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(56) Related Art
Anna Durbin ET AL, "Role of a ZIKV CHIM in vaccine evaluation", (2017-06-02), http://www.who.int/entity/blueprint/what/norms-standards/1_Durbin_CHIM.pdf?ua=1&usg=AOvVaw3sraJTiT8oBPlV6yWhMhVq, (2017-10-26)
Usp/institut Pasteur/fiocruz, "Workshop - Beyond Zika - A tripartite Initiative", (2016-08-29), URL: http://www.usp.br/aucani/zika/archive/Presentations_Afternoon_August_30.pdf, (2017-10-26)
PENELOPE KORAKA ET AL, "Bioinformatics in New Generation Flavivirus Vaccines", JOURNAL OF BIOMEDICINE AND BIOTECHNOLOGY, US, (2010-01-01), vol. 9, no. 5, doi:10.1155/2010/864029, ISSN 1110-7243, page 17PP

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(57) Abstract: The present invention relates to recombinant measles virus expressing Zika virus proteins and their applications, in particular in inducing preventive protection against Zika virus. The present invention is directed to recombinant measles virus (MV) expressing at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV), and the envelope (E) protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKVor a truncated version thereof, and concerns recombinant infectious particles of said MV-ZIKV able to replicate in a host after an administration, and also Virus Like Particles (VLPs) that contain these ZIKV proteins at their surface. The present invention provides means, in particular nucleic acids, vectors, cells and rescue systems to produce these recombinant infectious particles and VLPs. The present invention also relates to the use of these recombinant infectious particles and/ or VLPs, in particular under the form of a composition, more particularly in a vaccine formulation, for the prevention of an infection by ZIKV or for the preventive protection against clinical outcomes of ZIKV infection.

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RECOMBINANT MEASLES VIRUS EXPRESSING ZIKA VIRUS PROTEINS AND THEIR APPLICATIONS

The present invention relates to recombinant measles virus expressing Zika virus proteins and their applications, in particular in inducing preventive protection against Zika virus. The present invention is directed to recombinant measles virus (MV) expressing at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV), and the envelope (E) protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof, and concerns recombinant infectious particles of said MV-ZIKV able to replicate in a host after an administration, and also Virus Like Particles (VLPs) that contain these ZIKV proteins at their surface. The present invention provides means, in particular nucleic acids, vectors, cells and rescue systems to produce these recombinant infectious particles and VLPs. The present invention also relates to the use of these recombinant infectious particles and/or VLPs, in particular under the form of a composition, more particularly in a vaccine formulation, for the prevention of an infection by ZIKV or for the preventive protection against clinical outcomes of ZIKV infection.

ZIKV is an emerging mosquito-borne flavivirus. Although it was initially isolated in 1947, to date there are no specific treatments or any vaccines available against ZIKV disease, making it a truly neglected and emerging disease. The recent rapid spread of ZIKV in previously unaffected regions such as South Pacific islands and Latin America has provided strong epidemiological evidence that infection with this virus might be associated with neurological complications in adults and with an increase in severe congenital brain malformations of new-borns. Consequently, the World Health Organization (WHO) has declared the recent outbreak of the ZIKV a public health emergency.

ZIKV was initially isolated from a rhesus monkey in the Zika forest in Uganda in 1947 (*Gubler DJ, et al., eds. Fields Virology, 5th edn. Philadelphia, PA: Lippincott Williams & Wilkins Publishers, 2007: 1155–227; Dick GWA, et* *al. Trans R Soc Trop Med Hyg 1952; 46: 509–20*). The first human infection was reported in Nigeria in 1954 (*Macnamara FN. Trans R Soc Trop Med Hyg 1954; 48: 139–45*). Like dengue and chikungunya viruses, ZIKV adapted from an ancestral transmission cycle involving non-human primates and a broad spectrum of forest mosquito species as vectors to an urban cycle involving humans as reservoirs and the widely distributed Aedes mosquitoes as vectors (*Musso D, et al. Lancet 2015; 386: 243–44*). Since the 1950s, ZIKV had only been reported as circulating sporadically in Africa and Southeast Asia. In 2007, ZIKV was isolated for the first time in the Pacific, on the Micronesian island of Yap (*Duffy MR, et al. N Engl J Med 2009; 360: 2536–43*). Between October 2013 and April 2014, French Polynesia experienced the largest Zika outbreak ever reported at that time (*Cao-Lormeau VM, et al. Emerg Infect Dis 2013; 20: 1085–86*). More than 32,000 patients were suspected of ZIKV infection. Between 2014 and 2015, ZIKV spread to other Pacific islands, notably the Cook Islands and Easter Island (Chile). In March 2015, Brazil reported the autochthonous transmission of ZIKV (*Zanluca C, et al. Mem Inst Oswaldo Cruz 2015; 110: 569–72*) and declared an unprecedented outbreak 6 months later (*Dyer O. BMJ 2015; 351: h6983*) with preliminary estimates of 440,000 to 1.3 million cases of infection through December 2015 (*European Centre for Disease Prevention and Control, December 10, 2015*). As of March 2016, ZIKV infection has been reported from 43 countries and territories worldwide.

The current Zika epidemic is the largest epidemic ever recorded for this virus (*Abushouk et al. An updated review of Zika virus, J. Clin. Virol. 2016, 84, 53-58*). Although infection with ZIKV was usually associated with mild disease, its emergence in the Americas has coincided with a steep increase in patients developing Guillain-Barré syndrome. Moreover, infection with ZIKV has been linked to the birth of babies with neurological complications, in particular congenital microcephaly (*WHO. Guillain-Barré syndrome – El Salvador. Jan 21, 2016; ECDC. Rapid risk assessment. Zika virus epidemic in the Americas: potential association with microcephaly and Guillain-Barré syndrome. Dec 10, 2015; Soares de Araújo J, et al. Microcephaly in northeast Brazil: a review of 16 208 births between 2012 and 2015*), and it was shown that when pregnant women are exposed to ZIKV during the first trimester of pregnancy, the risk of microcephaly for the newborn is increased 50 times from 2/10 000 to 1/100 (*Cauchemez S, et al. Association between Zika virus and microcephaly in French Polynesia, 2013–15: a retrospective study. The Lancet 2016*). In February 2016, the WHO declared the suspected link between ZIKV and neurological disorders and neonatal malformations a Public Health Emergency of International Concern.

In this context, in March 2016, experts gathered at WHO agreed that the development of a preventive vaccine is a major priority to respond to Zika epidemics in the future. Pragmatic strategies were asked to fast track the development of a safe and effective vaccine. Due to the established link between ZIKV infection and the appearance of congenital microcephaly in babies born to infected mothers, one could argue that a Zika vaccine has to be suitable for use in pregnant women. However, no licensed vaccine is currently recommended for use during pregnancy. Moreover, with the demonstrated association of Zika infection with Guillain-Barré syndrome, the observation of possible sexual transmission, and the appearance of developmental defects probably appearing very early in pregnancy, it is very likely that the vaccine should be addressed to the general population. In any case a Zika vaccine will have to demonstrate an excellent safety profile, particularly concerning the risk of neurotropism.

To allow fast track development of a Zika vaccine, the inventors used one of the safest and most efficacious vaccines available, the live-attenuated measles vaccine, as a delivery vector for ZIKV protective antigens to ensure the timely availability of a preventive vaccine whenever a new epidemic occurs. This delivery platform technology has demonstrated proof of principle in humans and a preclinical track record of rapid adaptability and effectiveness for a variety of pathogens. Moreover, the manufacturing process for these measles vector-based vaccines has been optimized to give higher yields and purity than the standard manufacturing measles vaccine process. It uses standard equipment and thus lends itself to further scale up as well as technology transfer to low and middle-income countries.

Measles vaccination has been used for more than 40 years in over 1 billion children and is approximately 93% efficacious after one administration and 97% after 2 administrations. Attenuated measles vaccine strains have been shown to be genetically stable. Reversion to pathogenicity or integration into the host cell genome is virtually impossible and has never been observed. Taking advantage of these characteristics, the inventors previously cloned the attenuated measles Schwarz vaccine virus and developed a method to genetically manipulate this negative strand RNA virus into a versatile chimeric or recombinant vector (*Combredet, C. et al., 2003, J Virol, 77(21): 11546-11554*).

A prophylactic vaccine against ZIKV, as for any other target, has to be safe and efficacious. In addition, the special epidemiology of a rapidly emerging virus, affecting both industrialized and developing countries, and the threat of infections during pregnancy causing serious birth defects, calls for a number of additional features for an ideal ZIKV vaccine.

ZIKV infection during pregnancy is strongly suspected to cause birth defects. Although live vaccines are generally contraindicated during pregnancy, measles infections have not been connected to birth defects (*Rasmussen SA, et al. Obstet Gynecol. 2015 Jul;126 (1):163-70*), and accidental application of the MMR vaccine during pregnancy was not connected to congenital birth defects (*Swamy GK, et al. Obstet Gynecol. 2015 Jan;125(1):212-26*). In contrast to measles-based vaccine according to the invention, a live-attenuated Zika vaccine approach would raise very significant safety concerns if accidentally applied during pregnancy. It has to be seriously questioned, if a vaccine against Zika intended for use during pregnancy could be developed and licensed in any acceptable time frame to stop the current epidemic. Instead, a vaccine for adolescents with minimal safety concerns for accidental use during pregnancy seems the most practical and realistic intervention to eliminate Zika-induced disease. A measles-based vaccine would exactly meet that target profile.

The measles-based approach of the invention can meet all of the relevant criteria of a future ZIKV vaccine at least equally well or better than alternative approaches. In particular a non-adjuvanted measles-based ZIKV vaccine for children, adolescents and travelers represents one of the most likely candidates to be developed in a short time frame, has an excellent safety and efficacy profile, and has production and cost characteristics that are compatible with its use also in countries of limited economic strength.

To this end, a sequential development path was defined by the inventors. The first stage was the construction and characterisation of recombinant MV expressing at least ZIKV prM-E or E proteins as soluble secreted antigens. The characterisation included demonstration of Zika antigen expression, established growth characteristics in a production cell line, and analysis of genetic stability. Preclinical immunogenicity and protective efficacy of selected recombinant MV-Zika vaccine was evaluated in CD46-IFNAR mice susceptible to MV infection. The currently best candidate selected was evaluated for immunogenicity and protective efficacy in non-human primate model of ZIKV infection.

The inventors achieved the production of vaccines based on recombinant infectious replicative MV recombined with polynucleotides encoding at least ZIKV prM-E or E antigens, which are recovered when the recombinant virus replicates in particular in the host after administration. The invention thus relates to a live ZIKV vaccine active ingredient based on the widely used measles, in particular measles from the Schwarz strain, pediatric vaccine. In a preferred embodiment, this recombinant live MV-ZIKV vaccine yields ZIKV VLPs by replicating in infected cells.

MV is a non-segmented single-stranded, negative-sense enveloped RNA virus of the genus *Morbillivirus* within the family of *Paramyxoviridae*. This virus has been isolated in 1954 (*Enders, J. F., and T. C. Peebles. 1954. Propagation in tissue cultures of cytopathogenic agents from patients with measles. Proc. Soc. Exp. Biol. Med. 86:277-286*), and live-attenuated vaccines have been derived from this virus since then to provide vaccine strains, in particular from the Schwarz strain. Measles vaccines have been administered to hundreds of millions of children over the last 30 years and have proved its efficiency and safety. It is produced on a large scale in many countries and is

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distributed at low cost. For all these reasons, the inventors used attenuated MVs to generate recombinant MV particles stably expressing prM-E or E antigens of ZIKV, and possibly capable of expressing also VLPs.

According to a first aspect of the invention there is provided a nucleic acid construct comprising:

(1) a polynucleotide encoding at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV) and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 or SEQ ID NO: 32, or (ii) the E protein or truncated version of (i); and

(2) a cDNA molecule encoding a full-length, infectious antigenomic (+) RNA strand of a measles virus (MV);

wherein the polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof is operatively linked, in particular cloned into the cDNA molecule;

wherein the nucleic acid construct comprises the following polynucleotides from 5' to 3':

(a) a polynucleotide encoding the N protein of the MV;
(b) a polynucleotide encoding the P protein of the MV;
(c) the polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof;
(d) a polynucleotide encoding the M protein of the MV;
(e) a polynucleotide encoding the F protein of the MV;
(f) a polynucleotide encoding the H protein of the MV; and
(g) a polynucleotide encoding the L protein of the MV;

wherein said polynucleotides are operably linked in the nucleic acid construct and under a control of viral replication and transcription regulatory sequences such as MV leader and trailer sequences.

According to a second aspect of the invention there is provided a transfer vector plasmid comprising the nucleic acid construct according to the first aspect.

According to a third aspect of the invention there are provided transformed cells comprising inserted in their genome the nucleic acid construct according to the first aspect or comprising the transfer vector plasmid according to the second aspect.

According to a fourth aspect of the invention there are provided recombinant infectious replicating measles virus-Zika virus (MV-ZIKV) particles which comprise as their genome a nucleic acid construct according to the first aspect.

According to a fifth aspect of the invention there is provided a composition or an assembly of active ingredients comprising the recombinant infectious replicating MV-ZIKV particles according to the fourth aspect, in association with ZIKV-Virus Like Particles (VLPs) expressing the same ZIKV protein(s) as said MV-ZIKV particles, and a pharmaceutically acceptable vehicle.

According to a sixth aspect of the invention there is provided a method for preventing an infection by ZIKV in a subject or in the prevention of clinical outcomes of infection by ZIKV in a subject, such as in a human, comprising administering to the subject recombinant infectious replicating MV-ZIKV particles according to the fourth aspect in association with ZIKV-VLPs expressing the same ZIKV protein(s), or the composition or the assembly of active ingredients according to the fifth aspect.

According to a seventh aspect of the invention there is provided use of recombinant infectious replicating MV-ZIKV particles according to the fourth aspect in association with ZIKV-VLPs expressing the same ZIKV protein(s), or the composition or the assembly of active ingredients according to the fifth aspect for the manufacture of a medicament for the prophylactic treatment of infection by ZIKV or in the prevention of clinical outcomes of infection by ZIKV.

According to an eight aspect of the invention there is provided a process to rescue recombinant infections measles virus-Zika virus (MV-ZIKV) particles expressing at least (i) the precursor of membrane (prM) protein of a ZIKV and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 or SEQ ID NO: 32, or (ii) the E protein or truncated

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version of (i), and ZIKV Virus Like Particles (VLPs) expressing the same ZIKV protein(s), comprising:

1) co-transfecting helper cells, in particular HEK293 helper cells, that stably express T7 RNA polymerase, and measles N and P proteins with (i) the transfer vector plasmid according to the second aspect and with (ii) a vector, especially a plasmid, encoding the MV L polymerase;

2) cultivating said co-transfected helper cells in conditions enabling the production of recombinant MV-ZIKV particles;

3) propagating the thus produced recombinant MV-ZIKV particles by co-cultivating said helper cells of step 2) with cells enabling said propagation such as Vero cells;

4) recovering recombinant infectious replicating MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof, and ZIKV VLPs expressing the same ZIKV protein(s).

The invention thus relates to a nucleic acid construct which comprises:

(1) a polynucleotide encoding at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV), and the envelope (E) protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof; and

(2) a cDNA molecule encoding a full-length, infectious antigenomic (+) RNA strand of a measles virus (MV);

wherein the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof is operatively linked, in particular cloned into the cDNA molecule.

A nucleic acid construct according to the invention is in particular a purified DNA molecule, obtained or obtainable by recombination of various polynucleotides of different origins, operably linked together.

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The expression "*operably linked*" refers to the functional link existing between the different polynucleotides of the nucleic acid construct of the invention such that said different polynucleotides and nucleic acid construct are efficiently transcribed and if appropriate translated, in particular in cells or cell lines, especially in cells or cell lines used as part of a rescue system for the production of chimeric infectious MV particles of the invention or in host cells, especially in human cells.

In a particular embodiment of the invention, the construct is prepared by cloning a polynucleotide encoding at least (i) the prM protein of a ZIKV, and the E protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof, in the cDNA encoding a full-length, infectious antigenomic (+) RNA strand of a MV. Alternatively, a nucleic acid construct of the invention may be prepared using steps of synthesis of nucleic acid fragments or polymerization from a template, including by PCR

In a particular embodiment of the invention, the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, is cloned into an ATU (Additional Transcription Unit) inserted in the cDNA of the MV. ATU sequences are known from the skilled person and comprise, for use in steps of cloning into cDNA of MV, cis-acting sequences necessary for MV-dependent expression of a transgene, such as a promoter of the gene preceding, in MV cDNA, the insert represented by the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, and a multiple cloning sites cassette for insertion of said polynucleotide.

When used to carry out the invention, the ATU is advantageously located in the N-terminal sequence of the cDNA molecule encoding the full-length (+)RNA strand of the antigenome of the MV and is especially located between the P and M genes of this virus or between the H and L genes. It has been observed that the transcription of the viral RNA of MV follows a gradient from the 5' to the 3' end. This explains that, when inserted in the 5' end of the coding sequence of the cDNA, the ATU will enable a more efficient expression of the heterologous DNA sequence (*e.g.* the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof) that it contains.

The polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, may thus be inserted in any intergenic region of the cDNA molecule of the MV in particular in an ATU. Particular constructs of the invention are those illustrated in the examples.

In a preferred embodiment of the invention, the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, is inserted in the intergenic region of the P and M genes of the MV cDNA molecule, in particular in an ATU.

As used herein, the expression "*encoding*" defines the ability of the nucleic acid molecules to be transcribed and where appropriate translated for product expression into selected cells or cell lines. Accordingly, the nucleic acid construct may comprise regulatory elements controlling the transcription of the coding sequences, in particular promoters and termination sequences for the transcription and possibly enhancer and other cis-acting elements. These regulatory elements may be heterologous with respect to the ZIKV polynucleotide sequences.

The term "*protein*" is used interchangeably with the terms "*antigen*" or "*polypeptide*" and defines a molecule resulting from a concatenation of amino acid residues. In particular, the proteins disclosed in the application originate from the ZIKV and are structural proteins that may be identical to native proteins or alternatively that may be derived thereof by mutation, including by substitution (in particular by conservative amino acid residues) or by addition of amino acid residues or by secondary modification after translation or by deletion of portions of the native proteins(s) resulting in fragments having a shortened size with respect to the native protein of reference. Fragments are encompassed within the present invention to the extent that they bear epitopes of the native protein suitable for the elicitation of an immune response in a host in particular in a human host, preferably a response that enables the protection against ZIKV infection or against ZIKV associated disease. Epitopes are in particular of the type of B epitopes involved in the elicitation of a humoral immune response through the activation of the production of antibodies in a host to whom the protein has been administered or in whom it is expressed following administration of the infectious replicative particles of the invention. Epitopes may alternatively be of the type of T epitopes involved in elicitation of Cell Mediated Immune response (CMI response). Fragments may have a size representing more than 50% of the amino-acid sequence size of the native protein of ZIKV, preferably at least 90% or 95%. Alternatively, fragments may be short polypeptides with at least 10 amino acid residues, which harbor epitope(s) of the native protein. Fragments in this respect also include polyepitopes as defined herein.

In a particular embodiment of the invention, said nucleic acid construct complies with the rule of six (6) of the MV genome, *i.e.* the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, taken together with the cDNA molecule encoding the full-length, infectious antigenomic (+) RNA strand of the MV consist of a number of nucleotides that is a multiple of six.

The organization of the genome of MVs and their replication and transcription process have been fully identified in the prior art and are especially disclosed in Horikami S.M. and Moyer S.A. (*Curr. Top. Microbiol. Immunol. (1995) 191, 35-50*) or in Combredet C. *et al* (*Journal of Virology, Nov 2003, p11546-11554*) for the Schwarz vaccination strain of the virus or for broadly considered negative-sense RNA viruses, in Neumann G. et al (Journal of General Virology (2002) 83, 2635-2662).

