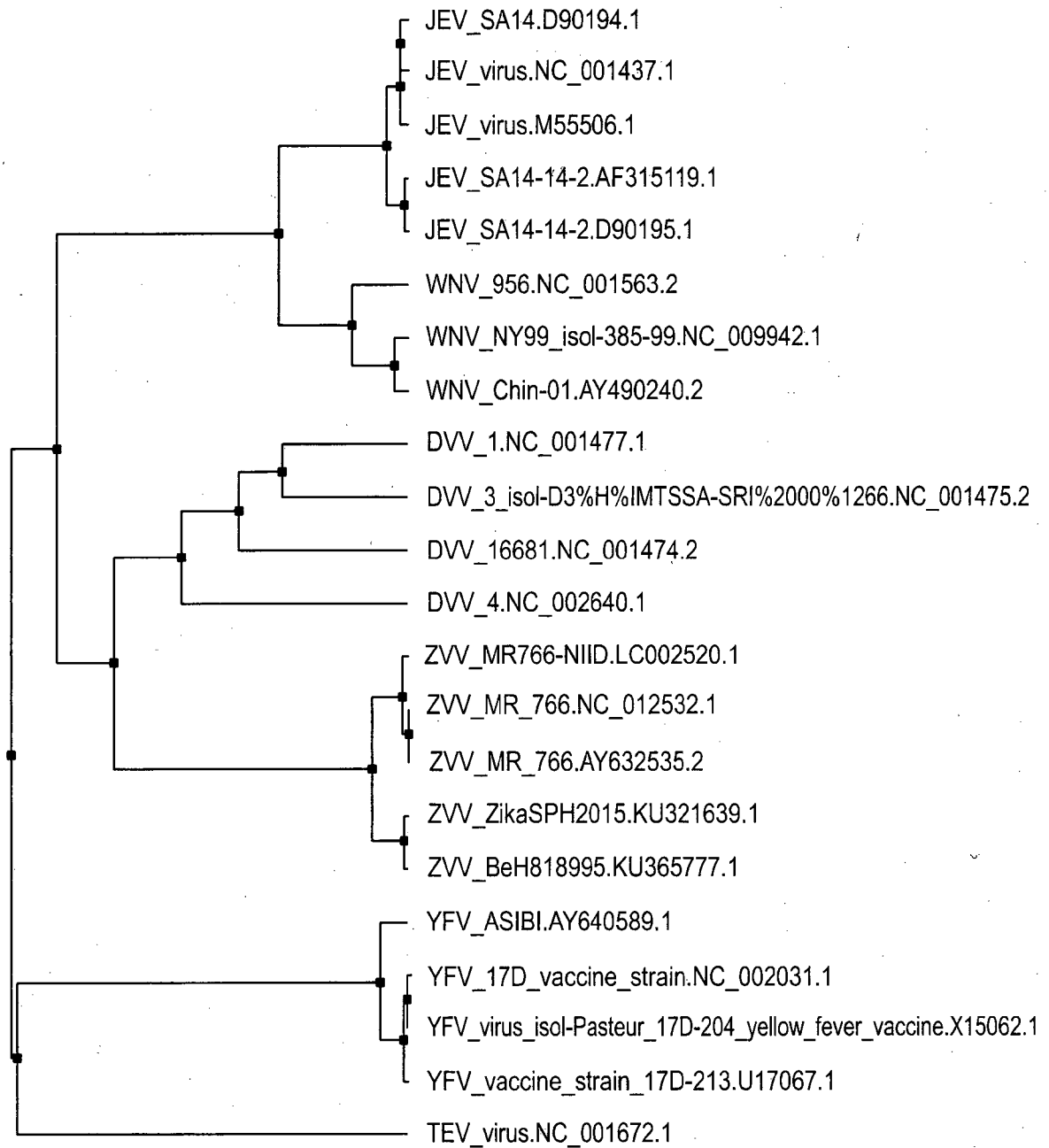


Figure 4

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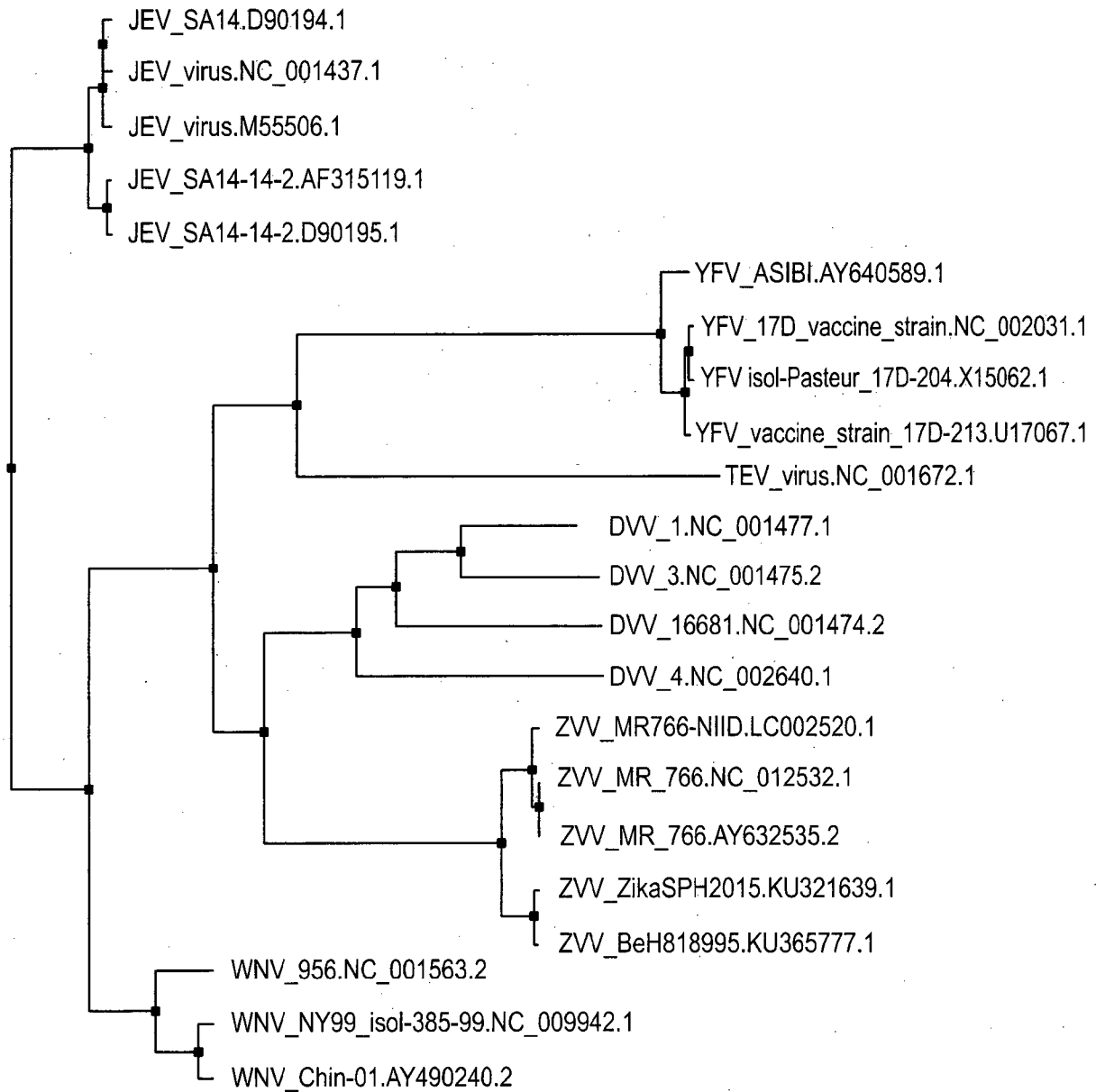


Figure 5

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
DV 1.NC 001477.1	0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
DV 16881.NC 001474.2	1	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
DV 3.NC 001475.2	2	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
DV 4.NC 002640.1	3	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
JEV SA14-14-2.AF315119.1	4	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
JEV SA14-14-2.D90195.1	5	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
JEV SA14.D90194.1	6	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
JEV virus.M55506.1	7	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
JEV virus.NC 001437.1	8	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
TEV virus.NC 001672.1	9	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
WNV 956.NC 001563.2	10	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
WNV Chin-01.AV490240.2	11	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
WNV NY99 isol-385-99.NC 009942.1	12	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
YFV 17D vaccine strain.NC 002031.1	13	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
YFV ASIB.AY640589.1	14	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
YFV isol-Pasteur 17D-204.X15062.1	15	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
YFV vaccine strain 17D-213.U17067.1	16	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
ZVBeH818995.KU365777.1	17	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
ZV MR766-NIID.LC002520.1	18	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
ZV MR 766.AY632535.2	19	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
ZV MR 766.NC 012532.1	20	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
ZV ZikaSPH2015.KU321639.1	21	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0