The "*rule of six*" is expressed in the fact that the total number of nucleotides present in a nucleic acid representing the MV(+) strand RNA genome or in nucleic acid constructs comprising same is a multiple of six. The "rule of six" has been acknowledged in the state of the art as a requirement regarding the total number of nucleotides in the genome of the MV, which enables efficient or optimized replication of the MV genomic RNA. In the embodiments of the present invention defining a nucleic acid construct that meets the rule of six, said rule applies to the nucleic acid construct specifying the cDNA encoding the full-length MV (+) strand RNA genome and all inserted sequences, when taken individually or collectively. In this regard the rule of six applies to the cDNA encoding the full-length infectious antigenomic (+) RNA strand of the MV possibly and to the polynucleotide cloned into said cDNA and encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof.

In a particular embodiment of the invention, the nucleic acid construct comprises the following polynucleotides from 5' to 3':

(a) a polynucleotide encoding the N protein of the MV;
(b) a polynucleotide encoding the P protein of the MV;
(c) the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof;
(d) a polynucleotide encoding the M protein of the MV;
(e) a polynucleotide encoding the F protein of the MV;
(f) a polynucleotide encoding the H protein of the MV; and
(g) a polynucleotide encoding the L protein of the MV;

wherein said polynucleotides are operably linked in the nucleic acid construct and under a control of viral replication and transcription regulatory sequences such as MV leader and trailer sequences.

The expressions "*N protein*", "*P protein*", "*M protein*", "F protein" , "*H protein*" and "*L protein*" refer respectively to the nucleoprotein (N), the phosphoprotein (P), the matrix protein (M), the fusion protein (F), the hemagglutinin protein (H) and the RNA polymerase large protein (L) of a MV. These components have been identified in the prior art and are especially disclosed in Fields, Virology (*Knipe & Howley, 2001*).

In a preferred embodiment of the invention, the measles virus is an attenuated virus strain.

An "*attenuated strain*" of measles virus is defined as a strain that is avirulent or less virulent than the parent strain in the same host, while maintaining immunogenicity and possibly adjuvanticity when administered in a host *i.e.*, preserving immunodominant T and B cell epitopes and possibly the adjuvanticity such as the induction of T cell costimulatory proteins or the cytokine IL-12.

An attenuated strain of a MV accordingly refers to a strain which has been serially passaged on selected cells and, possibly, adapted to other cells to produce seed strains suitable for the preparation of vaccine strains, harboring a stable genome which would not allow reversion to pathogenicity nor integration in host chromosomes. As a particular “attenuated strain”, an approved strain for a vaccine is an attenuated strain suitable for the invention when it meets the criteria defined by the FDA (US Food and Drug Administration) *i.e.*, it meets safety, efficacy, quality and reproducibility criteria, after rigorous reviews of laboratory and clinical data (www.fda.gov/cber/vaccine/vacappr.htm).

Particular attenuated strains that can be used to implement the present invention and especially to derive the MV cDNA of the nucleic acid construct are the Schwarz strain, the Zagreb strain, the AIK-C strain and the Moraten strain. All these strains have been described in the prior art and access to them is provided in particular as commercial vaccines.

In a particular embodiment of the invention, the cDNA molecule is placed under the control of heterologous expression control sequences. The insertion of such a control for the expression of the cDNA, is favorable when the expression of this cDNA is sought in cell types which do not enable full transcription of the cDNA with its native control sequences.

In a particular embodiment of the invention, the heterologous expression control sequence comprises the T7 promoter and T7 terminator sequences. These sequences are respectively located 5’ and 3’ of the coding sequence for the full length antigenomic (+)RNA strand of MV and from the adjacent sequences around this coding sequence.

In a particular embodiment of the invention, the cDNA molecule, which is defined hereabove is modified i.e., comprises additional nucleotide sequences or motifs.

In a preferred embodiment, the cDNA molecule of the invention further comprises, at its 5’-end, adjacent to the first nucleotide of the nucleotide sequence encoding the full-length antigenomic (+)RNA strand of the MV approved vaccine strain, a GGG motif followed by a hammerhead ribozyme sequence and which comprises, at its 3’-end, adjacent to the last nucleotide of said nucleotide sequence encoding the full length anti-genomic (+)RNA strand, the sequence of a ribozyme. The Hepatitis delta virus ribozyme (δ) is appropriate to carry out the invention.

The GGG motif placed at the 5' end, adjacent to the first nucleotide of the above coding sequence improves the efficiency of the transcription of said cDNA coding sequence. As a requirement for the proper assembly of measles virus particles is the fact that the cDNA encoding the antigenomic (+)RNA of the nucleic acid construct of the invention complies with the rule of six, when the GGG motif is added, a ribozyme is also added at the 5' end of the coding sequence of the cDNA, 3' from the GGG motif, in order to enable cleavage of the transcript at the first coding nucleotide of the full-length antigenomic (+)RNA strand of MV.

In a particular embodiment of the invention, in order to prepare the nucleic acid construct of the invention, the preparation of a cDNA molecule encoding the full-length antigenomic (+) RNA of a MV disclosed in the prior art is achieved by known methods. Said cDNA provides especially the genome vector when it is inserted in a vector such as a plasmid.

A particular cDNA molecule suitable for the preparation of the nucleic acid construct of the invention is the one obtained using the Schwarz strain of MV. Accordingly, the cDNA used within the present invention may be obtained as disclosed in WO2004/000876 or may be obtained from plasmid pTM-MVSchw deposited by Institut Pasteur at the Collection Nationale de Culture de Microorganismes (CNCM), 28 rue du Dr Roux, 75724 Paris Cedex 15, France, under No I-2889 on June 12, 2002, the sequence of which is disclosed in WO2004/000876 incorporated herein by reference. The plasmid pTM-MVSchw has been obtained from a Bluescript plasmid and comprises the polynucleotide coding for the full-length measles virus (+) RNA strand of the Schwarz strain placed under the control of the promoter of the T7 RNA polymerase. It has 18967 nucleotides and a sequence represented as SEQ ID NO: 1. cDNA molecules (also designated cDNA of the measles virus or MV cDNA for convenience) from other MV strains may be similarly obtained starting from the nucleic acid purified from viral particles of attenuated MV such as those described herein.

The cDNA used within the present invention may also be obtained from plasmid pTM2-MVSchw-gfp deposited by Institut Pasteur at the Collection

Nationale de Culture de Microorganismes (CNCM), 28 rue du Dr Roux, 75724 Paris Cedex 15, France, under No I-2890 on June 12, 2002. It has 19795 nucleotides and a sequence represented as SEQ ID NO: 2. This plasmid contains the sequence encoding the eGFP marker that may be deleted.

The nucleic acid construct of the invention is suitable and intended for the preparation of recombinant infectious replicative measles – Zika virus (MV-ZIKV) and accordingly said nucleic acid construct is intended for insertion in a transfer genome vector that as a result comprises the cDNA molecule of the measles virus, especially of the Schwarz strain, for the production of said MV-ZIKV and yield of at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, in particular ZIKV VLPs. The pTM-MVSchw plasmid or the pTM2-MVSchw plasmid is suitable to prepare the transfer vector, by insertion of the ZIKV polynucleotide(s) necessary for the expression of at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof. The recombinant infectious replicating MV-ZIKV particles may be recovered from rescue helper cells or in production cells and may optionally be recovered with VLP expressing the ZIKV antigens disclosed in accordance with the invention.

The invention thus relates to a transfer vector, which is used for the preparation of recombinant MV-ZIKV particles when rescued from helper cells. Advantageously, the transfer vector of the invention is a transfer vector plasmid suitable for transfection of said helper cells or of production cells, comprising the nucleic acid construct of the invention, in particular is a plasmid obtained from a Bluescript plasmid, such as pMV-ZIKV.

In a particular embodiment of the invention, the transfer vector plasmid has the sequence of SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167, preferably has the sequence of SEQ ID NO: 165.

The invention also concerns the use of said transfer vector to transform cells suitable for rescue of viral MV-ZIKV particles, in particular to transfect or to transduce such cells respectively with plasmids or with viral vectors harboring the nucleic acid construct of the invention, said cells being selected for their capacity to express required MV proteins for appropriate replication, transcription and encapsidation of the recombinant genome of the virus corresponding to the nucleic acid construct of the invention in recombinant infectious replicating MV-ZIKV particles.

In a preferred embodiment, the invention relates to transformed cells comprising inserted in their genome the nucleic acid construct according to the invention or comprising the transfer vector plasmid according to the invention, wherein said cells are in particular eukaryotic cells, such as avian cells, in particular CEF cells, mammalian cells such as HEK293 cells or yeast cells.

Polynucleotides are thus present in said cells, which encode proteins that include in particular the N, P and L proteins of a MV (*i.e.*, native MV proteins or functional variants thereof capable of forming ribonucleoprotein (RNP) complexes), preferably as stably expressed proteins at least for the N and P proteins functional in the transcription and replication of the recombinant viral MV-ZIKV particles. The N and P proteins may be expressed in the cells from a plasmid comprising their coding sequences or may be expressed from a DNA molecule inserted in the genome of the cell. The L protein may be expressed from a different plasmid. It may be expressed transitory. The helper cell is also capable of expressing a RNA polymerase suitable to enable the synthesis of the recombinant RNA derived from the nucleic acid construct of the invention, possibly as a stably expressed RNA polymerase. The RNA polymerase may be the T7 phage polymerase or its nuclear form (nlsT7).

In an embodiment of the invention, the cDNA clone of MV is from the same MV strain as the N protein and/or the P protein and/or the L protein. In another embodiment of the invention, the cDNA clone of a MV is from a different strain of virus than the N protein and/or the P protein and/or the L protein.

The invention also relates to a process for the preparation of recombinant infectious measles virus (MV) particles comprising:

1) transferring, in particular transfecting, the nucleic acid construct of the invention or the transfer vector containing such nucleic acid construct in a

helper cell line which also expresses proteins necessary for transcription, replication and encapsidation of the antigenomic (+)RNA sequence of MV from its cDNA and under conditions enabling viral particles assembly; and

2) recovering the recombinant infectious MV-ZIKV particles expressing at least (i) the prM protein of a ZIKV, and the E protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof.

In a particular embodiment of the invention, this process comprises:

1) transfecting helper cells with a nucleic acid construct according to the invention and with a transfer vector, wherein said helper cells are capable of expressing helper functions to express an RNA polymerase, and to express the N, P and L proteins of a MV virus ;
2) co-cultivating said transfected helper cells of step 1) with passaged cells suitable for the passage of the MV attenuated strain from which the cDNA originates ;
3) recovering the recombinant infectious MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof.

In another particular embodiment of the invention, the method for the production of recombinant infectious MV-ZIKV particles comprises :

1) recombining a cell or a culture of cells stably producing a RNA polymerase, the N protein of a MV and the P protein of a MV, with a nucleic acid construct of the invention and with a vector comprising a nucleic acid encoding the L protein of a MV, and

2) recovering the recombinant infectious MV-ZIKV particles from said recombinant cell or culture of recombinant cells.

In a particular embodiment of said process, recombinant MV are produced, which express at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, in particular ZIKV VLPs expressing the same ZIKV protein(s).

Preferably, the invention relates to a process to rescue recombinant infectious measles virus-Zika virus (MV-ZIKV) particles expressing at least (i) the precursor of membrane (prM) protein of a ZIKV, and the envelope (E) protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof, and ZIKV VLPs expressing the same ZIKV protein(s), comprising:

1) co-transfecting helper cells, in particular HEK293 helper cells, that stably express T7 RNA polymerase, and measles N and P proteins with (i) the transfer vector plasmid according to the invention and with (ii) a vector, especially a plasmid, encoding the MV L polymerase;

2) cultivating said co-transfected helper cells in conditions enabling the production of recombinant MV-ZIKV particles;

3) propagating the thus produced recombinant MV-ZIKV particles by co-cultivating said helper cells of step 2) with cells enabling said propagation such as Vero cells;

4) recovering replicating infectious replicating MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, and ZIKV VLPs expressing the same ZIKV protein(s).

According to a particular embodiment of said process, the transfer vector plasmid has the sequence of SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167, preferably has the sequence of SEQ ID NO: 165.

As used herein, the term "*recombining*" means introducing at least one polynucleotide into a cell, for example under the form of a vector, said polynucleotide integrating (entirely or partially) or not integrating into the cell genome (such as defined above).

According to a particular embodiment, recombination can be obtained with a first polynucleotide, which is the nucleic acid construct of the invention. Recombination can, also or alternatively, encompasses introducing a polynucleotide, which is a vector encoding a RNA polymerase large protein (L) of a MV, whose definition, nature and stability of expression has been described herein.

In accordance with the invention, the cell or cell lines or a culture of cells stably producing a RNA polymerase, a nucleoprotein (N) of a measles virus and a polymerase cofactor phosphoprotein (P) of a measles virus is a cell or cell line as defined in the present specification or a culture of cells as defined in the present specification, *i.e.*, are also recombinant cells to the extent that they have been modified by the introduction of one or more polynucleotides as defined above. In a particular embodiment of the invention, the cell or cell line or culture of cells, stably producing the RNA polymerase, the N and P proteins, does not produce the L protein of a measles virus or does not stably produce the L protein of a measles virus, *e.g.*, enabling its transitory expression or production.

The production of recombinant infectious replicating MV-ZIKV particles of the invention may involve a transfer of cells transformed as described herein. The term "*transfer*" as used herein refers to the plating of the recombinant cells onto a different type of cells, and particularly onto monolayers of a different type of cells. These latter cells are competent to sustain both the replication and the production of infectious MV-ZIKV particles, *i.e.*, respectively the formation of infectious viruses inside the cell and possibly the release of these infectious viruses outside of the cells. This transfer results in the co-culture of the recombinant cells of the invention with competent cells as defined in the previous sentence. The above transfer may be an additional, *i.e.*, optional, step when the recombinant cells are not efficient virus-producing culture, *i.e.*, when infectious MV-ZIKV particles cannot be efficiently recovered from these recombinant cells. This step is introduced after further recombination of the recombinant cells of the invention with nucleic acid construct of the invention, and optionally a vector comprising a nucleic acid encoding a RNA polymerase large protein (L) of a measles virus.

In a particular embodiment of the invention, a transfer step is required since the recombinant cells, usually chosen for their capacity to be easily recombined are not efficient enough in the sustaining and production of recombinant infectious MV-ZIKV particles. In said embodiment, the cell or cell line or culture of cells of step 1) of the above-defined methods is a recombinant cell or cell line or culture of recombinant cells according to the invention.

Cells suitable for the preparation of the recombinant cells of the invention are prokaryotic or eukaryotic cells, particularly animal or plant cells, and more particularly mammalian cells such as human cells or non-human mammalian cells or avian cells or yeast cells. In a particular embodiment, cells, before recombination of its genome, are isolated from either a primary culture or a cell line. Cells of the invention may be dividing or non-dividing cells.

According to a preferred embodiment, helper cells are derived from human embryonic kidney cell line 293, which cell line 293 is deposited with the ATCC under No. CRL-1573. Particular cell line 293 is the cell line disclosed in the international application WO2008/078198 and referred to in the following examples.

According to another aspect of this process, the cells suitable for passage are CEF cells. CEF cells can be prepared from fertilized chicken eggs as obtained from EARL Morizeau, 8 rue Moulin, 28190 Dangers, France, or from any other producer of fertilized chicken eggs.

The process which is disclosed according to the present invention is used advantageously for the production of infectious replicative MV-ZIKV particles and optionally VLPs expressing ZIKV antigens appropriate for use as immunization compositions.

The invention thus relates to an immunogenic composition whose active principle comprises infectious replicative MV-ZIKV particles rescued from the nucleic acid construct of the invention and in particular obtained by the process disclosed.

The nucleic acid construct of the invention and the MV-CHIKV of the invention encode or express at least (i) the prM protein of a ZIKV, and the E protein of a ZIKV or a truncated version thereof, or (ii) the E protein of a ZIKV or a truncated version thereof.

By "protein of a ZIKV" is meant a “protein” as defined herein, the sequence of which is identical to a counterpart in a strain of ZIKV, including a polypeptide which is a native mature or precursor of a protein of ZIKV or is a fragment thereof or a mutant thereof as defined herein. In the present invention, a "*protein of a ZIKV*" is in particular an antigen (prM or E or their derivatives as disclosed herein) designed using a consensus sequence for the ZIKV. In particular, said antigen is designed using the consensus amino acid sequence of Zika viruses as observed circulating from 2015 and onward, notably to include the S139N change that generated a novel potential N glycosylation site in prM that was absent from the African lineage, and the V763M in E. Thus the inventors included this S139N mutation that was present in all Asian lineage sequences, but did not include single mutations in particular isolates. The inventors observed that the amino acid sequence of the Asian strain BeH818995 (GenBank: KU365777) corresponded to the consensus amino acid sequence of Zika viruses as observed circulating from 2015 and onward.

In particular a fragment or a mutant having at least 50%, at least 80%, in particular advantageously at least 90% or preferably at least 95% amino acid sequence identity to a naturally occurring ZIKV capsid or envelope protein. Amino acid sequence identity can be determined by alignment by one skilled in the art using manual alignments or using the numerous alignment programs available. Fragments or mutants of ZIKV proteins of the invention may be defined with respect to the particular amino acid sequences illustrated herein.

According to a preferred embodiment, the invention also concerns modifications and optimization of the polynucleotide to allow an efficient expression of the at least (i) prM of ZIKV, and E protein of ZIKV or truncated version thereof, or (ii) E protein of ZIKV or truncated version thereof, at the surface of chimeric infectious particles of MV-ZIKV in the host, in particular the human host.

According to this embodiment, optimization of the polynucleotide sequence can be operated avoiding cis-active domains of nucleic acid molecules: internal TATA-boxes, chi-sites and ribosomal entry sites; AT-rich or GC-rich sequence stretches; ARE, INS, CRS sequence elements; repeat sequences and RNA secondary structures ; cryptic splice donor and acceptor sites, branch points.

The optimized polynucleotides may also be codon optimized for expression in a specific cell type. This optimization allows increasing the efficiency of chimeric infectious particles production in cells without impacting the expressed protein(s).

In a particular embodiment of the invention, the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, has been optimized for a Macaca codon usage or has been optimized for a human codon usage.

The optimization of the polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof may be performed by modification of the wobble position in codons without impacting the identity of the amino acid residue translated from said codon with respect to the original one.

Optimization is also performed to avoid editing-like sequences from Measles virus. The editing of transcript of Measles virus is a process which occurs in particular in the transcript encoded by the *P* gene of Measles virus. This editing, by the insertion of extra G residues at a specific site within the *P* transcript, gives rise to a new protein truncated compared to the P protein. Addition of only a single G residue results in the expression of the V protein, which contains a unique carboxyl terminus (*Cattaneo R et al., Cell. 1989 Mar 10;56(5):759-64*).

In a particular embodiment of the invention, *measles editing-like sequences* have been deleted from said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof. The following *measles editing-like sequences* can be mutated: AAAGGG, AAAAGG, GGGAAA, GGGGAA, TTAAA, AAAA, as well as their complementary sequence: TTCCCC, TTTCCC, CCTTTT, CCCCTT, TTTAA, TTTT. For example, AAAGGG can be mutated in AAAGGC, AAAAGG can be mutated in AGAAGG or in TAAAGG or in GAAAGG, and GGGAAA in GCGAAA.

In a particular embodiment of the invention, the native and codon-optimized nucleotide sequences of the polynucleotide encoding particular peptides/proteins/antigen as well as the amino acid sequences of these peptides/proteins/antigen of the invention are the sequences disclosed as SEQ ID Nos: 3-164 and mentioned in Table 1 below. These sequences are also represented in **Figures 3A-3D**.

In a particular embodiment of the invention, the transfer vector plasmid pTM2-MVSchw_A1_Zikasp_ZikaprME has the optimized sequence of SEQ ID NO: 165, the transfer vector plasmid pTM2-MVSchw_insert 4 has the native sequence of SEQ ID NO: 166 and the transfer vector plasmid pTM2-MVSchw_insert 5 has the native sequence of SEQ ID NO: 167, as mentioned in Table 1 below.

In another particular embodiment of the invention, the native nucleotide sequences of the polynucleotide encoding insert 4 or insert 5 as well as the amino acid sequences of said insert 4 or insert 5 of the invention are the sequences disclosed as SEQ ID Nos: 168-171 and mentioned in Table 1 below. Insert 4 (SEQ ID NO: 169) is similar to Zikasp_Zika_prMEd404 (SEQ ID NO: 54) but with a shorter sp in 5'. Insert 5 (SEQ ID NO: 171) is similar to Zikasp'_ZikaEd445 (SEQ ID NO: 75) with 2 minor differences in 5'.

Table 1. Native and codon-optimized nucleotide sequences of the polynucleotide encoding particular peptides/proteins as well as amino acid sequences of these peptides/proteins used in the invention.

Name of the compound, *i.e.* peptide/protein/antigen (abbreviation)	**SEQ ID NO of the native nucleotide sequence of the polynucleotide encoding the compound**	**SEQ ID NO of the codon-optimized nucleotide sequence of the polynucleotide encoding the compound**	**SEQ ID NO of the amino acid sequence of the compound**
Signal peptide from the capsid of ZIKV (**sp**)	3	4	5
Signal peptide from the membrane protein of ZIKV (**sp'**)	6	7	8
Signal peptide from the capsid of JEV (**JEVsp**)	9	10	11
Signal peptide from the fusion protein of MV (**MVsp**)	12	13	14
Modified signal peptide from the fusion protein of MV (**MVsp'**)	15	16	17
Precursor of membrane (**prM**) protein of ZIKV	18	19	20
Full-length **E** protein of ZIKV	21	22	23
E protein of ZIKV truncated at amino acid position 456 (**Ed456**)	24	25	26
E protein of ZIKV truncated at amino acid position 445 (**Ed445**)	27	28	29
E protein of ZIKV truncated at amino acid position 404 (**Ed404**)	30	31	32
E stem region of ZIKV	33	34	35
Intermediate domain between E stem and E anchor regions of ZIKV	36	37	38
E anchor region of ZIKV	39	40	41
Transmembrane (TM) and intracytoplasmic tail of MV F protein	42	43	44
Zikasp_ZikaprME protein (A1)	45	46	47
Zikasp_Zika_prMEd456 protein (A2)	48	49	50
Zikasp_Zika_prMEd445 protein (A3)	51	52	53
Zikasp_Zika_prMEd404 protein (A4)	54	55	56
Zikasp_ZikaE protein (A5)	57	58	59
Zikasp_ZikaEd456 protein (A6)	60	61	62
Zikasp_ZikaEd445 protein (A7)	63	64	65
Zikasp_ZikaEd404 protein (A8)	66	67	68
Zikasp'_ZikaE protein (A9)	69	70	71
Zikasp'_ZikaEd456 protein (A10)	72	73	74
Zikasp'_ZikaEd445 protein (A11)	75	76	77
Zikasp'_ZikaEd404 protein (A12)	78	79	80
JEVsp_ZikaprME protein (B1)	81	82	83
JEVsp_Zika_prMEd456 protein (B2)	84	85	86

JEVsp_Zika_prMEd445 protein (B3)	87	88	89
JEVsp_Zika_prMEd404 protein (B4)	90	91	92
JEVsp_ZikaE protein (B5)	93	94	95
JEVsp_ZikaEd456 protein (B6)	96	97	98
JEVsp_ZikaEd445 protein (B7)	99	100	101
JEVsp_ZikaEd404 protein (B8)	102	103	104
MVsp_ZikaprME (C1)	105	106	107
MVsp_Zika_prMEd456 (C2)	108	109	110
MVsp_Zika_prMEd445 (C3)	111	112	113
MVsp_Zika_prMEd404 (C4)	114	115	116
MVsp_ZikaE (C5)	117	118	119
MVsp_ZikaEd456 (C6)	120	121	122
MVsp_ZikaEd445 (C7)	123	124	125
MVsp_ZikaEd404 (C8)	126	127	128
MVsp_ZikaprME_MVTMintracyto (C9)	129	130	131
MVsp_Zika_MVTMintracytoE (C10)	132	133	134
MVsp'_ZikaprME (D1)	135	136	137
MVsp'_Zika_prMEd456 (D2)	138	139	140
MVsp'_Zika_prMEd445 (D3)	141	142	143
MVsp'_Zika_prMEd404 (D4)	144	145	146
MVsp'_ZikaE (D5)	147	148	149
MVsp'_ZikaEd456 (D6)	150	151	152
MVsp'_ZikaEd445 (D7)	153	154	155
MVsp'_ZikaEd404 (D8)	156	157	158
MVsp'_ZikaprME_MVTMintracyto (D9)	159	160	161
MVsp'_Zika_MVTMintracytoE (D10)	162	163	164

Name of the transfer vector plasmid	**SEQ ID NO**
pTM2-MVSchw_A1_Zikasp_ZikaprME (optimized sequence)	165
pTM2-MVSchw_insert 4 (native sequence)	166
pTM2-MVSchw_insert 5 (native sequence)	167

Name of the compound, *i.e.* peptide/protein/antigen (abbreviation)	**SEQ ID NO of the native nucleotide sequence of the polynucleotide encoding the compound**	**SEQ ID NO of the amino acid sequence of the compound**
Insert 4	168	169
Insert 5	170	171

In a particular embodiment of the invention, said ZIKV is from the African lineage, in particular from the African strain ArB1362 (GenBank: KF383115) or African isolate IbH_30656 (GenBank: HQ234500), or from the Asian lineage, in particular from the Asian strain BeH818995 (GenBank: KU365777), preferably is from ZIKV strains that circulated in the Pacific and Americas since 2013.

In another particular embodiment of the invention, said ZIKV corresponds to various lineages of ZIK viruses including strains that circulated in the Pacific and Americas since 2013.

In a preferred embodiment of the invention, the prM protein of the ZIKV has an amino acid sequence which is a consensus amino acid sequence representative of the prM sequences of a selection of various strains of ZIKV including from the Asian lineage, in particular is from the ZIKV strain BeH818995. The E protein of the ZIKV or the truncated version thereof has an amino acid sequence which is a consensus amino acid sequence representative of the E sequences of a selection of various strains of ZIKV including from the Asian lineage, in particular is from the ZIKV strain BeH818995.

In a particular embodiment of the invention, said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV (sp) or the signal peptide from the capsid of a JEV (JEVsp) or the signal peptide from the fusion protein of MV (MVsp) or the modified signal peptide from the fusion protein of MV (MVsp') and the signal peptide from the membrane protein of the ZIKV (sp'), or

said polynucleotide encoding at least (ii) the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV (sp) or the signal peptide from the membrane protein of the ZIKV (sp') or the signal peptide from the capsid of a JEV (JEVsp) or the signal peptide from the fusion protein of MV (MVsp) or the modified signal peptide from the fusion protein of MV (MVsp').

In a preferred embodiment of the invention, said polynucleotide encoding at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV and the signal peptide from the membrane protein of the ZIKV, or

said polynucleotide encoding at least (ii) the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV or the signal peptide from the membrane protein of the ZIKV.

In a particular embodiment of the invention, the polynucleotide encoding the E protein encodes either the full-length E protein or its soluble form lacking the two C-terminal transmembrane domains of the full-length E protein.

In a preferred embodiment of the invention, the polynucleotide encoding the truncated version of the E protein is selected from the group consisting of (i) the polynucleotide encoding the E protein truncated at amino acid position 456 of the full-length E protein of the ZIKV, *i.e.* the E protein lacking the anchor region and the intermediate domain between the stem and anchor regions, (ii) the polynucleotide encoding the E protein truncated at position 445 of the full-length E protein of the ZIKV, *i.e.* the E protein lacking the anchor region, the intermediate domain between the stem and anchor regions and a fragment of the second helix that composed the stem region, and (iii) the polynucleotide encoding the E protein truncated at position 404 of the full-length E protein of the ZIKV, *i.e.* the E protein lacking the stem region, the intermediate domain between the stem and anchor regions, and the anchor region.

In a preferred embodiment of the invention, the polynucleotide encodes the prM protein of the ZIKV whose sequence is SEQ ID NO: 20, and the polynucleotide encodes the E protein of the ZIKV or the truncated version thereof whose sequence is selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 26, SEQ ID NO: 29 and SEQ ID NO: 32.

In a preferred embodiment of the invention, the polynucleotide encoding the prM protein of the ZIKV has the sequence of SEQ ID NO: 19, and the polynucleotide encoding the E protein of the ZIKV or a truncated version thereof has a sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28 and SEQ ID NO: 31.

In a particular embodiment of the invention, said nucleic acid construct comprises a sequence selected from the group consisting of SEQ ID NOs: 45-164 and 168-171.

In a preferred embodiment of the invention, said nucleic acid construct comprises a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170, preferably has the sequence of SEQ ID NO: 46, SEQ ID NO: 55 or SEQ ID NO: 76, more preferably has the sequence of SEQ ID NO: 46.

In a preferred embodiment of the invention, the nucleic acid construct comprises the sequence from nucleotide at position 83 to nucleotide at position 18404 in the sequence of SEQ ID NO: 165, or the sequence from nucleotide at position 83 to nucleotide at position 18074 in the sequence of SEQ ID NO: 166, or the sequence from nucleotide at position 83 to nucleotide at position 17702 in the sequence of SEQ ID NO: 167.

The invention also concerns recombinant infectious replicating measles virus-Zika virus (MV-ZIKV) particles, which comprise as their genome a nucleic acid construct according to the invention.

In a particular embodiment of the invention, said recombinant infectious replicating MV-ZIKV particles are rescued from a helper cell line expressing an RNA polymerase recognized by said cell line, for example a T7 RNA polymerase, a nucleoprotein (N) of a MV, a phosphoprotein (P) of a MV, and optionally an RNA polymerase large protein (L) of a MV, and which is further transfected with the transfer vector plasmid according to the invention.

Said recombinant infectious replicating MV-ZIKV particles are thus produced by a method comprising expressing the nucleic acid construct according to the invention in a host cell comprising an RNA polymerase recognized by said host cell, for example a T7 RNA polymerase, a nucleoprotein (N) of a MV, a phosphoprotein (P) of a MV, and optionally an RNA polymerase large protein (L) of a MV.

According to a particular embodiment of the invention, said particles comprise in their genome a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170, preferably has the sequence of SEQ ID NO: 46, SEQ ID NO: 55 or SEQ ID NO: 76, more preferably has the sequence of SEQ ID NO: 46.

The obtained at least (i) prM protein of the ZIKV, and E protein of the ZIKV or truncated version thereof, or (ii) E protein of the ZIKV or truncated version thereof, are also able to auto-assemble into ZIK virus-like-particles (VLPs), with the MV-ZIKV particles.

As used herein, the term "*virus-like particle*" (VLP) refers to a structure that in at least one attribute resembles a virus but which has not been demonstrated to be infectious as such. VLPs in accordance with the invention do not carry genetic information encoding the proteins of the VLPs, in general, VLPs lack a viral genome and, therefore, are non-infectious and non-replicative. In accordance with the present invention, VLPs can be produced in large quantities and are expressed together with recombinant infectious MV-ZIKV particles. Said VLPs are VLPs of ZIKV.

According to another aspect, the invention relates to recombinant infectious MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, in particular by reference to their nucleic acid and polypeptide sequences. The recombinant infectious MV-ZIKV advantageously expresses at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, as VLPs.

The invention also relates to a composition or an assembly of active ingredients comprising the recombinant infectious replicating MV-ZIKV particles according to the invention, and a pharmaceutically acceptable vehicle.

The invention also concerns the association, in a composition, of VLPs comprising at least (i) the prM protein of the ZIKV, and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein of the ZIKV or the truncated version thereof, with recombinant infectious replicating MV-ZIKV-MV particles.

According to a preferred embodiment of the invention, the recombinant MV vector is designed in such a way and the production process involves cells such that the virus particles produced in helper cells transfected or transformed with said vector, originated from a MV strain adapted for vaccination, enable the production of recombinant infectious replicating MV and the production of ZIKV-VLPs for use in immunogenic compositions, preferably protective or even vaccine compositions.

Advantageously, the genome of the recombinant infectious MV-ZIKV particles of the invention is replication competent. By "replication competent', it is meant a nucleic acid, which when transduced into a helper cell line expressing the N, P and L proteins of a MV, is able to be transcribed and expressed in order to produce new viral particles.

Replication of the recombinant virus of the invention obtained using MV cDNA for the preparation of the recombinant genome of MV-ZIKV can also be achieved *in vivo* in the host, in particular the human host to which recombinant MV-ZIKV is administered.

The invention also concerns a composition or an assembly of active ingredients comprising the recombinant infectious replicating MV-ZIKV particles according to the invention, in association with ZIKV-VLPs expressing the same ZIKV protein(s) as said MV-ZIKV particles.

According to a preferred embodiment of the invention, said composition or assembly of active ingredients is used in the elicitation of an immune response, in particular a protective immune response, against ZIKV by the elicitation of antibodies directed against said ZIKV protein(s), and/or of a cellular immune response, in a host, in particular a human host in need thereof.

Said composition or assembly of active ingredients accordingly may comprise a suitable vehicle for administration *e.g.* a pharmaceutically acceptable vehicle to a host, especially a human host and may further comprise but not necessarily adjuvant to enhance immune response in a host. The inventors have indeed shown that the administration of the active ingredients of the invention may elicit an immune response without the need for adjuvantation.

According to a particular embodiment of the invention, said composition or assembly of active ingredients comprises a pharmaceutically acceptable vehicle.

The invention relates in particular to a composition, in particular an immunogenic composition, preferably a vaccine composition for administration to children, adolescents or travelers.

In a particular embodiment, said composition or vaccine is used for preventive protection against African and Asian strains of ZIKV.

Said composition or vaccine is used for protection against ZIKV infection or against clinical outcomes of infection by ZIKV (protection against ZIKV disease) in a prophylactic treatment. Such a vaccine composition has advantageously active principles (active ingredients) which comprise recombinant infectious replicating MV-ZIKV particles rescued from the vector as defined herein optionally associated with VLPs comprising the same ZIKV proteins.

In the context of the invention, the terms “associated” or “*in association*” refer to the presence, in a unique composition, of both recombinant infectious replicating MV-ZIKV particles and the above-mentioned ZIKV proteins, in particular as VLPs, usually as physically separate entities.

The invention also concerns the recombinant infectious replicating MV-ZIKV particles according to the invention in association with the above-mentioned ZIKV proteins, in particular in association with ZIKV-VLPs expressing the same ZIKV proteins, or the composition or the assembly of active ingredients according to the invention, for use in the prevention of an infection by ZIKV in a subject, or in the prevention of clinical outcomes of infection by ZIKV in a subject, in particular in a human.

The invention also concerns the recombinant infectious replicating MV-ZIKV particles according to the invention in association with the above-mentioned ZIKV proteins, in particular in association with ZIKV-VLPs expressing the same ZIKV proteins, for use in an administration scheme and according to a dosage regime that elicit an immune response, advantageously a protective immune response, against ZIKV infection or induced disease, in particular in a human host.

The administration scheme and dosage regime may require a unique administration of a selected dose of the recombinant infectious replicating MV-ZIKV particles according to the invention in association with the above-mentioned ZIKV proteins, in particular in association with ZIKV-VLPs expressing the same ZIKV proteins.

Alternatively it may require multiple administration doses in a prime-boost regimen. Priming and boosting may be achieved with identical active ingredients consisting of said recombinant infectious replicating MV-ZIKV particles in association with the above-mentioned ZIKV proteins, in particular in association with ZIKV-VLPs expressing the same ZIKV proteins.

Alternatively priming and boosting administration may be achieved with different active ingredients, involving said recombinant infectious replicating MV-ZIKV particles in association with the above-mentioned ZIKV proteins, in particular in association with ZIKV-VLPs expressing the same ZIKV proteins, in at least one of the administration steps and other active immunogens of ZIKV, such as the above-mentioned ZIKV proteins or ZIKV-VLPs expressing the same ZIKV proteins, in other administration steps.

Administration of recombinant infectious replicating MV-ZIKV particles according to the invention in association with ZIKV-VLPs expressing the same ZIKV proteins elicits an immune response and especially elicits antibodies that are cross-reactive for various ZIKV strains. Accordingly, it has been shown that administration of the active ingredients according to the invention, when prepared with the coding sequences of a particular strain of ZIKV, can elicit an immune response against a group of strains of ZIKV.

Considering available knowledge on doses of vaccines suitable for other pathogens (such as HBV or HPV) which involve the administration of VLPs and also for known human MV vaccines, the inventors have determined that the recovery of ZIKV-VLPs with the recombinant MV-ZIKV enables proposing administration of effective low doses of the active ingredients. Indeed, considering that the recombinant MV-ZIKV enables production of around 10^4 ZIKV-VLPs per recombinant infectious replicating MV-ZIKV particle, and considering that the currently known doses for human MV vaccines are in the range of 10^3 to 10^5 TCID50, a suitable dose of recombinant MV-ZIKV to be administered may be in the range of 0.1 to 10ng, in particular 0.2 to 6ng, and possibly as low as 0.2 to 2ng. For comparison doses of VLPs administered in the case of HBV or HPV vaccines are in the range of 10µg which means that a dose of recombinant MV-ZIKV vaccine could comprise around 2 000 or up to 5 000 to 10 000 times less VLPs.

According to a particular embodiment of the invention, the immunogenic or vaccine composition defined herein may also be used for protection against an infection by the measles virus.

Other features and advantages of the invention will be apparent from the examples which follow and will also be illustrated in the figures.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Schematic representation of Zika virus genome.

Figure 2. Phylogenetic trees of the main human pathogenic flaviviruses based on the amino acid sequences of the E protein (left) and of the polymerase NS5 protein (right). JEV, Japanese encephalitis virus; MVEV, Murray Valley encephalitis virus; POWV, Powassan virus; SLEV, Saint Louis encephalitis virus; TBEV, tick-borne encephalitis virus; YFV, yellow fever virus; WNV, West Nile virus.

Figure 3. Schematic representation of Zika virus antigens. Protein domains are drawn to scale. Zika, Zika virus; JEV, Japanese encephalitis virus; MV, Measles virus. A. 12 variants of the Zika antigen, where the native signal peptide from the capsid (sp) or from the membrane protein (sp') of Zika virus is used. B. 8 variants of the chimeric JEV-Zika antigen, where a signal peptide of the capside of JEV is used. C. 10 variants of the MV-Zika antigen, where the signal peptide of the fusion protein of MV (MVsp) is used. D. 10 variants of the MV Zika antigen, where a modified signal peptide of the fusion protein of MV (MVsp') is used.

Figure 4. **Schematic representation of MV Vector.** MV genes are indicated: N (nucleoprotein), PVC (phoshoprotein and V/C proteins), M (matrix), F (fusion), H (hemagluttinin), L (polymerase), T7 (T7 RNA polymerase promoter), hh (hammerhead ribozyme), T7t (T7 RNA polymerase terminator), ∂ (hepatitis delta virus ribozyme), red arrows (additional transcription units).

Figure 5. **Single immunization in mice.** A) Zika antibody response measured in mice sera by ELISA at one month after a single immunization. MV-prMEd404 (native sequence, insert 4); MV-ssEd445 (native sequence, insert 5). B) Survival of immunized mice after challenge by Zika virus. C) Zika virus viremia in serums of immunized mice (determined by RT-qPCR) at different days after challenge. D) IFN-gamma Elispot detected in splenocytes of mice one week after immunization with MV-Zika or control MVSchw viruses. Elispots are detected against MV (Schwarz), Zika virus (Zika) and Concanavalin A as a control.