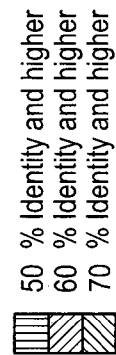


Figure 6

YFV_YASBI_AY640589.1292-784
YFV_Y7D_vaccine_strain_NC_002031.1292-784
YFV_vaccine_strain_17D-213.U17067.1292-784
YFV_Yisol-Pasteur_17D-204.X15062.1292-784
YEV_S414.D90194.1307-806
YEV_virus_NC_001437.1307-806
YEV_virus_M55506.1307-806
YEV_S414-14-2.AF315119.1307-806
YEV_S414-14-2.D90195.1307-806
DVV_1_NC_001477.1294-788
DVV_Y16681_NC_001474.1287-781
DVV_Y16681_NC_001474.1287-781
DVV_4_NC_002640.1313-807
DVV_3_NC_001475.1294-786
YEV_virus_NC_001672.1292-787
WNV_Y56_NC_001563.2906-802
WNV_Y199_isol-385-99_NC_009942.1306-806
WNV_Chin-01_AY90240.2806-806
WNV_H766-H1D.LC002520.1326-829
ZVV_ZikaSPH2015.KU21639.1326-829
ZVV_MR_766_NC_012532.1326-825
ZVV_MR_766.AY632535.1326-825
ZVV_B84H18995.KU35777.1308-811
YFV_YASBI_AY640589.1292-784
YFV_Y7D_vaccine_strain_NC_002031.1292-784
YFV_vaccine_strain_17D-213.U17067.1292-784
YFV_Yisol-Pasteur_17D-204.X15062.1292-784
YEV_S414.D90194.1307-806
YEV_virus_NC_001437.1307-806
YEV_virus_M55506.1307-806
YEV_S414-14-2.AF315119.1307-806
YEV_S414-14-2.D90195.1307-806
DVV_1_NC_001477.1294-788
DVV_Y16681_NC_001474.1287-781
DVV_4_NC_002640.1313-807
DVV_3_NC_001475.1294-786
YEV_virus_NC_001672.1292-787
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WNV_Chin-01_AY90240.2806-806
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ZVV_MR_766.AY632535.1326-825
ZVV_B84H18995.KU35777.1308-811

SUBSTITUTE SHEET (RULE 26)

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748	MS	AV	L	I	V	G	I	N	T	R	N	M	T	M	S	M	I	L	V	G	V	I	M	M	F	L	S	L	G	V	G	A			
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748	MS	AV	L	I	V	G	I	N	T	R	N	M	T	M	S	M	I	L	V	G	V	I	M	M	F	L	S	L	G	V	G	A			
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745	IG	VI	I	T	I	G	M	N	S	R	S	T	S	L	S	V	T	L	V	L	V	G	I	M	T	L	Y	L	G	V	M	Q	A		
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770	LG	AL	L	L	M	G	I	N	A	R	D	R	S	I	A	L	T	F	L	A	I	G	G	V	L	L	F	L	S	V	N	H	A		
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793	IG	TL	L	M	W	L	G	L	N	T	K	N	G	S	I	S	L	M	C	L	A	L	G	G	V	L	I	F	L	S	T	A	M	S	A
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775	IG	TL	L	M	W	L	G	L	N	T	K	N	G	S	I	S	L	M	C	L	A	L	G	G	V	L	I	F	L	S	T	A	M	S	A

YFV_ASBI.AY640589.1/292-784
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Figure 7 (Part 3 of 3)

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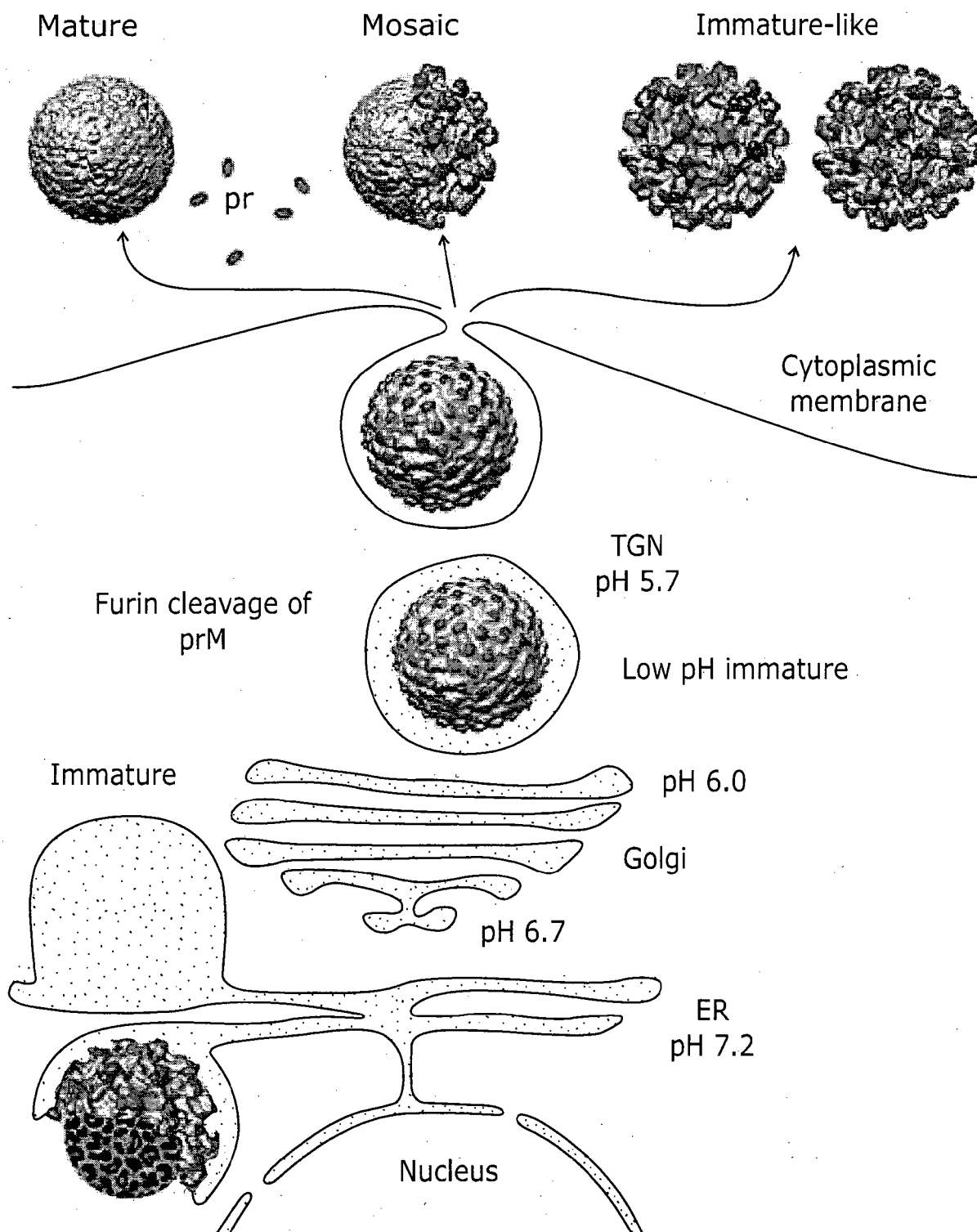