Figure 6. **Prime-boost immunization in mice.** A) Zika antibody response measured in mice sera by ELISA at day 30, 45 and 55 after two immunizations. B) Detection of Zika virus neutralizing antibodies in the sera of mice immunized with two injections of MV-prMEd404 (native sequence, insert 4), MV-ssEd445 (native sequence, insert 5). C) Survival of immunized mice after challenge with

low dose of Zika virus. D) Zika virus viremia in serums of immunized mice (determined by RT-qPCR) at different days after challenge.

Figure 7. **Recombinant MV expressing the full-length prME Zika antigen (construct A1) produces Zika VLPs**. Vero cells were infected with three different clones of rMV-Zika_A1 (1, 2, 3) for 48 hours. Cell lysates and medium were collected. Supernatant medium was clarified by low-speed centrifugation (1500 rpm) then concentrated by ultracentrifugation on a 20% sucrose cushion for 3 hours (36000 rpm). All material was analyzed by western blot to detect the Zika E protein (50 kD) with 4G2 panflavi monoclonal antibody. (A) Cell lysates, (B) Concentrated medium, (C) Non-concentrated medium and positive and negative controls. Positive control is a lysate of Vero cells transfected for 48 hours with pcDNA5 plasmid expressing the Zika A1 antigen. The positive E protein recovered in panel B after ultracentrifugation demonstrates that high density VLPs were produced in the supernatant of infected Vero cells.

Figure 8. Zika virus antigen expression assay. HEK293T cells were transfected with each codon-optimized construct, and cell lysates and medium were collected after 48h. Supernatant medium was clarified by low-speed centrifugation (1500 rpm), and then a fraction was concentrated by ultracentrifugation on a 20% sucrose cushion for 3 hours (36000 rpm). All material was analyzed by western blot to detect the Zika virus E protein (~50 kD) with the 4G2 pan-flavivirus antibody. (L) Cell lysates, (S) non-concentrated medium, and (U) ultracentrifugated medium.

Figure 9. Expression of Zika virus antigen A1 from measles vector and growth curve of recombinant MV-Zika-A1. (A) Immunofluorescence analysis showed large syncytia in Vero cells infected for 24 hours with MV-Zika-A1 (the Zika virus E protein was detected with the 4G2 pan-flavivirus antibody). (B) Replication of recombinant MV-Zika-A1 virus on Vero cells at 32°C after infection with a multiplicity of infection of 0.01 (titers were determined by limiting dilution and the Karber method).

Figure 10. Antibody response to ZIKV in immunized CD46-IFNAR$^{-/-}$ mice. The antibody titers against ZIKV EDIII were determined using indirect ELISA in mice sera collected after prime and boost with MV-ZIKV-A1, MV-prMEd404 (native sequence, insert 4), MV-ssEd445 (native sequence, insert 5), MV-ZIKV-A12 or control empty MV-Schwarz. Readings from wells coated with mock antigens were subtracted from wells with ZIKV-EDIII and the ZIKV specific IgG titers were calculated as the reciprocal of the highest dilution of an individual serum giving an absorbance of 0.5. A strong antibody response to ZIKV was induced in immunized mice with slightly higher values for A1 (highly reproducible) and A12 (more variability).

Figure 11. ZIKV neutralizing antibody titers in immunized CD46-IFNAR$^{-/-}$ mice. Neutralizing antibody titers against ZIKV were determined by using plaque reduction neutralizing tests ($PRNT_{50}$) in mice sera collected after last boost with MV-ZIKV-A1, MV-prMEd404 (native sequence, insert 4), MV-ssEd445 (native sequence, insert 5), MV-ZIKV-A12 or control empty MV-Schwarz and before challenge. The strongest neutralizing titers were observed with the MV-ZIKV-A1 construct.

Figure 12. Protection of immunized CD46-IFNAR$^{-/-}$ mice from ZIKV non-lethal challenge. Mice immunized twice with MV-ZIKV-A1, MV-ZIKV-A12 or control empty MV-Schwarz were challenged with 10^3 ffu of ZIKV (Asian-South American lineage, isolated in December 2015) one month after the last immunization. Viral loads were determined by RT-qPCR. LOD indicates the limit of detection of the RT-qPCR. Mice immunized with construct MV-ZIKV-A1 were all protected from viremia while mice immunized with MV-ZIKV-A12 or empty MV Schwarz control were infected.

Figure 13. Protection of immunized CD46-IFNAR$^{-/-}$ mice from ZIKV lethal challenge. Mice immunized twice with MV-ZIKV-A1, or control empty MV-Schwarz were challenged with 10^3 ffu of ZIKV (Mouse adapted strain of the African lineage) one month after the last immunization. Animals were

monitored for morbidity and mortality for 15 days. All animals immunized with MV-ZIKV-A1 survived without presenting signs of disease, while all control mice died by day 8.

<u>EXAMPLES</u>

Generation of vaccine candidates

Previous experiences with different flaviviruses (dengue, West Nile, Japanese encephalitis, tick-borne encephalitis) widely demonstrated that the flaviviral surface envelope (E) proteins are able to elicit protective neutralizing antibodies that allow reducing virus infectivity. The ZIKV genome consists of a single-stranded positive sense RNA molecule of ~10800 kb of length with 2 flanking non-coding regions (5' and 3' NCR) and a single long open reading frame encoding a polyprotein that is cleaved into three structural proteins (capsid (C), precursor of membrane (prM), envelope (E)) and seven non-structural proteins (NS) (**Figure 1**). The E protein (53 kDa) is the major virion surface protein involved in various aspects of the viral cycle, mediating binding to target cells and membrane fusion.

The inventors therefore chose to express the Zika virus E protein. Several forms of E protein were selected in order to express either soluble secreted proteins or anchored proteins onto the surface of VLPs. The following Zika virus antigens were cloned and expressed from a mammalian expression plasmid in human cells: prM-E and different forms of E with or without the stem or anchor region. These proteins contain either the original signal peptide sequence of Zika virus E or a heterologous signal peptide sequence from JEV or MV fusion protein. These proteins contain the signalase cleavage site located between the prM and the E sequences (**Figures 3A, 3B, 3C, 3D**).

Antigens selection and design

The Zika antigens were selected based on previous works concurring into suggesting that envelope antigens of flaviviruses may be able to elicit neutralizing antibodies and T cell responses. Selecting a suitable antigen should however take into consideration the evolution of the virus over time and the variety of existing virus strains. To this end, the inventors reconstructed the phylogeny of representative members of the flavivirus family, including Zika virus, using only the amino acid region of the flavivirus polyprotein corresponding to the envelope (E) gene. Unlike phylogenetic analyses based on the full genome, or the polymerase (NS5) of flaviviruses, where the closest relative of Zika virus are neurotropic viruses such as Saint-Louis Encephalitis virus, the inventors noticed that Zika E appeared closer to DENV E (**Figure 2**) (*Barba-Spaeth, et al. Nature 2016, 536, 48-53)*. The inventors then proceeded to identify the different domains of Zika membrane (M), its precursor (prM) and E proteins through structural homology modelling based on available data on DENV (*Ekins et al. Illustrating and homology modeling the proteins of the Zika virus, F1000Research 2016, 5:275*). The inventors also identified the signal peptides at the end of the Capsid (C) gene, just upstream of prM, using again homology modelling with dengue virus as a reference, as well as publicly available algorithms to predict signal peptide sequences (http://sigpep.services.came.sbg.ac.at/signalblast.html; http://www.cbs.dtu.dk/services/SignalP/; http://www.predisi.de/). The inventors chose to include the signal peptide sequence to induce the export and secretion of the candidate antigen, either the full-length prM-E, or the E only, outside the cells. For the E antigen, the inventors also predicted the signal peptide at the end of M, just upstream of E, and designed versions of the antigen using this native signal (**Figure 3A**). In addition, the inventors also designed chimeric antigens where the native signal peptide of Zika virus was replaced with the signal peptide present at the end of JEV C (**Figure 3B**), or the signal peptide present at the N-terminal of the fusion protein (F) of MV (**Figure 3C**), hypothesizing that these sequences would provide enhanced export of the candidate antigens. The inventors designed an additional version of the chimeric antigen including the signal peptide of F from MV, where two amino acids corresponding to the junction between the end of the signal peptide of F and the beginning of F itself were removed (**Figure 3D**).

Secondly, the inventors also designed shorter variations of the antigens by removing C terminal fragments of the E protein corresponding to the predicted stem and/or anchor domains, including the intermediate region between the stem and anchor (as predicted by comparison to DENV). The aim of these modifications that reduced antigens size was to generate antigens that were able to form VLPs. For a third variant, the inventors removed the anchor, the intermediate domain between the anchor and the stem, as well as a fragment of the second helix that composed the stem, this time in homology modelling with WNV (variant Ed445).

Finally, the inventors designed chimeric prM-E and E antigens using the signal peptide from MV F protein, and replacing Zika E anchor by the transmembrane (TM) and intracytoplasmic tail of MV F protein (**Figures 3C and 3D**).

For the selection sequence of the antigen itself, the inventors analyzed all publicly available sequences of Zika virus (both Asian and African lineages), as well as unpublished sequences generated by the inventors, from the epidemic in South America and Pacific. Based on the epidemiological data reporting an association of congenital syndromes and neurological afflictions in adults with only the Asian lineage, the inventors designed an antigen using the consensus amino acid sequence of Zika viruses as observed circulating from 2015 and onward, notably to include the S139N change that generated a novel potential N glycosylation site in prM that was absent from the African lineage, and the V763M in E.

The sequences were codon-optimized for Homo sapiens expression and adapted to measles vector cloning and to the "rule of six" (total number of nucleotides divisible by 6). Regions very rich (> 80%) or very poor (< 30%) in GC were avoided to increase RNA stability, a high CAI value (0.97) was obtained to increase translation efficacy, the following CIS active sequences were avoided: internal TATA-boxes, chi-sites, ribosomal entry sites, AT- or GC-rich sequence stretches, ARE, INS, CRS elements, repeat sequences, RNA secondary structures, cryptic splice donor and acceptor sites, branch points. The following measles virus editing sequences were avoided where possible: AAAGGG, AAAAGG, GGGAAA, GGGGAA, TTAAA, AAAA, and also their complementary sequences on the same strand: TTCCCC, TTTCCC, CCTTTT, CCCTT, TTTAA, TTTT. The enzyme restriction sites BssHII, BsiWI were avoided internally and inserted at both ends for cloning purpose.

Antigen expression in mammalian cells

The optimized antigen sequences were cloned into pcDNA5 mammalian expression plasmid and transfected into HEK293 cells. The size and level of expression of each antigen were characterized after western blotting using appropriate antibodies for detection.

Antigen expression in measles vector

The optimized Zika antigen sequences were inserted into the MV vector in different additional transcription units, according to the desired level of expression. After sequencing of the measles vector plasmids expressing the different Zika antigens, the replicating recombinant vectors were generated by reverse genetics using a cell-based system previously developed (*Combredet, C. et al., 2003, J Virol, 77(21): 11546-11554*), and the rescued viruses were amplified and titrated on Vero cells. The recombinant viruses were grown on Vero cells to document the expression of Zika proteins detected both in supernatants and in cells by using Western Blot and indirect immunofluorescence staining with appropriate antibodies. The presence of Zika virus VLPs (in prM/E expressing vectors) was identified after ultracentrifugation of culture medium and western blot (**Figure 7**). The correct processing of antigens in infected cells was checked by Western Blot. The vectors with the best expression capacity of Zika antigens were isolated by serial dilution and single plaque cloning before amplification on Vero cells.

Growth capacity of recombinant vaccine virus

The growth capacity of selected vaccine viruses was compared with standard MV Schwarz. Growth curve analysis was performed in Vero cell culture by using different multiplicity of infection then titration.

Stability of recombinant vaccine virus

The best vaccine vectors selected were tested for their genetic stability by serial passaging over 10 cell culture passages on Vero cell culture followed by western blot for antigen expression and full sequencing analysis.

Preclinical evaluation of first MV-Zika recombinant in mice

Single immunization

The two recombinant vectors MV-prMEd404 (native sequence, insert 4) and MV-ssEd445 (native sequence, insert 5) were evaluated in CD46/IFNAR mice susceptible to measles infection. Mice were immunized with one or two intraperitoneal injections with defined infectious units of vaccine virus and functional antibodies and cell-mediated immune responses were analysed using both standard and specifically developed assays. Binding antibodies to Zika virus were determined with ELISA and neutralizing antibodies with specific plaque reduction neutralization test (PRNT). The T cell responses were analysed by Elispot assay using Zika virus-specific peptides for *ex vivo* stimulation of splenic cells. The vaccine vectors were then tested for protective efficacy: immunized mice were challenged with a lethal dose of Zika virus. A dose-response challenge was previously established in CD46/IFNAR mice showing that doses between 10^2 and 10^6 focus forming unit (ffu) of Zika virus African strain HD78788 (adapted to mouse) efficiently kill these mice.

In a first experiment 6 mice per group were immunized with a single intraperitoneal injection of 10^6 TCID50 of MV-prMEd404 (native sequence, insert 4), MV-ssEd445 (native sequence, insert 5) or empty MVSchw as a control. Blood was taken before immunization and at day 30 after immunization, and Zika virus ELISA titers were determined (**Figure 5A**).

The immunized mice were then challenged at day 30 by intraperitoneal injection of 10^6 ffu of Zika virus African strain HD78788 (mouse adapted). Morbidity and mortality were controlled during 12 days (**Figure 5B**) and Zika virus viremia was determined in serum by qRT-PCR (**Figure 5C**).

To determine T-cell response to the vaccine, another group of CD46/IFNAR mice were immunized by MV-prMEd404 (insert 4) or empty

MVSchw and spleens were collected at 8 days after immunization. Elispot assay was performed on freshly extracted splenocytes using MVSchw or Zika virus to re-stimulate T-cells or concanavalin A as a control (**Figure 5D**).

Prime-boost immunization

In a second set of experiments, groups of CD46/IFNAR mice were immunized with two successive intraperitoneal injections of 10^6 TCID50 of MV-prMEd404 (native sequence, insert 4), MV-ssEd445 (native sequence, insert 5) or empty MVSchw as a control. Blood was taken before immunization and at day 30, 45 and 55 after immunizations and Zika virus ELISA titers were determined (**Figure 6A**). Neutralizing antibodies were determined in sera collected at day 50 using a specific neutralization test of Zika virus (**Figure 6B**). The immunized mice were then challenged at day 60 by intraperitoneal injection of 10^6 ffu of Zika virus African strain HD78788 (mouse adapted). Morbidity and mortality were controlled during 12 days (**Figure 6C**) and Zika virus viremia was determined in serum by qRT-PCR at days 2, 4 and 6 post infection (**Figure 6D**).

Preclinical evaluation in Non-Human Primates (NHP)

Validation of the ZIKV strain used in the NHP challenge study

Because little is known about the physiopathology of ZIKV in cynomolgus macaque (*Macaca fascicularis*), two animals were inoculated in a preliminary assay with three doses of Zika wild-type virus (10^4, 10^5 and 10^6 pfu) to assess the viral stock and associated clinics in macaques. These two animals were submitted to the same follow-up than vaccinated and challenged animals but for a 6-month period. The following points were addressed: Virology (qRT-PCR; clinics (Rash, Fever); Blood cell count (Lymphocytes, Monocytes, Granulocytes, platelettes); Biochemistry (ASAT, ALAT, CRP); Non-specific (innate and inflammatory) and specific immune response: Cytokines/chemokines by luminex, NK, B and T cell profile (14 colors flow cytometry), Antibodies (neutralizing, binding) on serial sera samples, T cells functional response and memory cells (ELISpot, ICS). Shedding of the virus in biological fluid (saliva, tears, genital fluids) was assessed by qRT-PCR and/or isolation methods at various time-points.

Vaccine immunogenicity study in NHP

Macaques were immunized with one or two subcutaneous injections at 3 months interval of defined infectious units of vaccine virus. Humoral and cell-mediated immune responses were determined at different times post immunization. Macaques were then challenged with infectious doses of ZIKV. Infectious viremia and clinical signs were determined. For this task, twenty-one adult cynomolgus macaques were selected to be negative for anti-flaviviruses and anti-measles antibodies; Two groups of 7 animals were vaccinated with a single dose or a prime boost regiment with the best MV-ZIKV recombinant virus (MV-prMEd404 native) selected. Immunity (Humoral and cell associated) was explored and virology was followed up to 1 month post vaccination. Clinics and biological parameters are assessed in parallel to a third group of 7 animals vaccinated with the control empty MVSchw strain following the prime boost schedule. Antibody neutralization titer was determined.

Vaccine Efficacy study in NHP

Immunized NHP were challenged with ZIKV two months after immunization. ZIKV viremia level (qRT-PCR) was analyzed in blood, saliva and tears. Inflammation and immune response was assessed in plasma (neutralizing Ab, cytokines).

Expression assays

The expression assays performed for all constructs generated (**Figure 8**) showed a strong expression for several of them. Signal was detected in the ultracentrifugated fraction, which was compatible with the generation of virus-like particles, in varying amounts for some candidate antigens, notably A1 and A12. These two antigens were thus further cloned into the measles vector and demonstrated high-level expression as shown by immunofluorescence

(**Figure 9A**). The recombinant MV-ZIKV-A1 vector replicated similarly to standard MV Schwarz virus, although with a lower final titer (**Figure 9B**).

Tested for their immunogenicity in CD46/IFNAR mice, MV-ZIKV-A1 and MV-ZIKV-A12 vectors elicited strong immune responses following a prime and boost regimen with 1-month interval, comparable to MV-prMEd404 and MV-ssEd445 vectors, as detected by ELISA (**Figure 10**). However, different amounts of neutralizing antibodies were induced (**Figure 11**). Only the candidate MV-ZIKV-A1 induced a strong neutralizing response (2 log stronger). This correlated with the complete protection conferred to mice by immunization with MV-ZIKV-A1 (**Figure 12**) against viremia, as well as protection from a lethal challenge (**Figure 13**).

In conclusion, this study demonstrated that the A1 full-length Zika antigen expressed in MV vector was able to provide sterile protection from infectious and lethal challenge of immunized animals, correlating with strong neutralizing antibody induction.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as, an acknowledgement or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

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The claims defining the invention are as follows:

1. A nucleic acid construct which comprises:

(1) a polynucleotide encoding at least (i) the precursor of membrane (prM) protein of a Zika virus (ZIKV) and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 or SEQ ID NO: 32, or (ii) the E protein or truncated version of (i); and

(2) a cDNA molecule encoding a full-length, infectious antigenomic (+) RNA strand of a measles virus (MV);

wherein the polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof is operatively linked to the cDNA molecule;

wherein the nucleic acid construct comprises the following polynucleotides from 5' to 3':

(a) a polynucleotide encoding the N protein of the MV;
(b) a polynucleotide encoding the P protein of the MV;
(c) the polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof;
(d) a polynucleotide encoding the M protein of the MV;
(e) a polynucleotide encoding the F protein of the MV;
(f) a polynucleotide encoding the H protein of the MV; and
(g) a polynucleotide encoding the L protein of the MV;

wherein said polynucleotides are operably linked in the nucleic acid construct and under a control of viral replication and transcription regulatory sequences such as MV leader and trailer sequences.

2. The nucleic acid construct according to claim 1, wherein the polynucleotide of (1) and the cDNA molecule of (2) together consist of a number of nucleotides that is a multiple of six.

3. The nucleic acid construct according to claim 1 or 2, wherein said measles virus is an attenuated virus strain selected from the group consisting

of the Schwarz strain, the Zagreb strain, the AIK-C strain and the Moraten strain.