Figure 8

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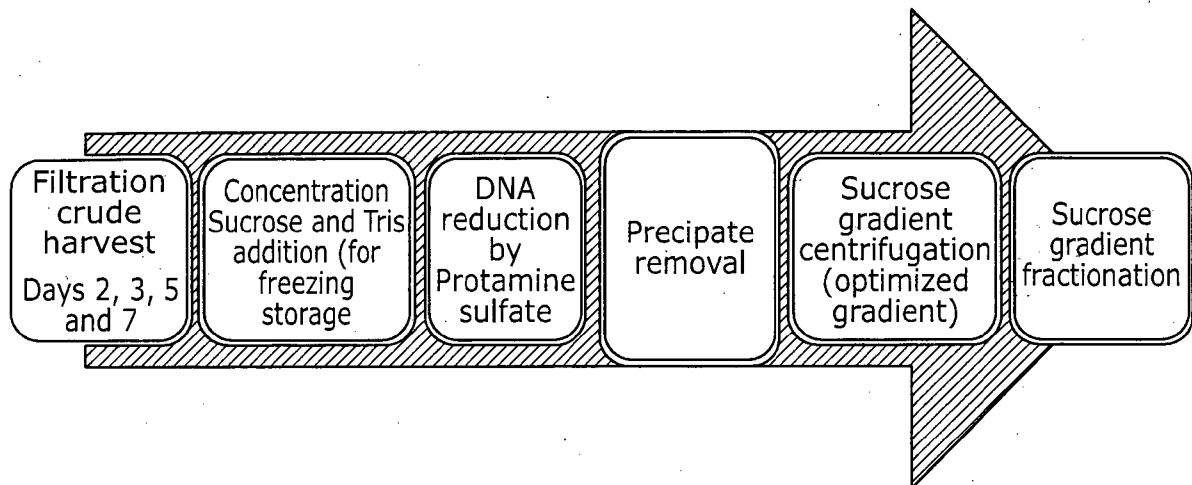


Figure 9A

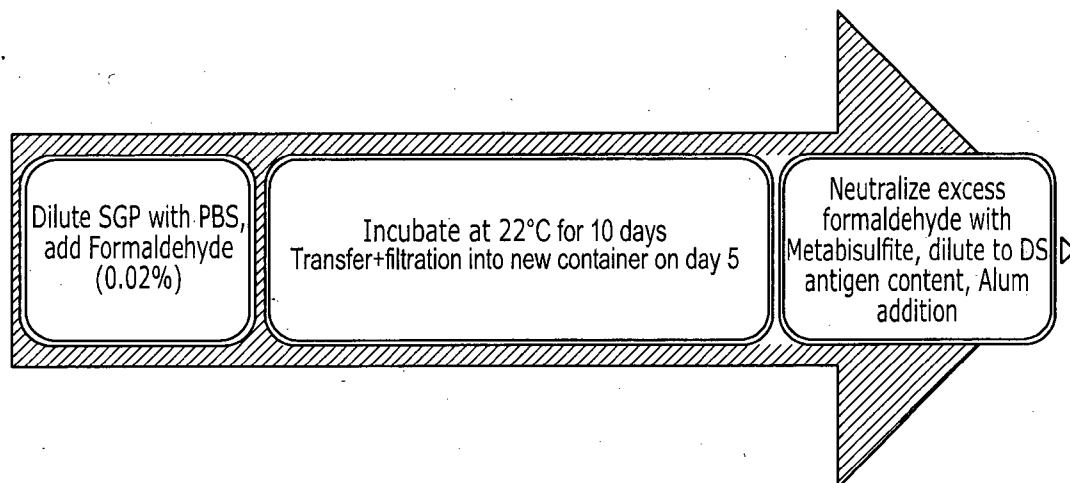


Figure 9B

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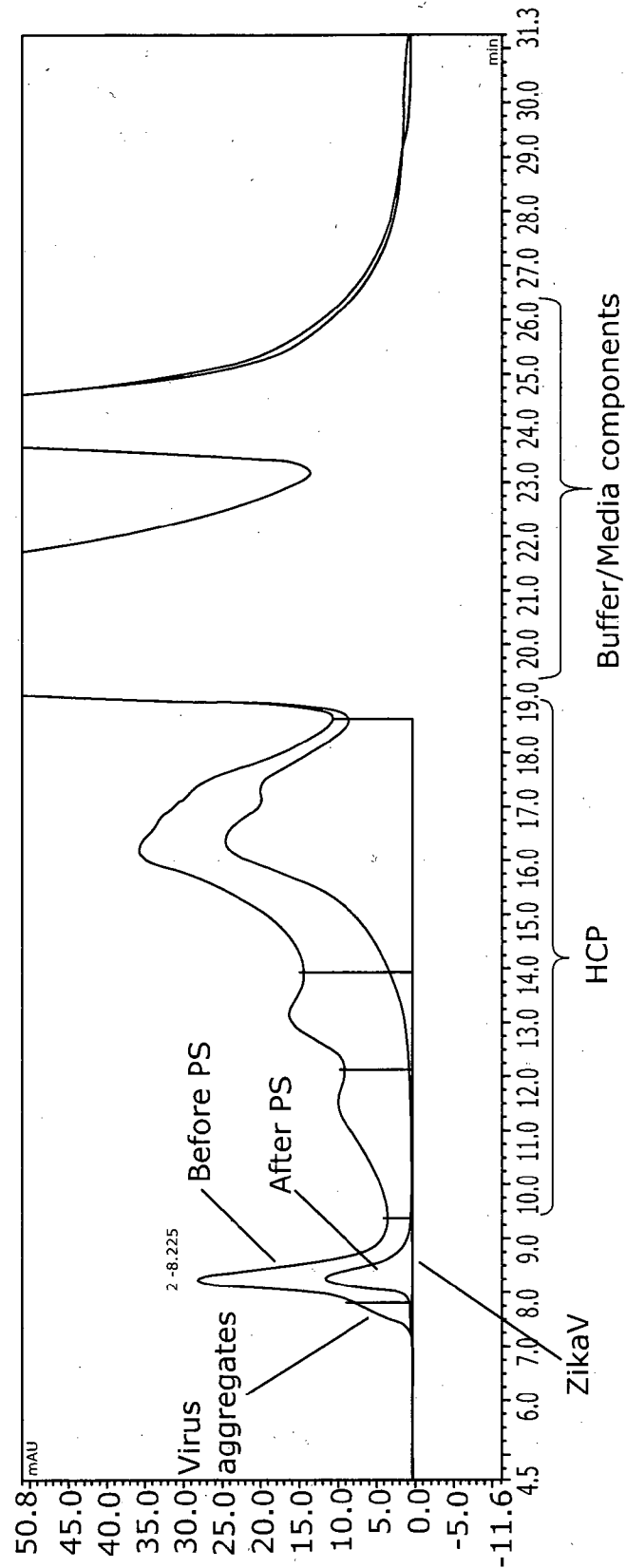
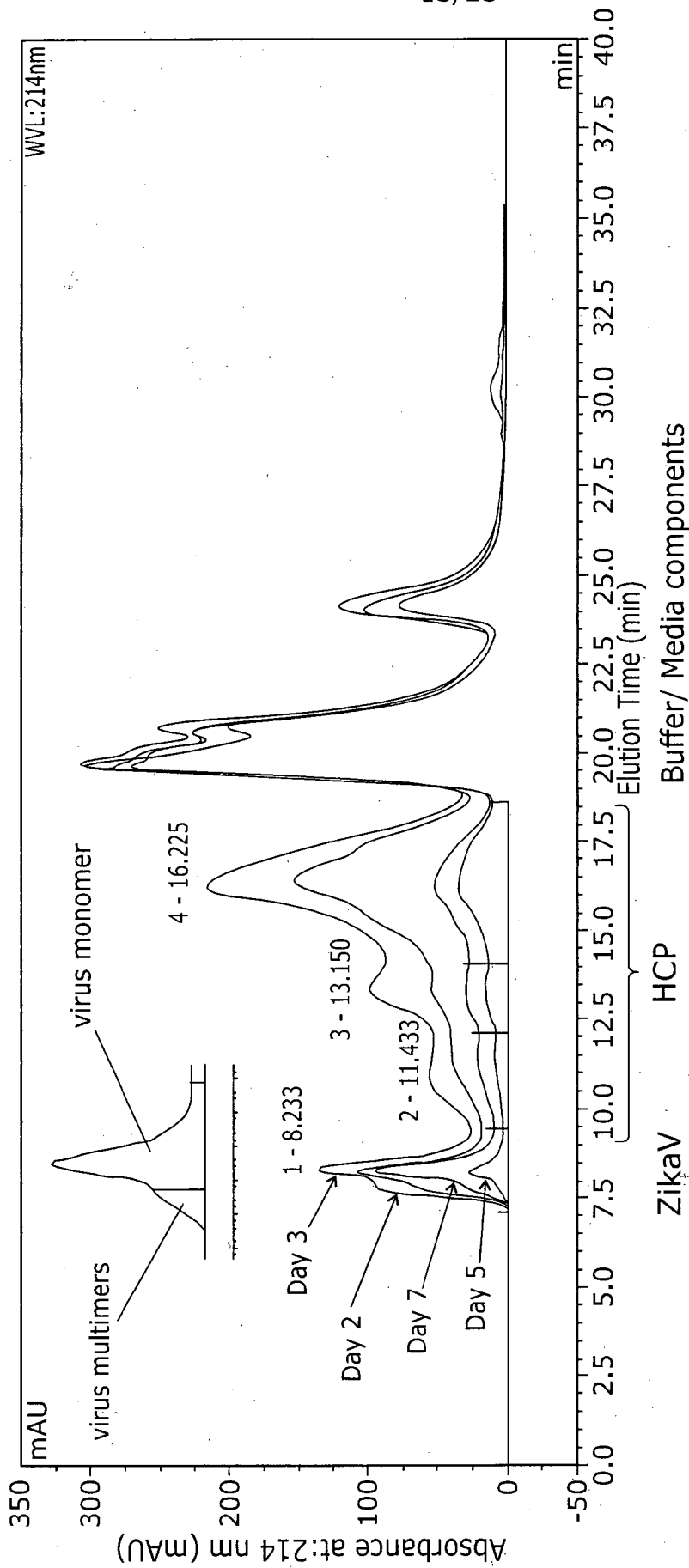