4. The nucleic acid construct according to any one of claims 1 to 3, wherein said polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof, has been optimized for a Macaca codon usage or has been optimized for a human codon usage.

5. The nucleic acid construct according to any one of claims 1 to 4, wherein measles editing-like sequences have been deleted from said polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof.

6. The nucleic acid construct according to any one of claims 1 to 5, wherein said ZIKV is from the African lineage or the Asian lineage.

7. The nucleic acid construct according to any one of claims 1 to 6, wherein said polynucleotide encoding at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV and the signal peptide from the membrane protein of the ZIKV, or
wherein said polynucleotide encoding at least (ii) the E protein or truncated version thereof, further encodes (iii) the signal peptide from the capsid of the ZIKV or the signal peptide from the membrane protein of the ZIKV.

8. The nucleic acid construct according to any one of claims 1 to 7, wherein the polynucleotide encoding the E protein as defined in (i) or (ii) of claim 1 encodes either the full-length E protein or its soluble form lacking the two C-terminal transmembrane domains of the full-length E protein.

9. The nucleic acid construct according to any one of claims 1 to 7, wherein the polynucleotide encoding the truncated version of the E protein as defined in (i) or (ii) of claim 1 is selected from the group consisting of (i) the polynucleotide encoding the E protein truncated at amino acid position 456 of the full-length E protein of the ZIKV of SEQ ID NO: 23, (ii) the polynucleotide encoding the E protein truncated at amino acid position 445 of the full-length E protein of the ZIKV of SEQ ID NO: 23 and (iii) the polynucleotide encoding the E protein truncated at amino acid position 404 of the full-length E protein of the ZIKV of SEQ ID NO: 23.

10. The nucleic acid construct according to any one of claims 1 to 9, wherein the polynucleotide encodes the prM protein of the ZIKV whose sequence is SEQ ID NO: 20, and the polynucleotide encodes the E protein of the ZIKV or the truncated version thereof whose sequence is selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 26, SEQ ID NO: 29 and SEQ ID NO: 32.

11. The nucleic acid construct according to any one of claims 1 to 10, wherein the polynucleotide encoding the prM protein of the ZIKV has the sequence of SEQ ID NO: 19, and the polynucleotide encoding the E protein of the ZIKV or the truncated version thereof has a sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28 and SEQ ID NO: 31.

12. The nucleic acid construct according to any one of claims 1 to 11, wherein said nucleic acid construct comprises a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170.

13. The nucleic acid construct according to claim 12, wherein said nucleic acid construct comprises a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 55 and SEQ ID NO: 76.

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14. The nucleic acid construct according to any one of claims 1 to 13, which comprises the sequence from nucleotide at position 83 to nucleotide at position 18404 in the sequence of SEQ ID NO: 165, or the sequence from nucleotide at position 83 to nucleotide at position 18074 in the sequence of SEQ ID NO: 166, or the sequence from nucleotide at position 83 to nucleotide at position 17702 in the sequence of SEQ ID NO: 167.

15. A transfer vector plasmid, comprising the nucleic acid construct according to any one of claims 1 to 14.

16. The transfer vector plasmid according to claim 15, whose sequence is SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167.

17. Transformed cells comprising, inserted in their genome, the nucleic acid construct according to any one of claims 1 to 14 or comprising the transfer vector plasmid according to claim 15 or 16.

18. Transformed cells according to claim 17, wherein said cells are eukaryotic cells, such as avian cells, mammalian cells or yeast cells.

19. Recombinant infectious replicating measles virus-Zika virus (MV-ZIKV) particles, which comprise as their genome a nucleic acid construct according to any one of claims 1 to 14.

20. The recombinant infectious replicating MV-ZIKV particles according to claim 19, which are rescued from a helper cell line expressing an RNA polymerase recognized by said cell line, for example a T7 RNA polymerase, a nucleoprotein (N) of a MV, a phosphoprotein (P) of a MV, and which is further transfected with the transfer vector plasmid according to claim 15 or 16.

21. The recombinant infectious replicating MV-ZIKV particles according to claim 20, wherein the helper cell line further expresses an RNA polymerase large protein (L) of a MV.

22. The recombinant infectious replicating MV-ZIKV particles according to any one of claims 19 to 21, wherein said particles comprise in their genome a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 70, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 168 and SEQ ID NO: 170.

23. The recombinant infectious replicating MV-ZIKV particles according to claim 22, wherein said particles comprise in their genome a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO: 46, SEQ ID NO: 55 and SEQ ID NO: 76.

24. A composition or an assembly of active ingredients comprising the recombinant infectious replicating MV-ZIKV particles according to any one of claims 19 to 23, in association with ZIKV-Virus Like Particles (VLPs) expressing the same ZIKV protein(s) as said MV-ZIKV particles, and a pharmaceutically acceptable vehicle.

25. The composition or the assembly of active ingredients according to claim 24 for use in the elicitation of a protective immune response against ZIKV by the elicitation of antibodies directed against said ZIKV protein(s), and/or of a cellular immune response, in a host in need thereof, such as a human host.

26. A method for preventing an infection by ZIKV in a subject or in the prevention of clinical outcomes of infection by ZIKV in a subject, such as in a human, comprising administering to the subject recombinant infectious replicating MV-ZIKV particles according to any one of claims 19 to 23 in association with ZIKV-VLPs expressing the same ZIKV protein(s), or the composition or the assembly of active ingredients according to claim 24 or 25.

27. Use of recombinant infectious replicating MV-ZIKV particles according to any one of claims 19 to 23 in association with ZIKV-VLPs expressing the same ZIKV protein(s), or the composition or the assembly of active ingredients

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according to claim 24 or 25 for the manufacture of a medicament for the prophylactic treatment of infection by ZIKV or in the prevention of clinical outcomes of infection by ZIKV.

28. A process to rescue recombinant infectious measles virus-Zika virus (MV-ZIKV) particles expressing at least (i) the precursor of membrane (prM) protein of a ZIKV and the envelope (E) protein of a ZIKV or a truncated version thereof of SEQ ID NO: 26, SEQ ID NO: 29 or SEQ ID NO: 32, or (ii) the E protein or truncated version of (i), and ZIKV Virus Like Particles (VLPs) expressing the same ZIKV protein(s), comprising:
1) co-transfecting helper cells, in particular HEK293 helper cells, that stably express T7 RNA polymerase, and measles N and P proteins with (i) the transfer vector plasmid according to claim 15 or 16 and with (ii) a vector encoding the MV L polymerase;
2) cultivating said co-transfected helper cells in conditions enabling the production of recombinant MV-ZIKV particles;
3) propagating the thus produced recombinant MV-ZIKV particles by co-cultivating said helper cells of step 2) with cells enabling said propagation such as Vero cells;
4) recovering recombinant infectious replicating MV-ZIKV particles expressing at least (i) the prM protein of the ZIKV and the E protein of the ZIKV or the truncated version thereof, or (ii) the E protein or truncated version thereof, and ZIKV VLPs expressing the same ZIKV protein(s).

29. The process according to claim 28, wherein the transfer vector plasmid has the sequence of SEQ ID NO: 165, SEQ ID NO: 166 or SEQ ID NO: 167.

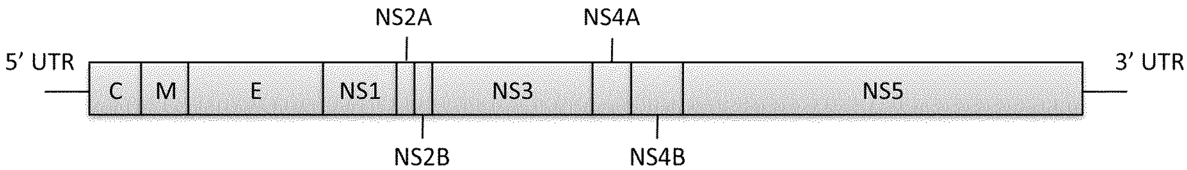


Figure 1

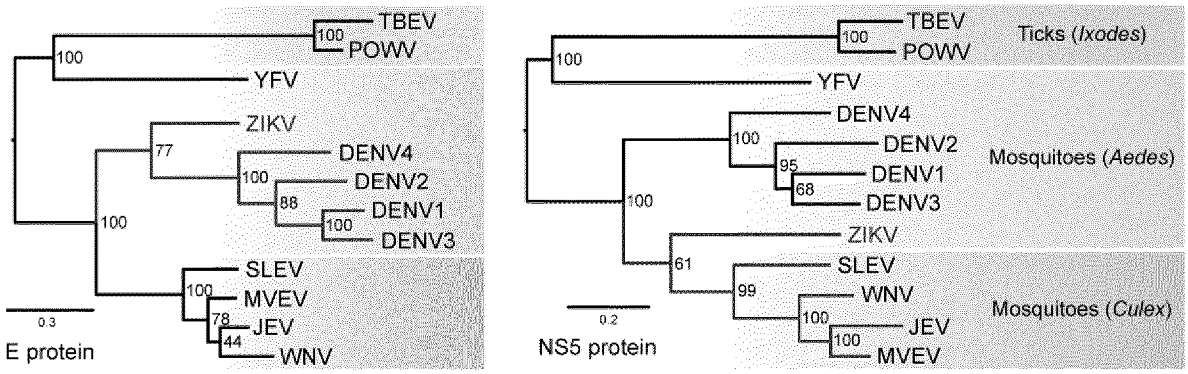


Figure 2

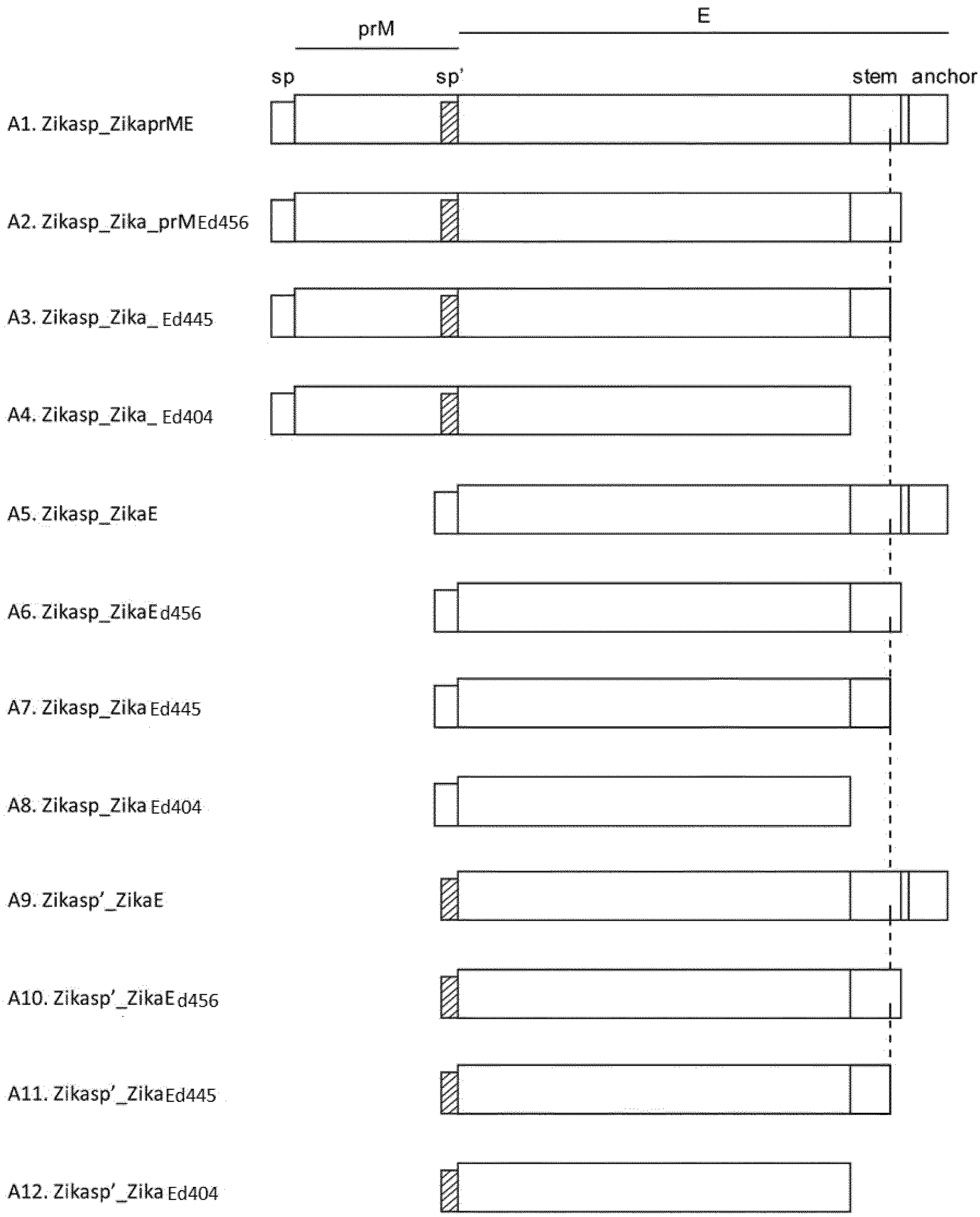

prM
E
sp
sp'
stem
anchor
A1. Zikasp_ZikaprME
A2. Zikasp_Zika_prMEd456
A3. Zikasp_Zika_ Ed445
A4. Zikasp_Zika_ Ed404
A5. Zikasp_ZikaE
A6. Zikasp_ZikaEd456
A7. Zikasp_Zika Ed445
A8. Zikasp_Zika Ed404
A9. Zikasp'_ZikaE
A10. Zikasp'_ZikaEd456
A11. Zikasp'_ZikaEd445
A12. Zikasp'_Zika Ed404

Figure 3A

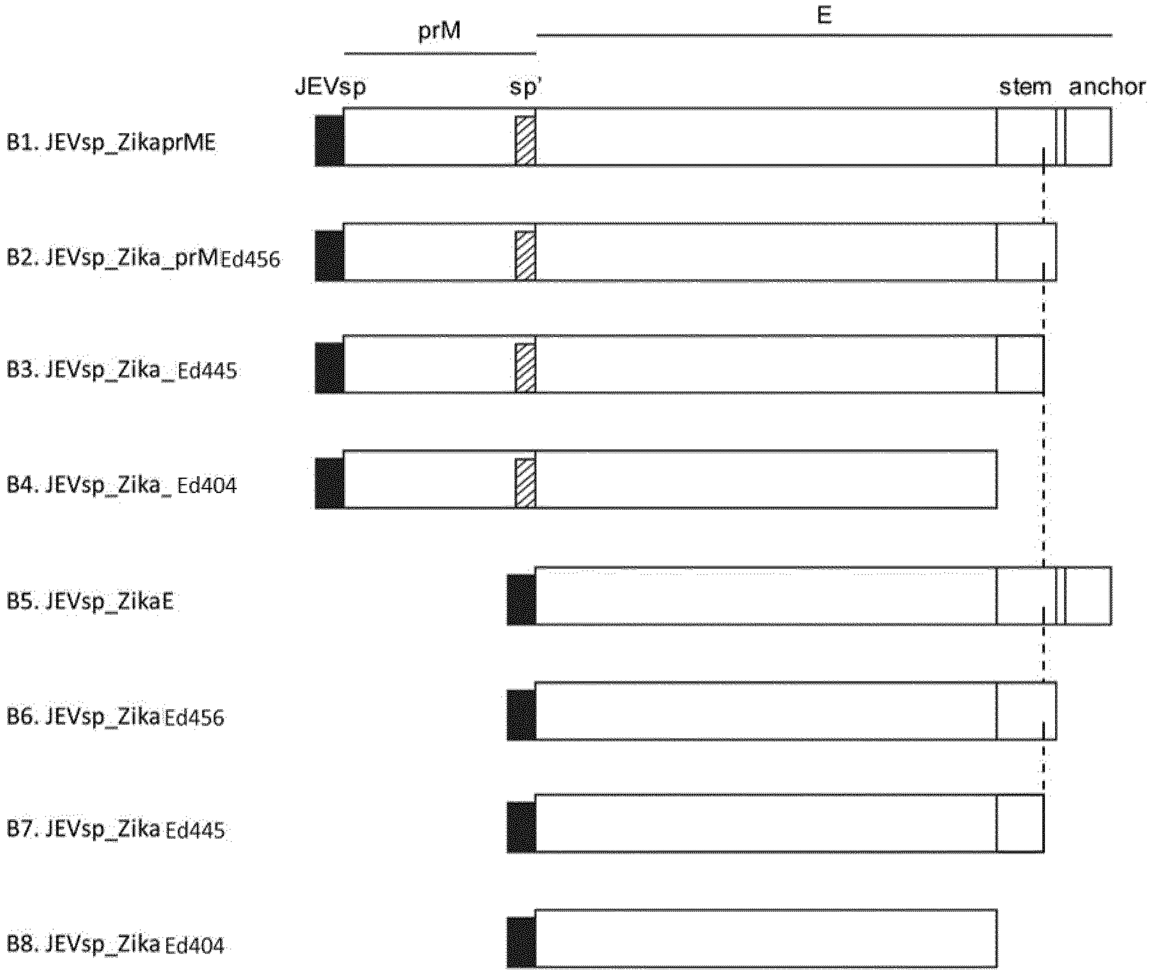

prM
E
JEVsp
sp'
stem
anchor
B1. JEVsp_ZikaprME
B2. JEVsp_Zika_prMEd456
B3. JEVsp_Zika_Ed445
B4. JEVsp_Zika_ Ed404
B5. JEVsp_ZikaE
B6. JEVsp_ZikaEd456
B7. JEVsp_ZikaEd445
B8. JEVsp_ZikaEd404