Figure 10



- + Similar virus concentration in harvests Day 2, Day 3, Day 7; lower virus concentration in harvest Day 5
- + Day 2 and Day 3 harvests contained more HCP than Days 5/7 (correlates with observed CPE)
- + Minor amount of virus multimers observed

Figure 11

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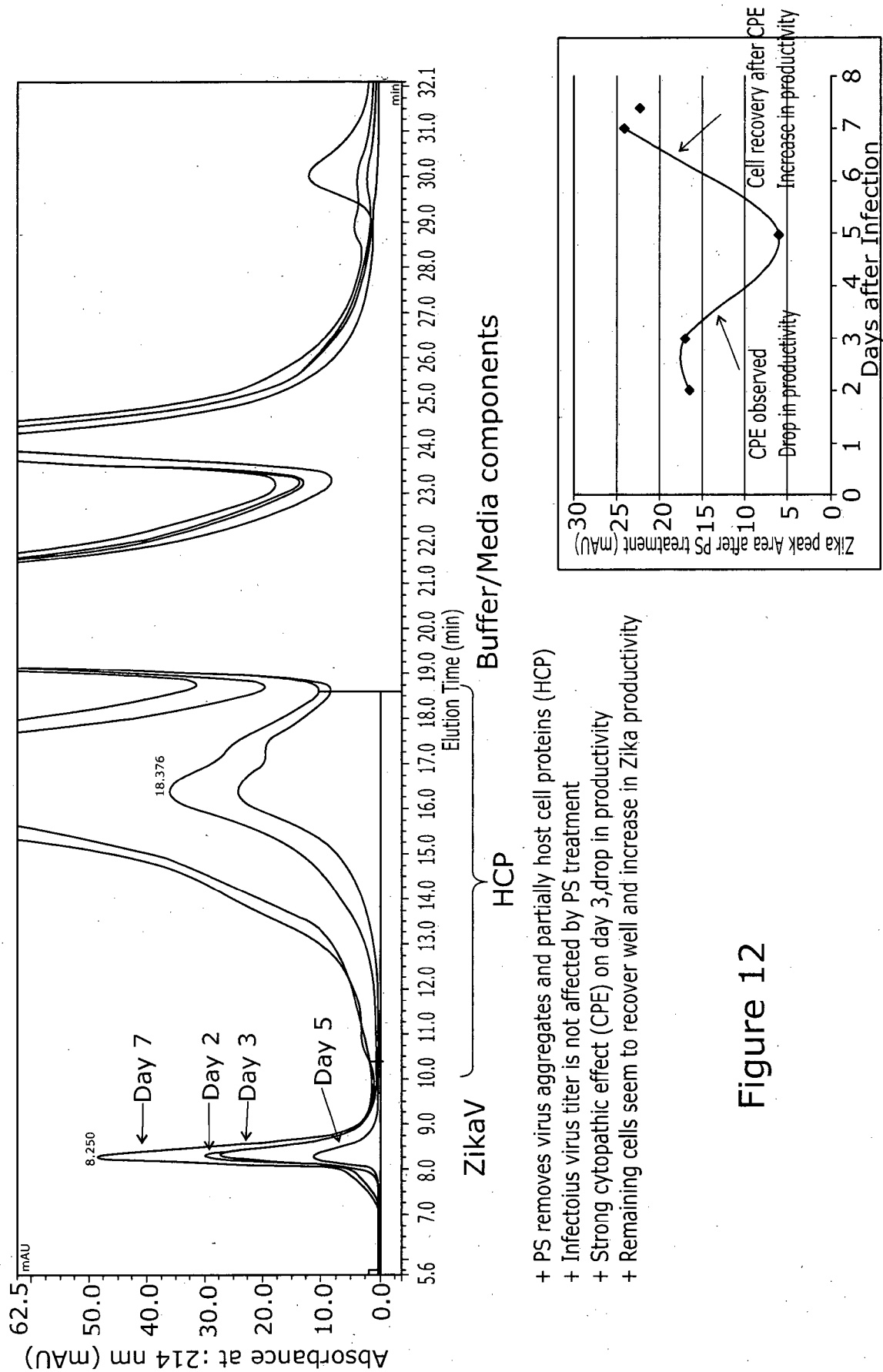


Figure 12

- + PS removes virus aggregates and partially host cell proteins (HCP)
- + Infectious virus titer is not affected by PS treatment
- + Strong cytopathic effect (CPE) on day 3, drop in productivity
- + Remaining cells seem to recover well and increase in Zika productivity