Figure 3B

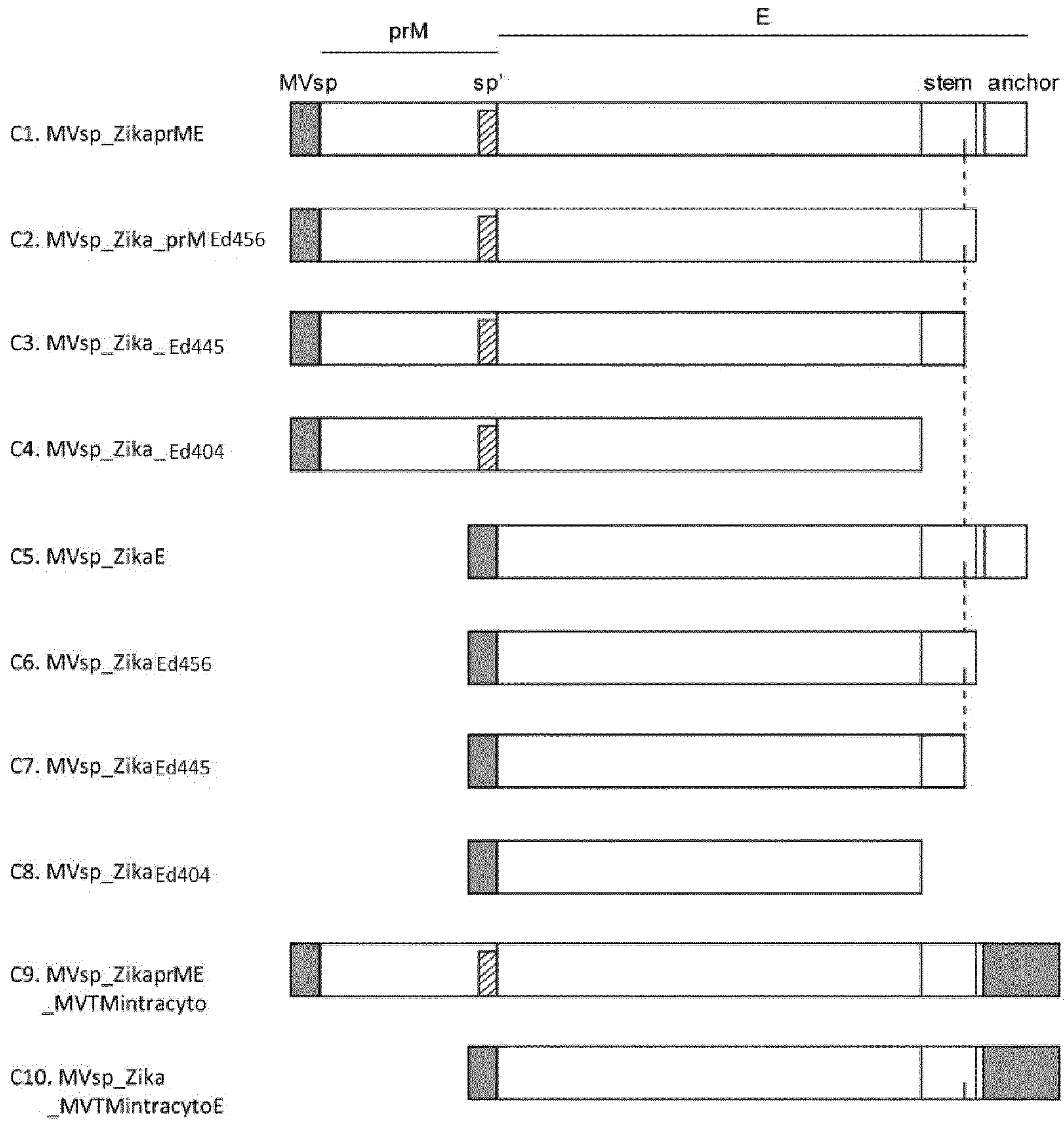
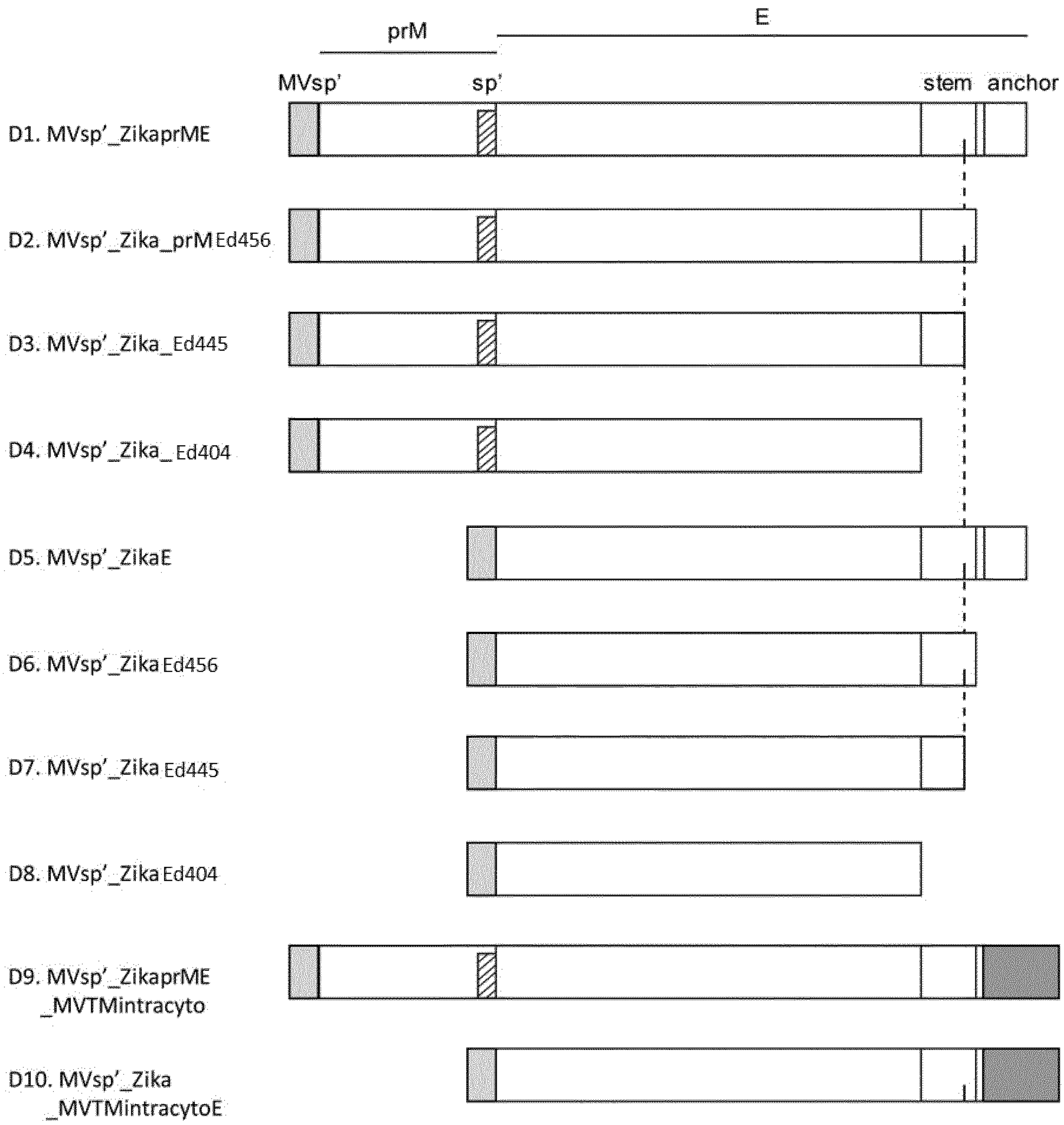

prM
E
MVsp
sp'
stem
anchor
C1. MVsp_ZikaprME
C2. MVsp_Zika_prM Ed456
C3. MVsp_Zika_ Ed445
C4. MVsp_Zika_ Ed404
C5. MVsp_ZikaE
C6. MVsp_Zika Ed456
C7. MVsp_Zika Ed445
C8. MVsp_Zika Ed404
C9. MVsp_ZikaprME _MVTMintracyto
C10. MVsp_Zika _MVTMintracytoE

Figure 3C


prM
E
MVsp'
sp'
stem
anchor
D1. MVsp'_ZikaprME
D2. MVsp'_Zika_prMEd456
D3. MVsp'_Zika_Ed445
D4. MVsp'_Zika_ Ed404
D5. MVsp'_ZikaE
D6. MVsp'_Zika Ed456
D7. MVsp'_Zika Ed445
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D9. MVsp'_ZikaprME _MVTMintracyto
D10. MVsp'_Zika _MVTMintracytoE

Figure 3D

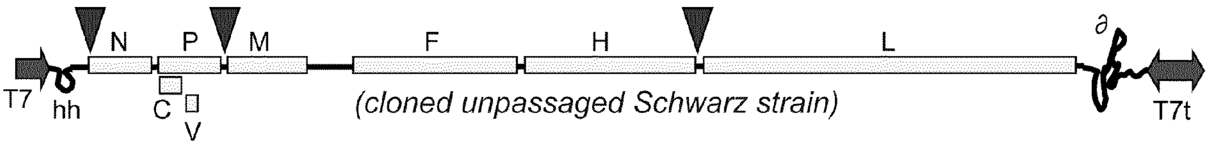
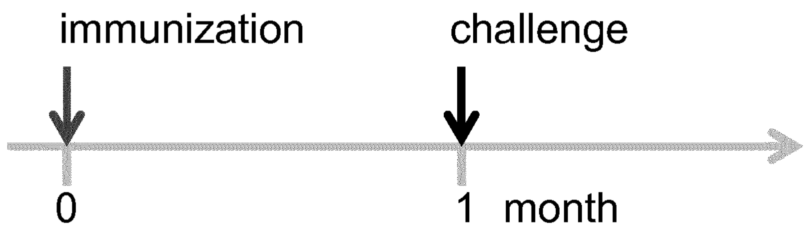


Figure 4



6 CD46-IFNAR mice per group

Immunization: MV vectors 10^6 $TCID_{50}$/mouse

Challenge: ZIKV African strain 10^6 pfu/mouse

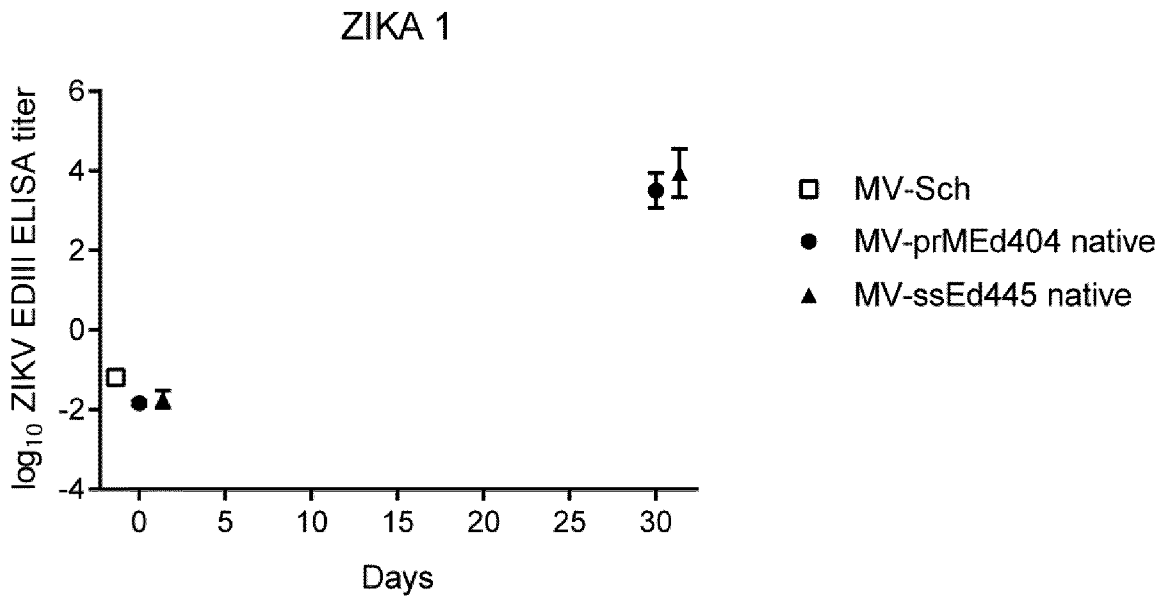


Figure 5A

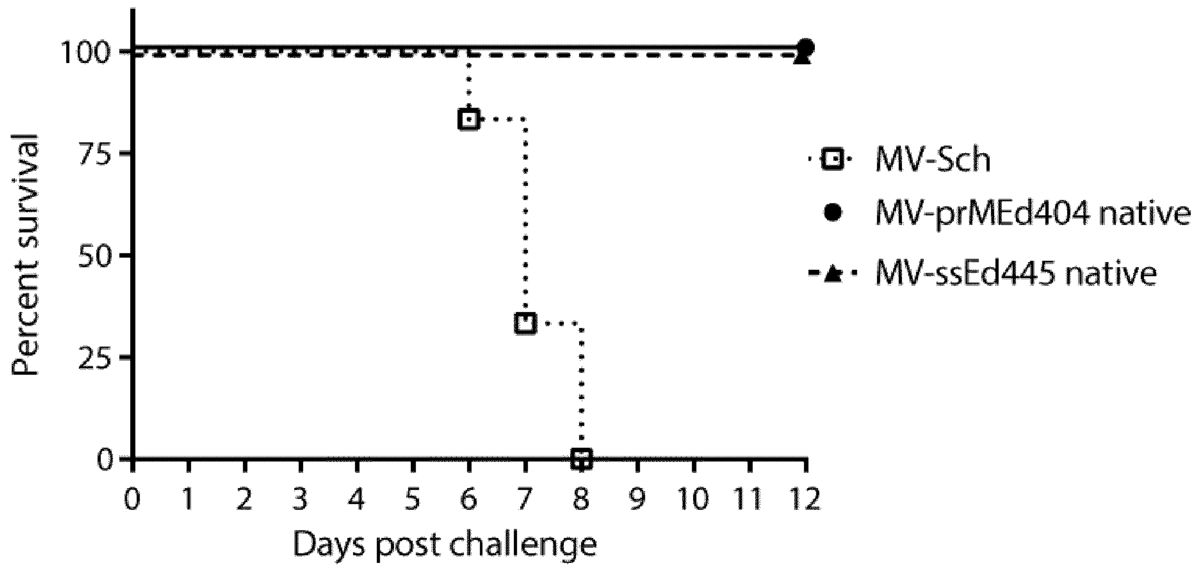


Figure 5B

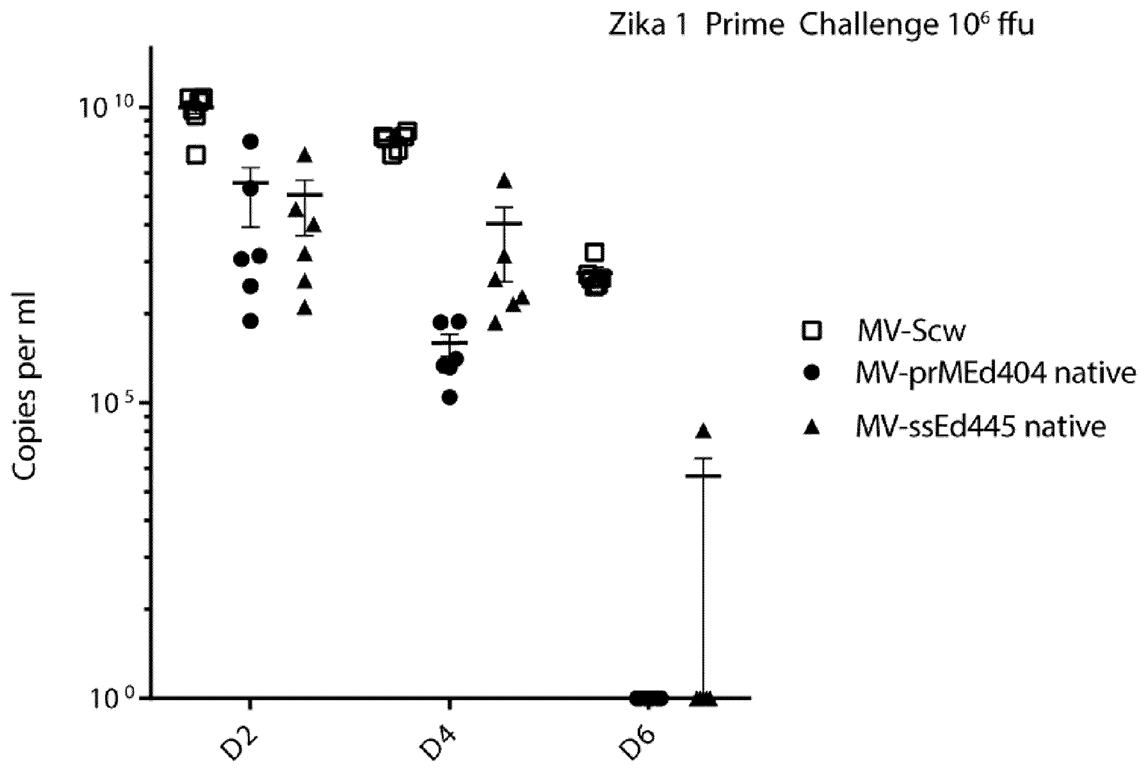


Figure 5C

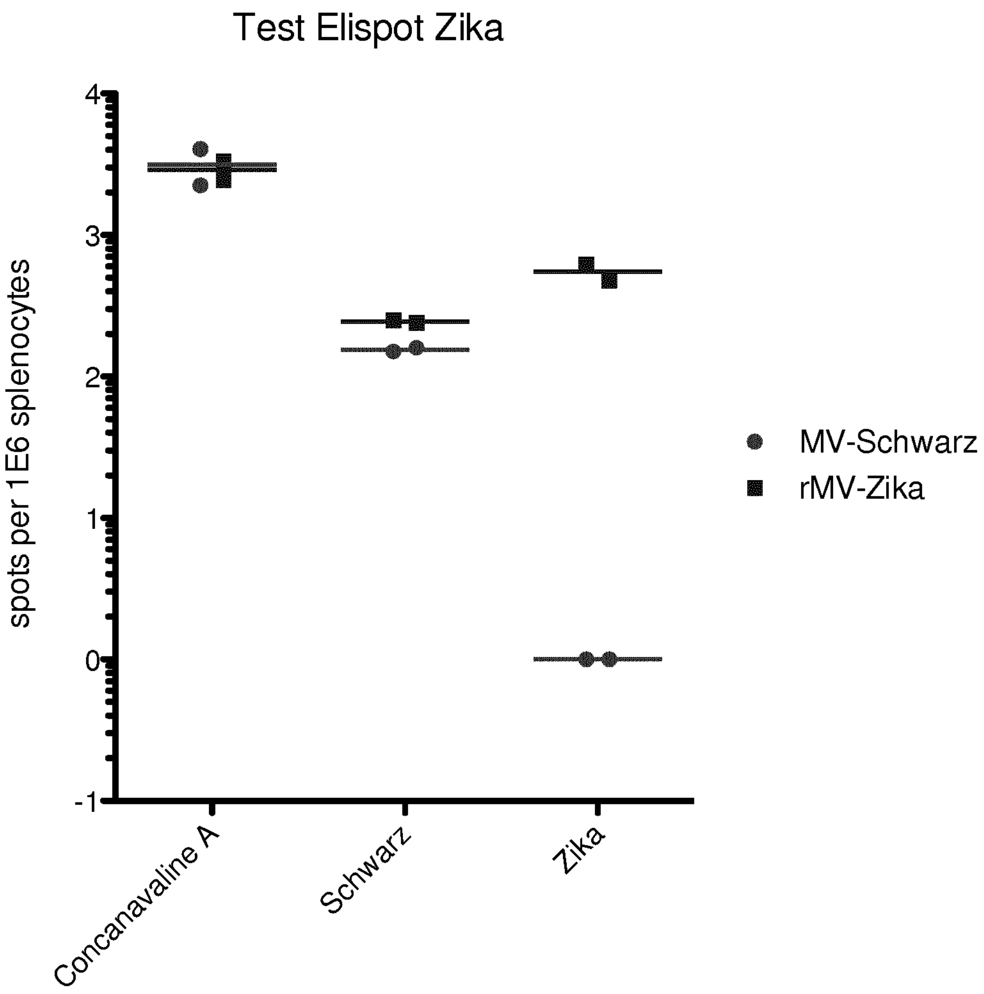

Test Elispot Zika
spots per 1E6 splenocytes
4
3
2
1
0
-1
Concanavaline A
Schwarz
Zika
MV-Schwarz
rMV-Zika

Figure 5D

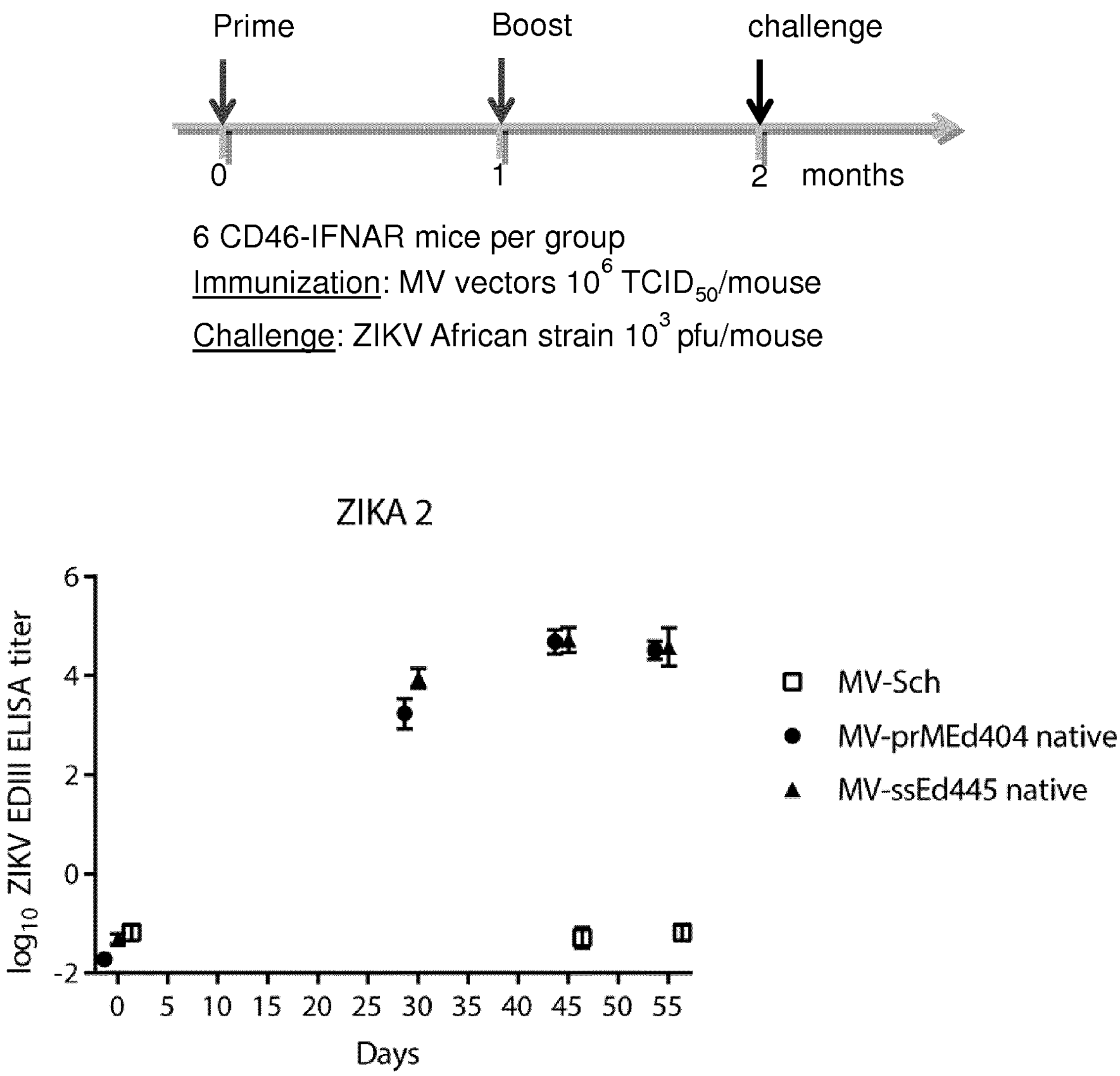
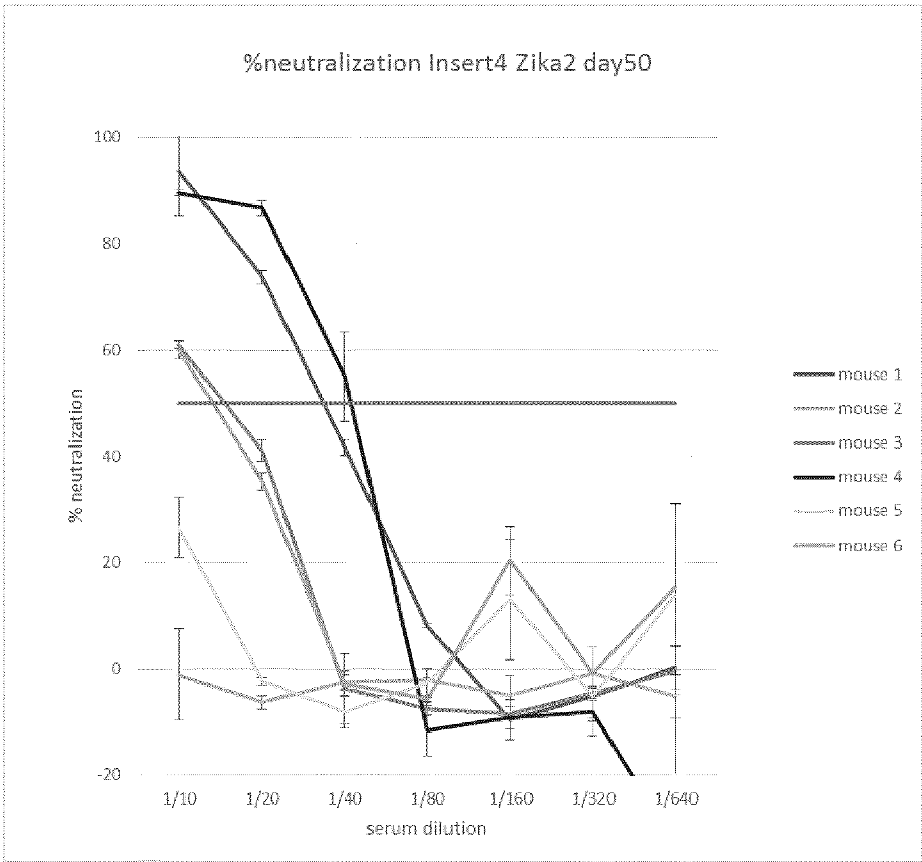

Prime
Boost
challenge
0
1
2 months
6 CD46-IFNAR mice per group
Immunization: MV vectors 10^6 $TCID_{50}$/mouse
Challenge: ZIKV African strain 10^3 pfu/mouse
ZIKA 2
log_{10} ZIKV EDIII ELISA titer
6
4
2
0
-2
0 5 10 15 20 25 30 35 40 45 50 55
Days
MV-Sch
MV-prMEd404 native
MV-ssEd445 native

Figure 6A


%neutralization Insert4 Zika2 day50
100
80
60
40
20
0
-20
% neutralization
1/10
1/20
1/40
1/80
1/160
1/320
1/640
serum dilution
mouse 1
mouse 2
mouse 3
mouse 4
mouse 5
mouse 6

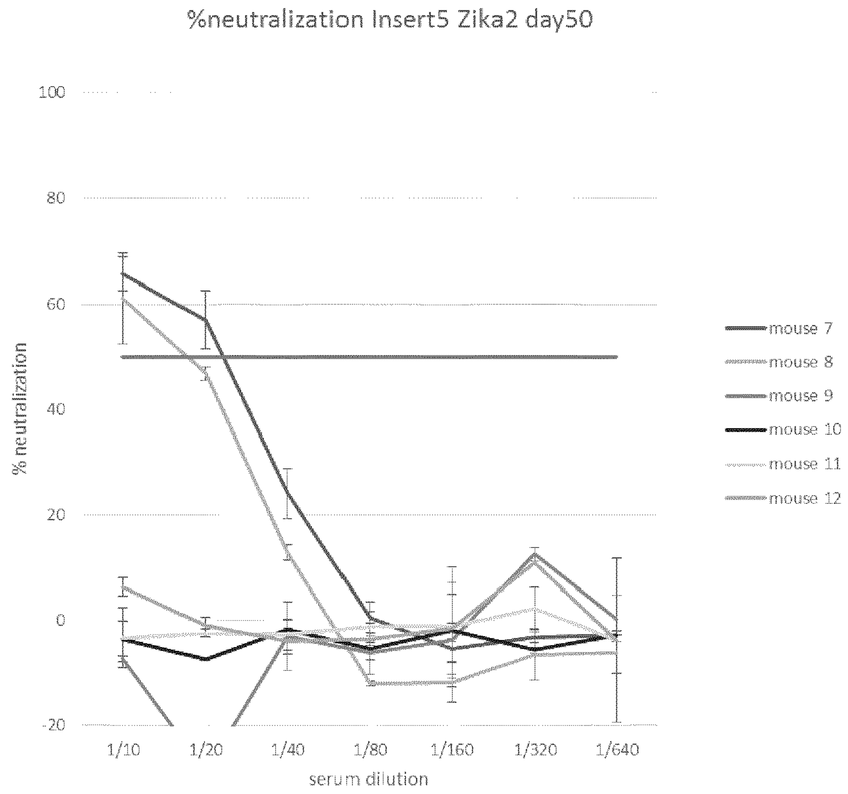

%neutralization Insert5 Zika2 day50
100
80
60
40
20
0
-20
% neutralization
1/10
1/20
1/40
1/80
1/160
1/320
1/640
serum dilution
mouse 7
mouse 8
mouse 9
mouse 10
mouse 11
mouse 12

Figure 6B

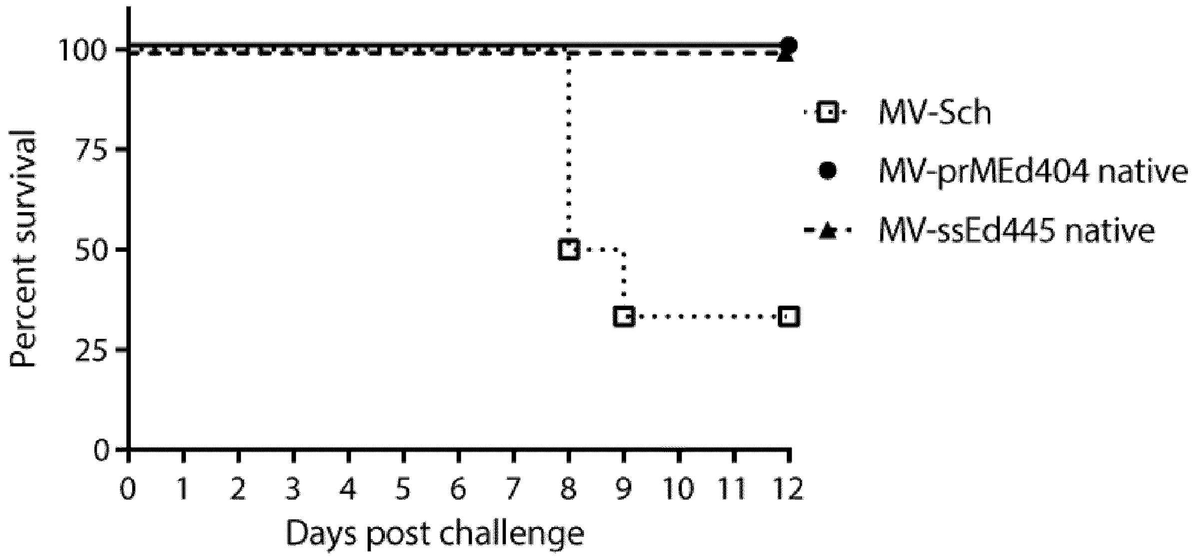


Figure 6C

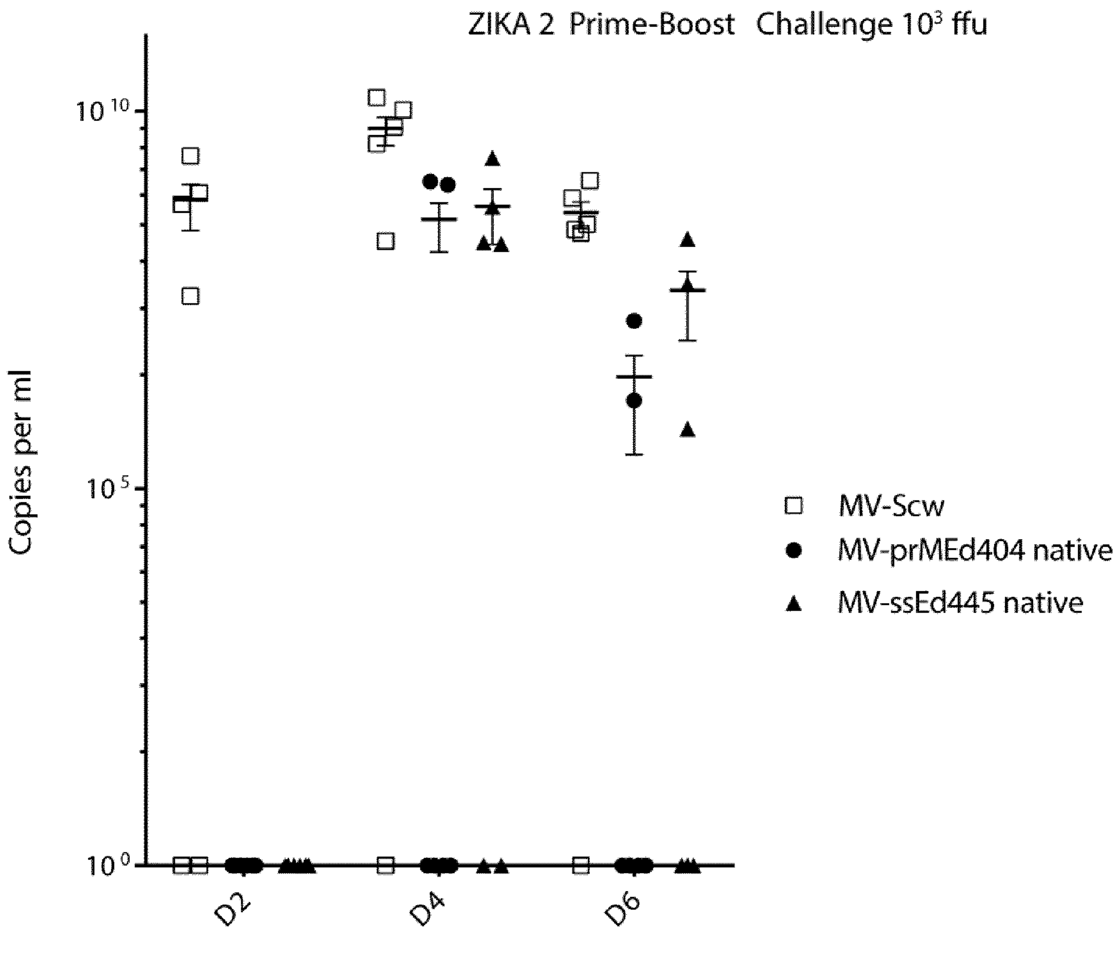


Figure 6D

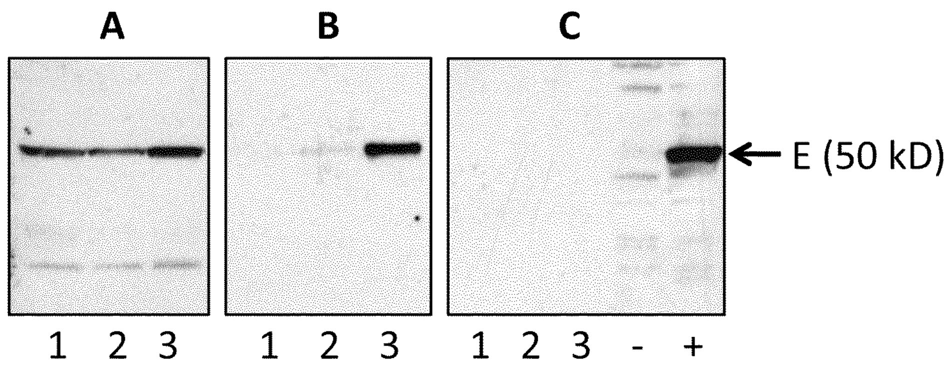
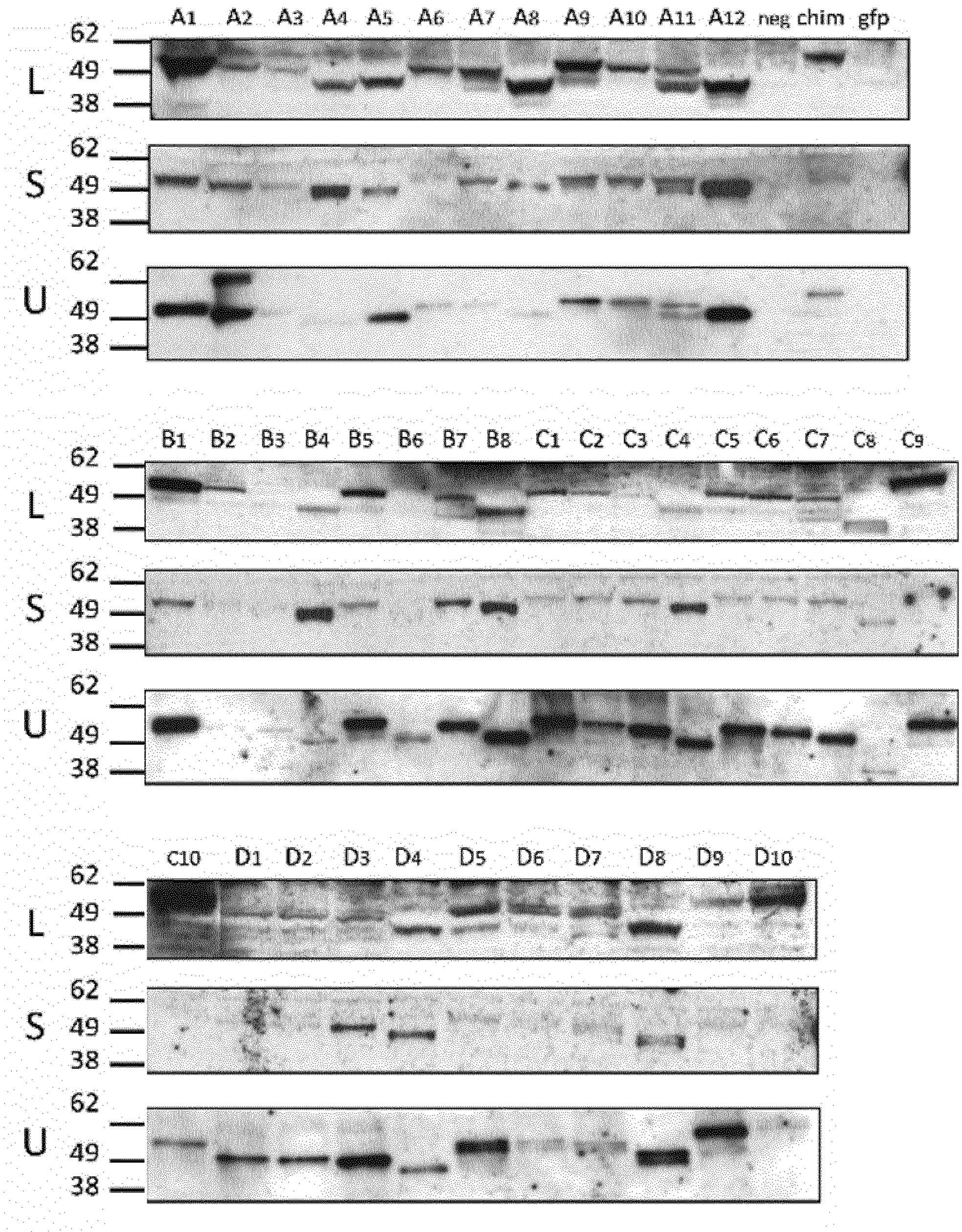


Figure 7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A2
A3
A4
A5
A6
A7
A8
A9
A10
A11
A12
neg
chim
gfp
62
49
38
L
S
U
B1
B2
B3
B4
B5
B6
B7
B8
C1
C2
C3
C4
C5
C6
C7
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D8
D9
D10