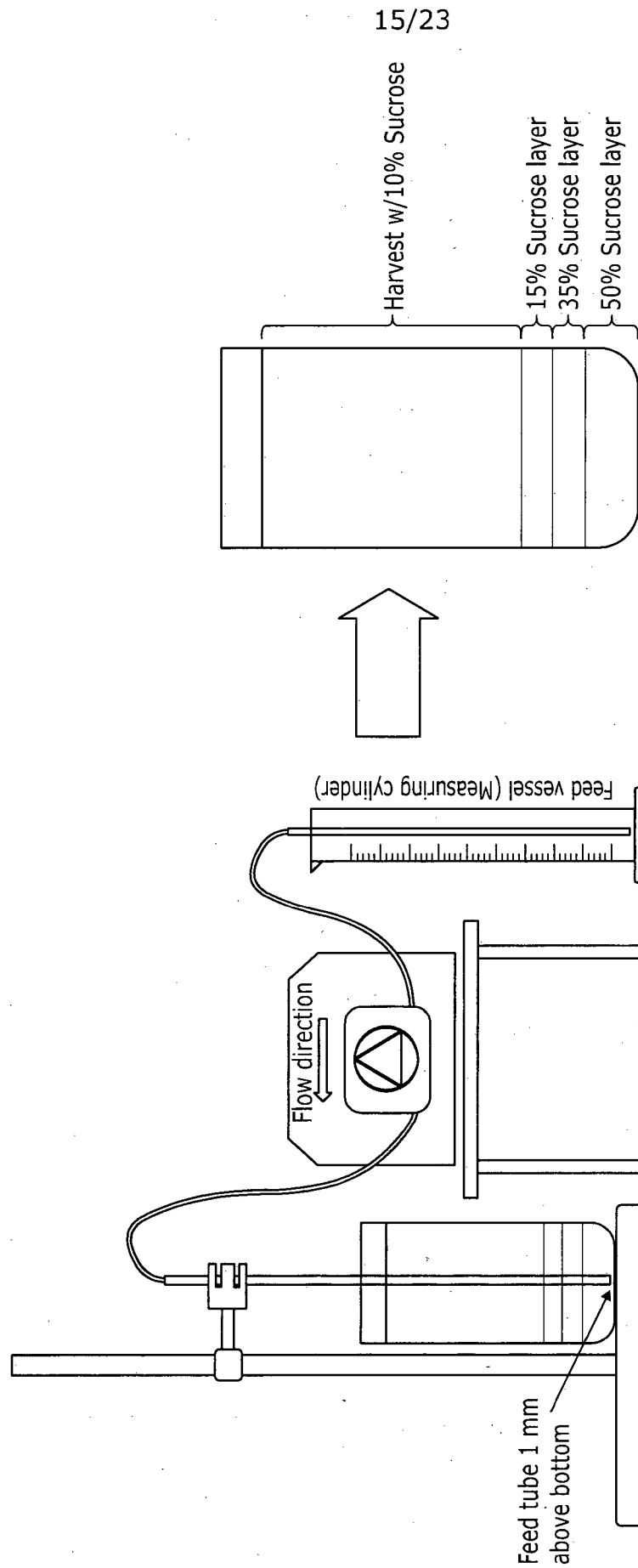
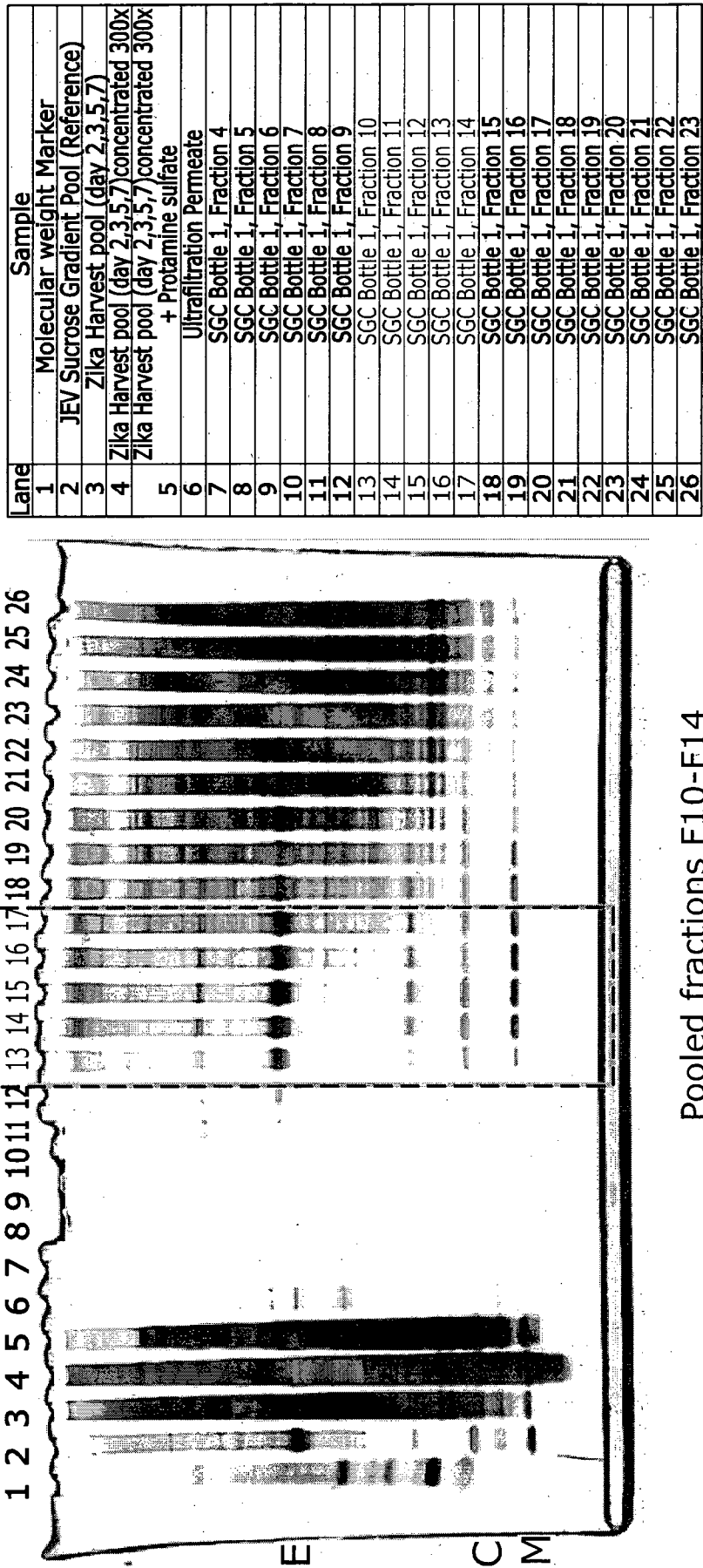


Figure 13



Pooled fractions F10-F14
(10mL total volume per bottle)

Figure 14

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Comparison of harvest schedules

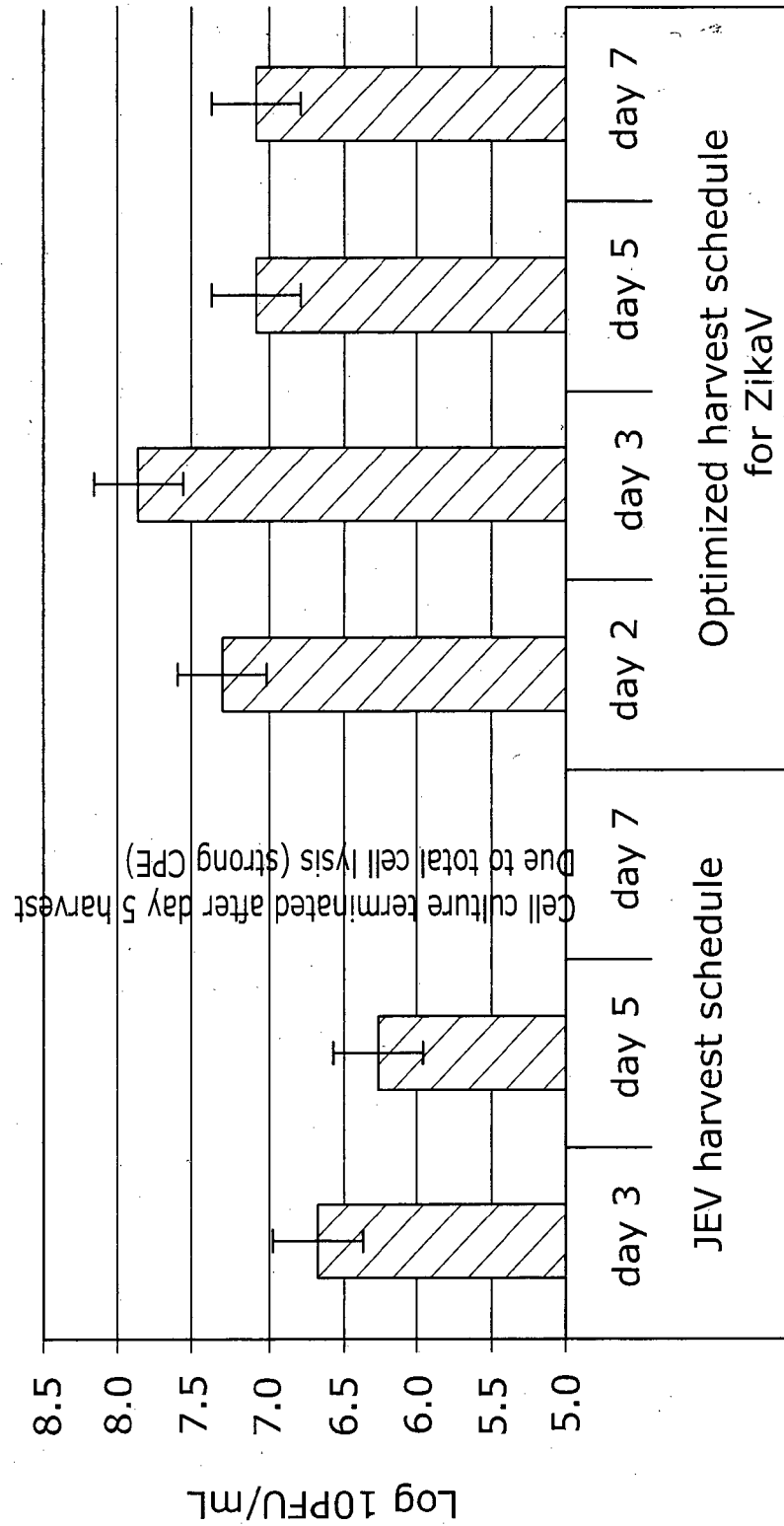


Figure 15

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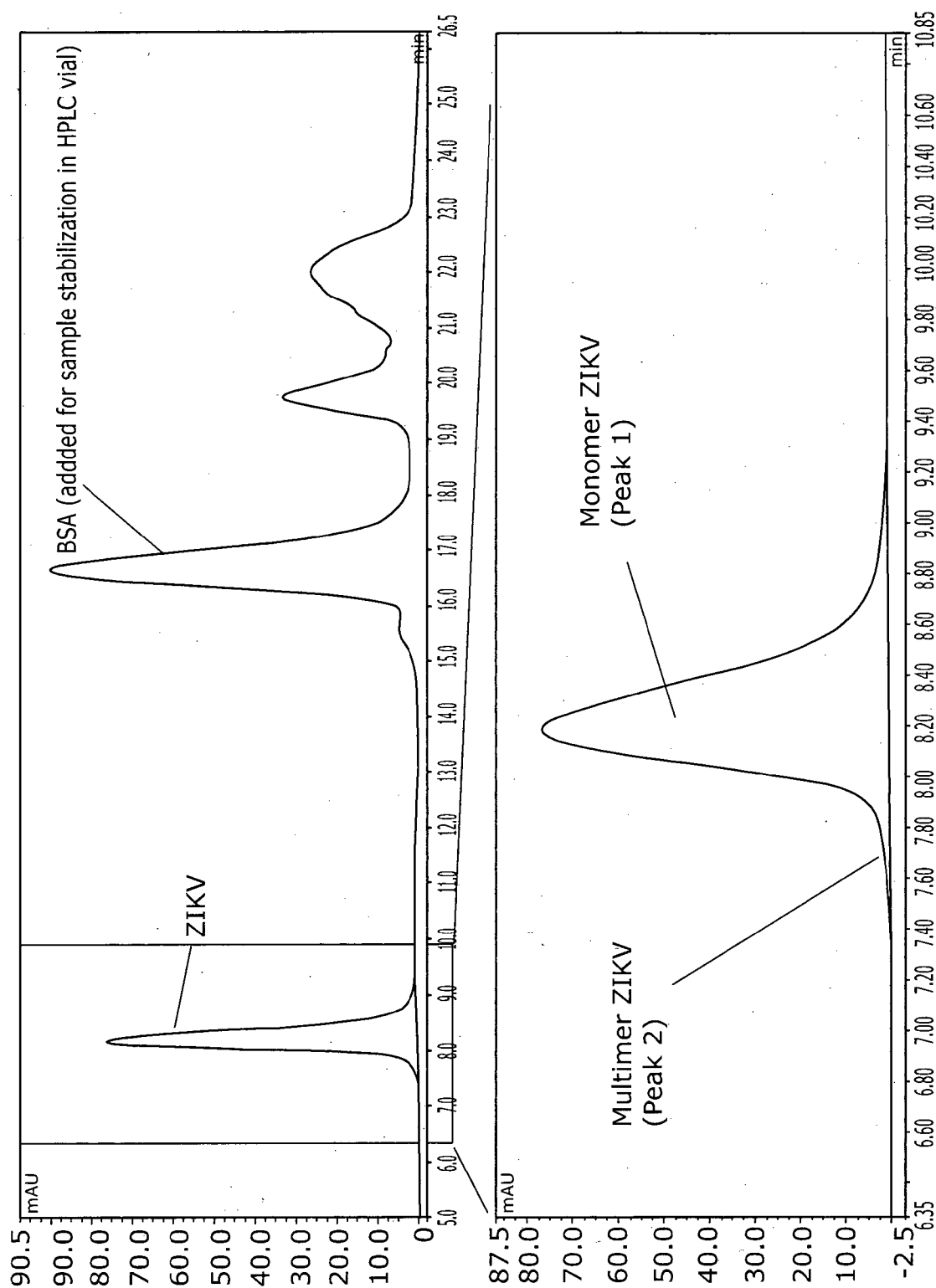


Figure 16

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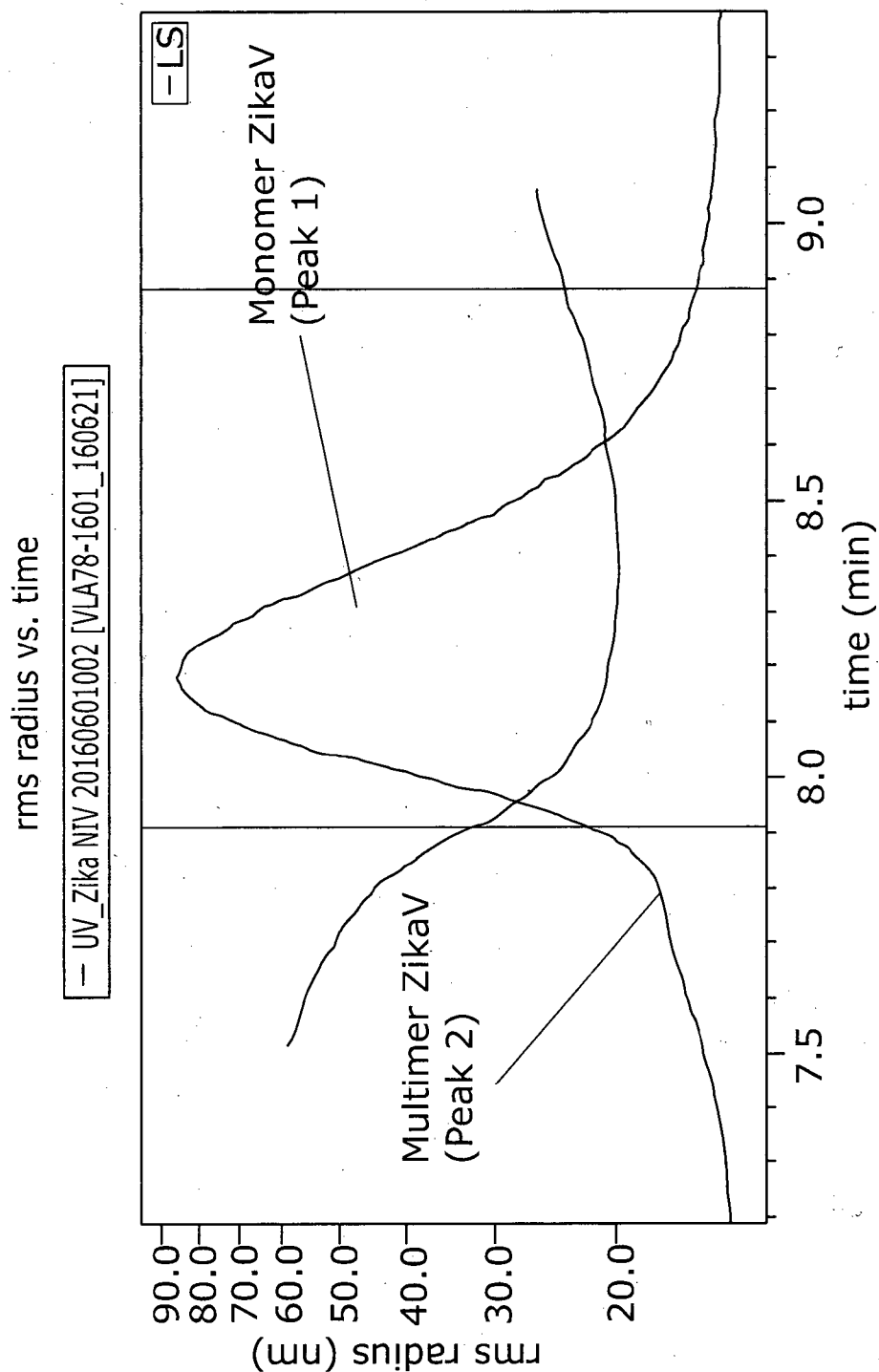


Figure 17

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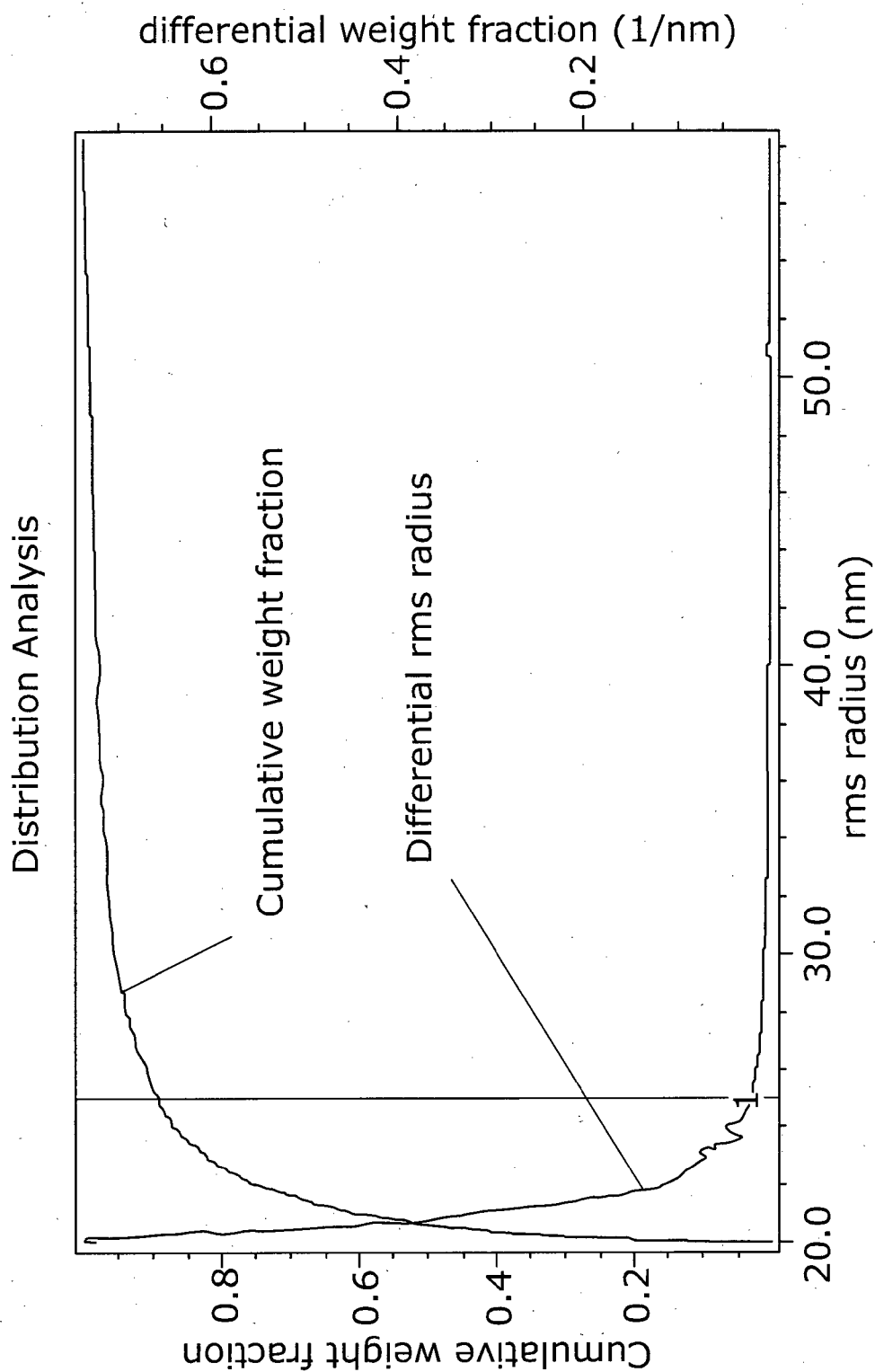


Figure 18

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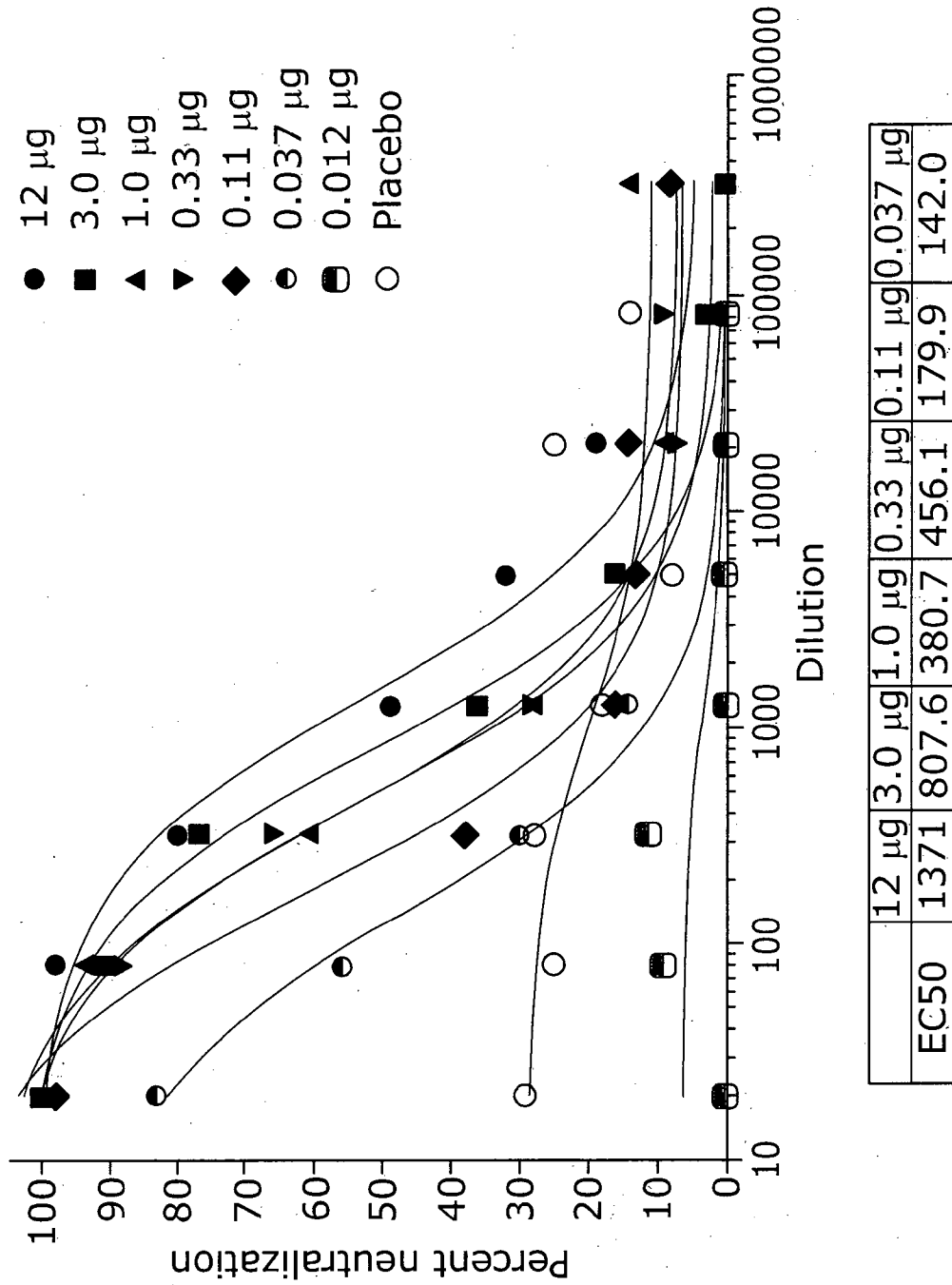


Figure 19

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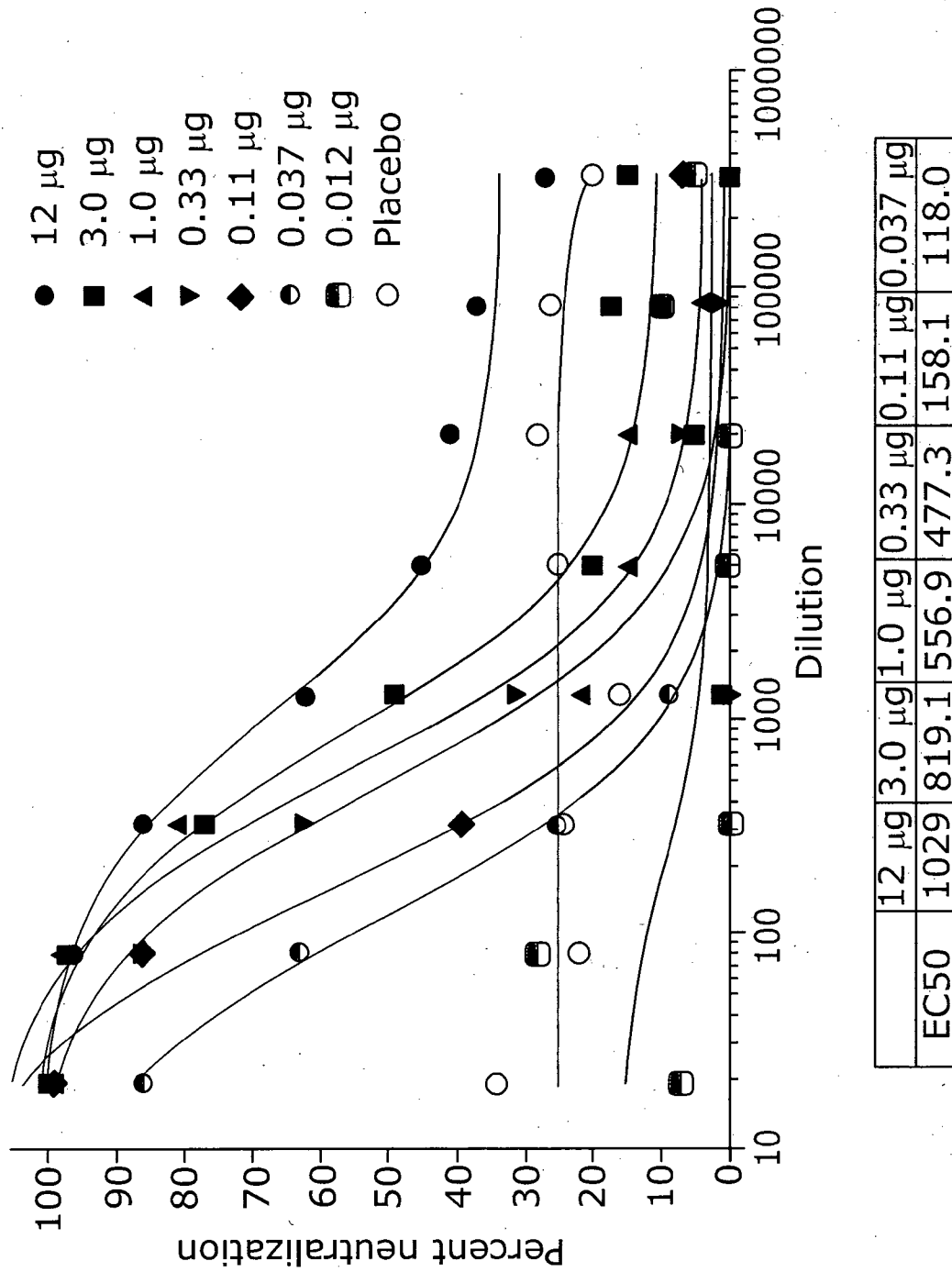


Figure 20

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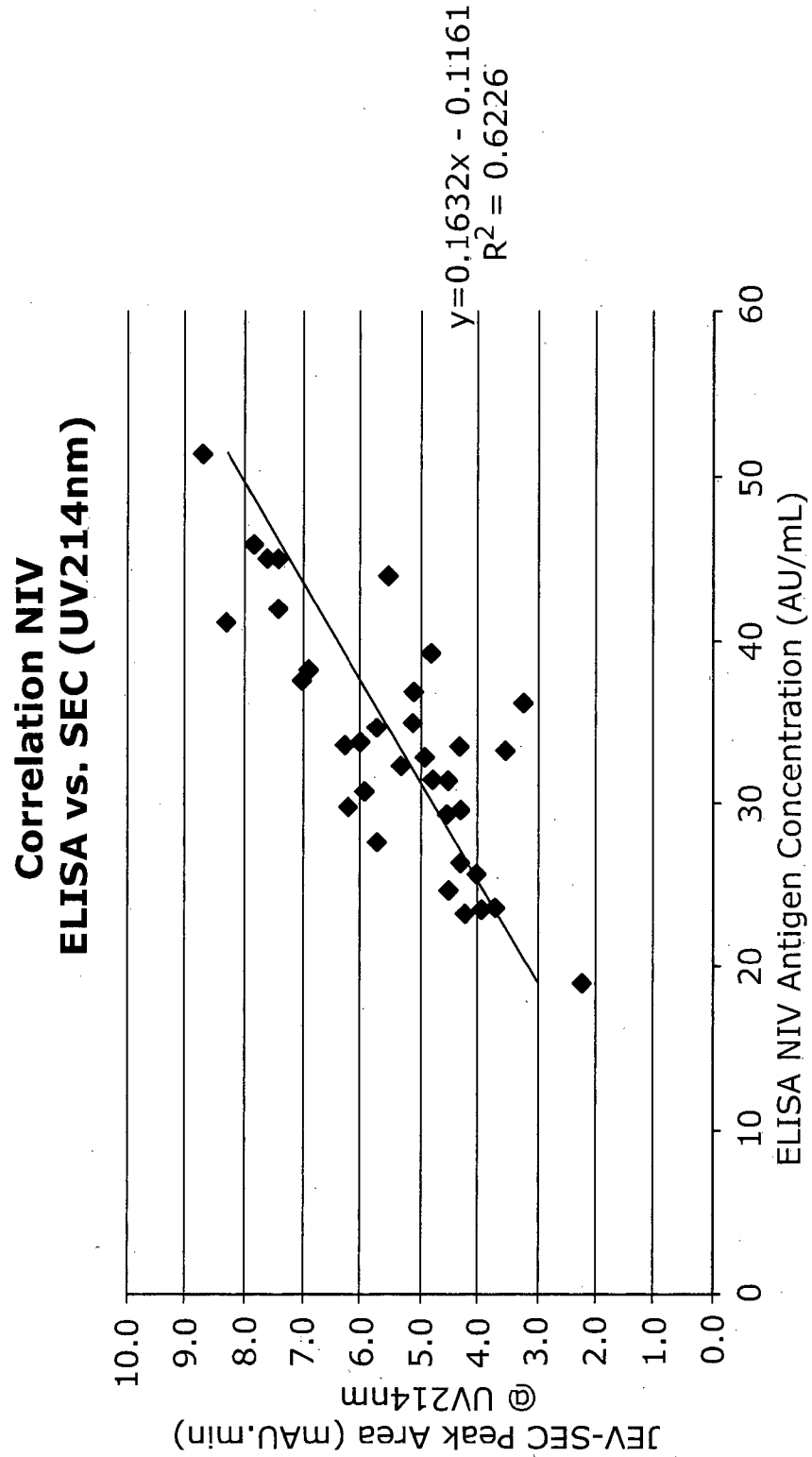


Figure 21

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/082667

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K39/12 C07K14/005
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, CHEM ABS Data, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	B. D. COX ET AL: "Predicting Zika virus structural biology: Challenges and opportunities for intervention", ANTIVIRAL CHEMISTRY & CHEMOTHERAPY., vol. 24, no. 3-4, 1 August 2015 (2015-08-01), pages 118-126, XP055328128, GB ISSN: 0956-3202, DOI: 10.1177/2040206616653873 the whole document ----- -/--	3-20



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

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"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

5 April 2017

Date of mailing of the international search report

19/04/2017

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040,
Fax: (+31-70) 340-3016

Authorized officer

Lewis, Birgit

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2016/082667

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SRIVASTAVA A K ET AL: "A purified inactivated Japanese encephalitis virus vaccine made in vero cells", VACCINE, vol. 19, no. 31, 14 August 2001 (2001-08-14), pages 4557-4565, XP027321987, ISSN: 0264-410X [retrieved on 2001-08-14] cited in the application abstract page 4559, left-hand column, paragraph 3 - page 4560, left-hand column, paragraph 2 page 4564, left-hand column, paragraph 2 -----	3-20
X,P	WO 2016/145149 A1 (THE US SECRETARY OF THE ARMY ON BEHALF OF THE WALTER REED ARMY INST OF) 15 September 2016 (2016-09-15) page 5, lines 8-17 paragraphs [0037] - [0040] paragraph [0048] claims 1-19 -----	3-20
A	US 6 309 650 B1 (KIM HYUN SU ET AL) 30 October 2001 (2001-10-30) cited in the application examples 3,4; table 3 -----	1-20
T	RAFAEL A. LAROCCA ET AL: "Vaccine protection against Zika virus from Brazil", NATURE, vol. 536, no. 7617, 28 June 2016 (2016-06-28), pages 474-478, XP055314483, United Kingdom ISSN: 0028-0836, DOI: 10.1038/nature18952 abstract page 475, right-hand column, last paragraph - page 476, left-hand column, paragraph 1 -----	

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2016/082667

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2016145149	A1	15-09-2016	NONE

US 6309650	B1	30-10-2001	AU 748730 B2 13-06-2002
		CA 2301000 A1 11-03-1999	
		CN 1272879 A 08-11-2000	
		DE 69837211 T2 06-12-2007	
		DE 122009000037 I1 05-11-2009	
		DK 1025209 T3 25-06-2007	
		DK 1604685 T3 18-06-2012	
		EP 1025209 A1 09-08-2000	
		EP 1604685 A2 14-12-2005	
		ES 2281929 T3 01-10-2007	
		ES 2382946 T3 14-06-2012	
		JP 4161017 B2 08-10-2008	
		JP 2001514844 A 18-09-2001	
		MY 129773 A 30-04-2007	
		NL 300391 I1 03-08-2009	
		NZ 503522 A 29-06-2001	
		US 6309650 B1 30-10-2001	
		WO 9911762 A1 11-03-1999	