Figure 8

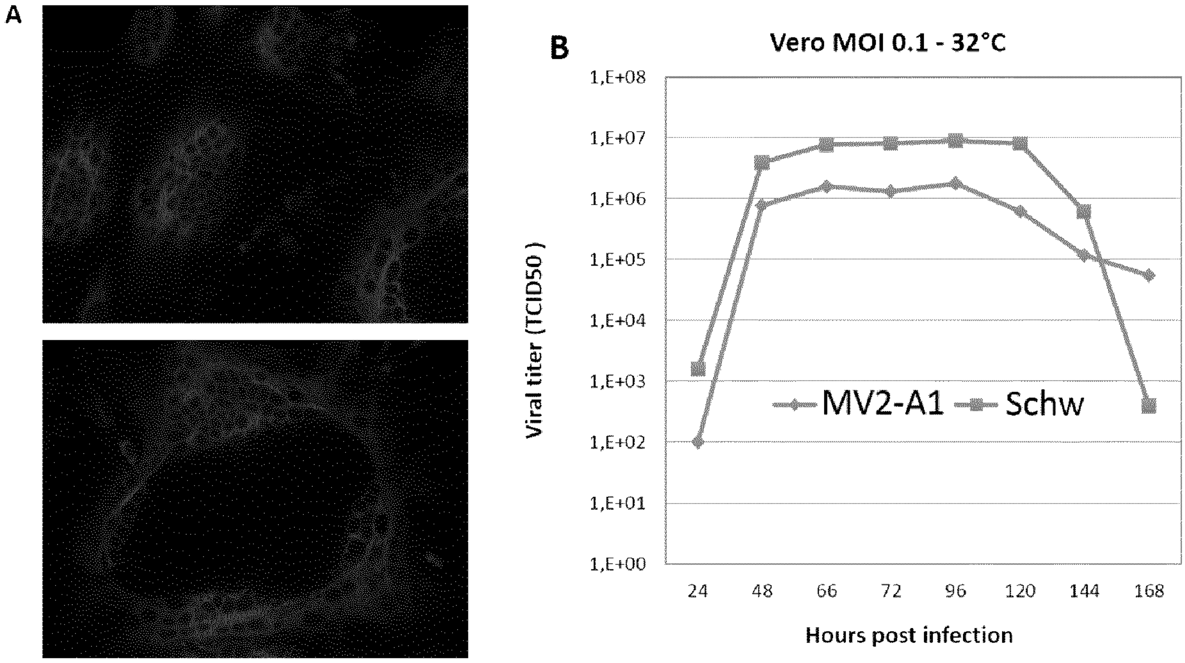

Figure 9

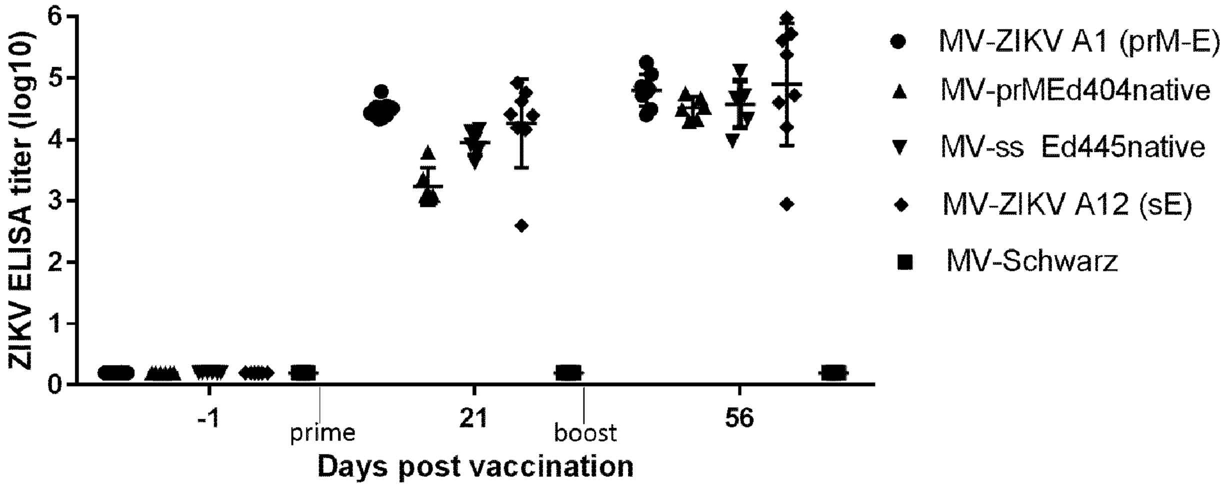

Figure 10

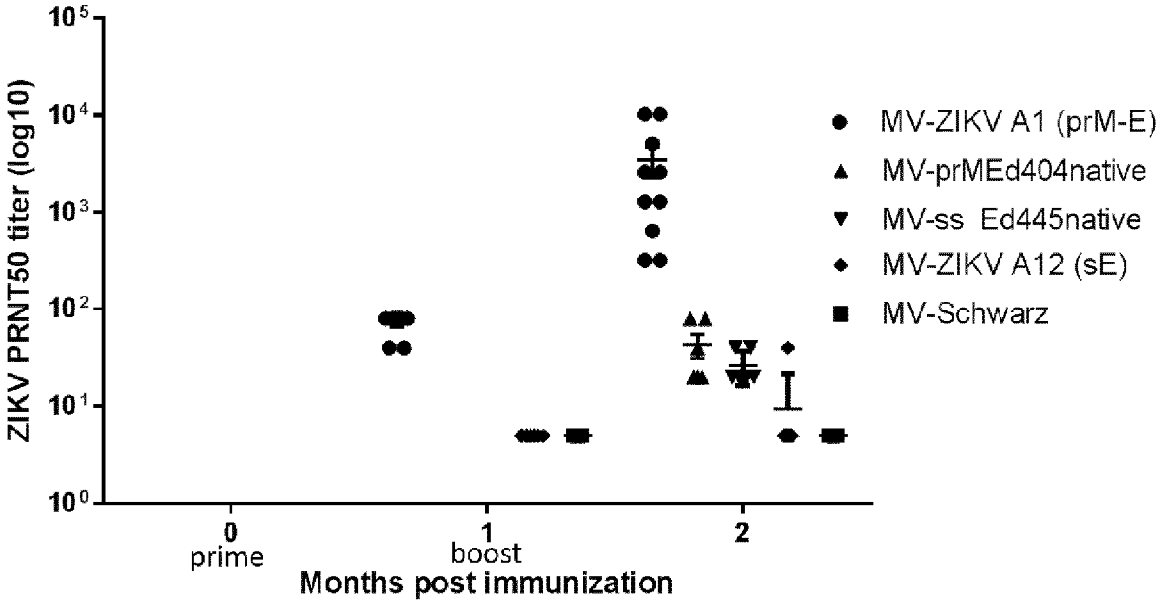

Figure 11

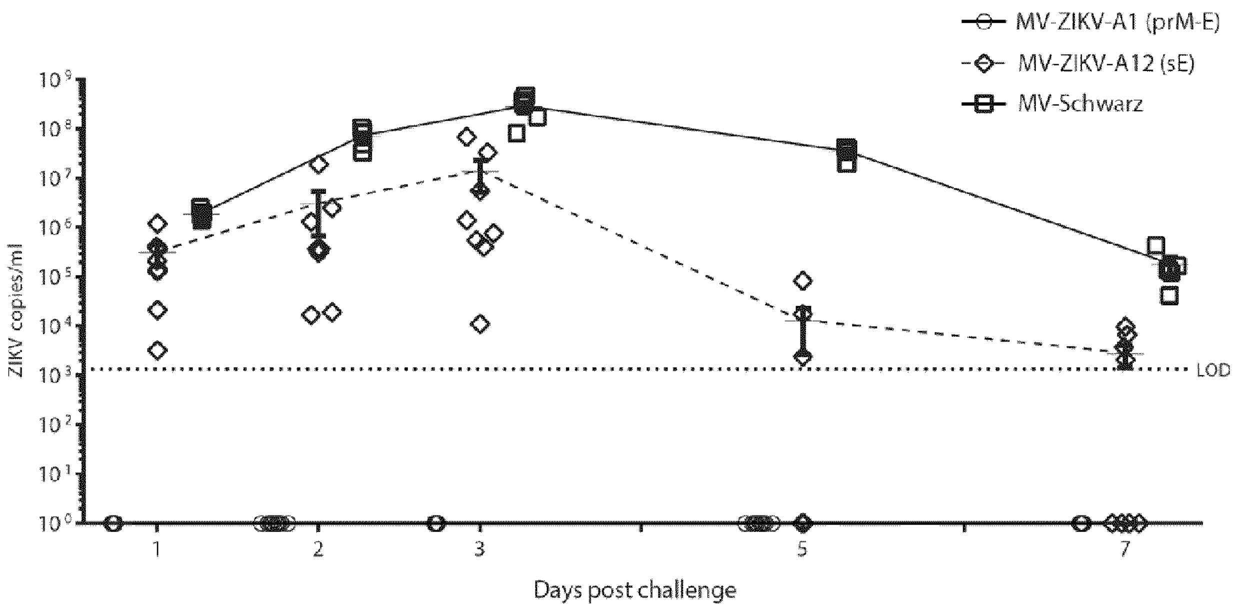

Figure 12

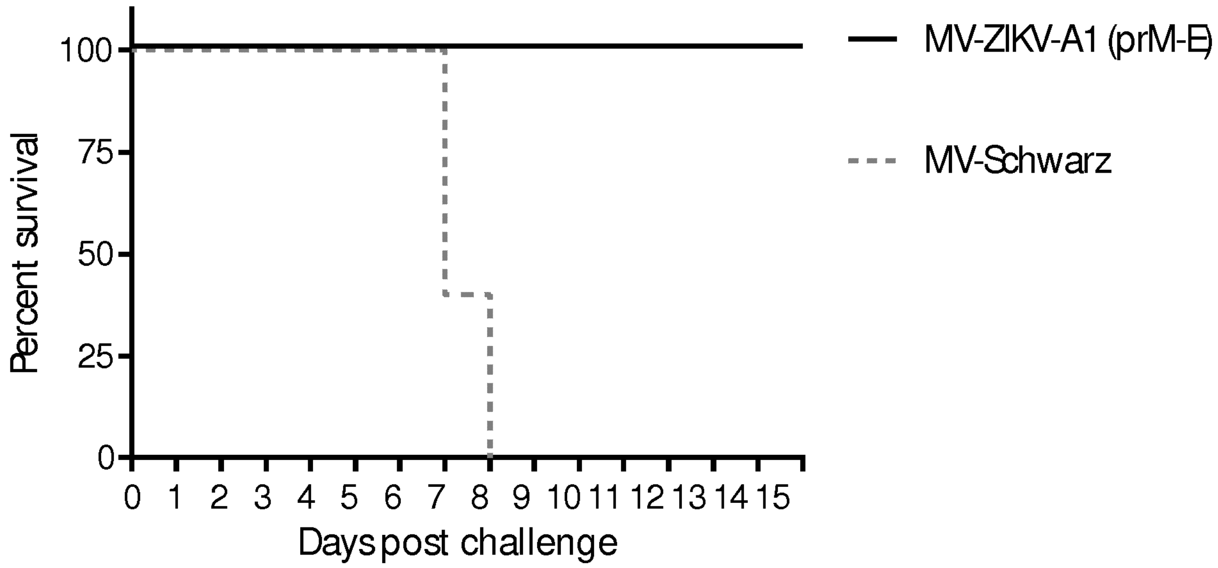
MV-ZIKV-A1 (prM-E)
MV-Schwarz
Percent survival
100
75
50
25
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Days post challenge

Figure 13

SEQUENCE LISTING

<110> INSTITUT PASTEUR
       CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> RECOMBINANT MEASLES VIRUS EXPRESSING ZIKA VIRUS PROTEINS AND
       THEIR APPLICATIONS

<130> B12291A/AD/DP/KN

<140> PCT/EP
<141> 2018-06-06

<150> EP17305676.3
<151> 2017-06-07

<160> 171

<170> PatentIn version 3.5

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catcttctag tgcacttagg attcaagatc ctattatcag ggacaagagc aggattaggg   180

atatccgaga tggccacact tttaaggagc ttagcattgt tcaaaagaaa caaggacaaa   240

ccacccatta catcaggatc cggtggagcc atcagaggaa tcaaacacat tattatagta   300

ccaatccctg gagattcctc aattaccact cgatccagac ttctggaccg gttggtgagg   360

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agcataaggc tgttagaggt tgtccagagt gaccagtcac aatctggcct taccttcgca   540

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ctggatatca agagaacacc cggaaacaaa cccaggattg ctgaaatgat atgtgacatt 960

gatacatata tcgtagaggc aggattagcc agttttatcc tgactattaa gtttgggata 1020

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aactcaattc agaacaagtt cagtgcagga tcataccctc tgctctggag ctatgccatg 1200

ggagtaggag tggaacttga aaactccatg ggaggtttga actttggccg atcttacttt 1260

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<220>
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acagctatgg ca 72

<210> 4
<211> 72
<212> DNA

<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of signal peptide from the capsid of ZIKV (sp)

<400> 4
atggagaaga agcggagagg agcagacaca agcgtgggaa tcgtgggcct gctgctgacc   60

acagcaatgg ca   72

<210> 5
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> Signal peptide from the capsid of ZIKV (sp)

<400> 5

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

Leu Leu Leu Thr Thr Ala Met Ala
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<210> 6
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of signal peptide from the membrane protein of ZIKV (sp’)

<400> 6
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<210> 7
<211> 52
<212> DNA
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<220>
<223> Codon-optimized nucleotide sequence of signal peptide from the membrane protein of ZIKV (sp’)

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cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc ta   52

<210> 8
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Signal peptide from the membrane protein of ZIKV (sp’)

<400> 8

Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr
1   5   10   15

Ser

<210> 9
<211> 72
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of signal peptide from the capsid of JEV (JEVsp)

<400> 9
atgggcaaac gatcagccgg ctcaatcatg tggctcgcga gcttggcagt tgtcatagct   60

tgtgcaggag cc   72

<210> 10
<211> 72
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of signal peptide from the capsid of JEV (JEVsp)

<400> 10
atgggcaaga ggtccgcagg gagcattatg tggctggcat ctctggcagt cgtcatcgct   60

tgtgcaggag ca   72

<210> 11
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> Signal peptide from the capsid of JEV (JEVsp)

<400> 11

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15


Val Val Ile Ala Cys Ala Gly Ala
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<210> 12
<211> 87
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of signal peptide from the fusion protein of MV (MVsp)

<400> 12

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atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact       60

ctccaaacac ccaccggtca aatccat                                           87
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<210> 13
<211> 87
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of signal peptide from the fusion protein of MV (MVsp)

<400> 13

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atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc       60

ctgcagacac caacaggcca gatccac                                           87
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<210> 14
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<212> PRT
<213> Artificial sequence

<220>
<223> Signal peptide from the fusion protein of MV (MVsp)

<400> 14

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His
            20                  25
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<210> 15
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of modified signal peptide from the fusion protein of MV (MVsp’)

<400> 15

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atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact       60

ctccaaacac ccaccggtca a                                                 81
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<210> 16
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of modified signal peptide from the fusion protein of MV (MVsp’)

<400> 16

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ctgcagacac caacaggcca g                                                 81
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<210> 17
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> Modified signal peptide from the fusion protein of MV (MVsp’)

<400> 17

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln
            20   25

<210> 18
<211> 504
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of precursor of membrane (prM) protein of ZIKV

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gaggccatat cttttccaac cacattgggg atgaataagt gttatataca gatcatggat   120

cttggacaca tgtgtgatgc caccatgagc tatgaatgcc ctatgctgga tgagggggtg   180

gaaccagatg acgtcgattg ttggtgcaac acgacgtcaa cttgggttgt gtacggaacc   240

tgccatcaca aaaaaggtga agcacggaga tctagaagag ctgtgacgct cccctcccat   300

tccactagga agctgcaaac gcggtcgcaa acctggttgg aatcaagaga atacacaaag   360

cacttgatta gagtcgaaaa ttggatattc aggaaccctg gcttcgcgtt agcagcagct   420

gccatcgctt ggcttttggg aagctcaacg agccaaaaag tcatatactt ggtcatgata   480

ctgctgattg ccccggcata cagc   504

<210> 19
<211> 505
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of precursor of membrane (prM) protein of ZIKV

<400> 19
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gcaatcgcat ggctgctggg aagctccacc agccagaaag tgatctacct ggtcatgatc 480

ctgctgatcg ctcctgccta ttcta 505

<210> 20
<211> 168
<212> PRT
<213> Artificial sequence

<220>
<223> Precursor of membrane (prM) protein of ZIKV

<400> 20

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

Asn Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn
            20   25   30

Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr
        35   40   45

Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp
    50   55   60

Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr
65   70   75   80

Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr
                85   90   95

Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp
            100   105   110

Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp
        115   120   125

Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp
    130   135   140

Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile
145   150   155   160

Leu Leu Ile Ala Pro Ala Tyr Ser
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<210> 21
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<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of full-length E protein of ZIKV

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gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt   780 caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga 1260

atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatccatca aatttttgga gcagctttca aatcattgtt tggaggaatg 1380

tcctggttct cacaaattct cattggaacg ttgctgatgt ggttgggtct gaacacaaag 1440

aatggatcta tttcccttat gtgcttggcc ttagggggag tgttgatctt cttatccaca 1500

gccgtctctg ct 1512

<210> 22
<211> 1511
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of full-length E protein of ZIKV

<400> 22
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480 atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catccaccag atcttcggcg ccgcctttaa gtccctgttc ggcggcatga 1380

gctggttctc acagatcctg atcggcacac tgctgatgtg gctgggcctg aacaccaaga 1440

atggctctat cagcctgatg tgcctggccc tgggaggcgt gctgatcttc ctgtccaccg 1500

ccgtgtctgc c 1511

<210> 23
<211> 504
<212> PRT
<213> Artificial sequence

<220>
<223> Full-length E protein of ZIKV

<400> 23

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

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

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
        35                  40                  45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
    50                  55                  60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65                  70                  75                  80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
                85                  90                  95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
        115                 120                 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145                 150                 155                 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220
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Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340                 345                 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405                 410                 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420                 425                 430
```

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
        435   440   445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
    450   455   460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465   470   475   480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
                485   490   495

Phe Leu Ser Thr Ala Val Ser Ala
            500

<210> 24
<211> 1368
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position x (Edx)

<400> 24
atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg   60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact   120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc   180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc   240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc   300

tggggaaatg gatgtggact tttggcaaa gggagcctgg tgacatgcgc taagtttgca   360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg   420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact   480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg   540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat   600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac   660 attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga 1260

atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatccatca aatttttgga gcagctttca aatcattg 1368

<210> 25
<211> 1367
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position x (Edx)

<400> 25
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540 gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catccaccag atcttcggcg ccgcctttaa gtccctg 1367

<210> 26
<211> 456
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position x (Edx)

<400> 26

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

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

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

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Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
    50                  55                  60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65                  70                  75                  80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
                85                  90                  95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
        115                 120                 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145                 150                 155                 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255
```

```
Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340                 345                 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405                 410                 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420                 425                 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
        435                 440                 445

Phe Gly Ala Ala Phe Lys Ser Leu
    450                 455
```

<210> 27
<211> 1335
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 27
atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg   60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact   120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc   180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc   240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc   300

tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc taagtttgca   360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg   420

ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact   480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg   540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat   600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac   660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa   720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt   780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca   840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg   900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa   960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag   1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc   1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca   1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg   1200

cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg tgccaagaga   1260 atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc tctcaactca 1320

ttgggcaagg gcatc 1335

<210> 28
<211> 1334
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 28
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420

tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140 catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg ctccacaatc ggcaaggcct ttgaggcaac cgtgcgcgga gcaaagagaa 1260

tggccgtgct gggcgacacc gcatgggatt tcggatctgt gggaggcgcc ctgaacagcc 1320

tgggcaaggg catc 1334

<210> 29
<211> 445
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position 411 (Ed411)

<400> 29

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

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

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

```
Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145                 150                 155                 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335
```

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340   345   350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355   360   365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370   375   380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385   390   395   400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
                405   410   415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
            420   425   430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
        435   440   445

<210> 30
<211> 1212
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 30
atcaggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacttgg 60

gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact 120

gtcgacatag agctggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc 180

tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc 240

taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc 300

tggggaaatg gatgtggact tttggcaaa gggagcctgg tgacatgcgc taagtttgca 360

tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg 420 ctgtcagttc atggctccca gcacagtggg atgatcgtta atgacacagg acatgaaact 480

gatgagaata gagcgaaggt tgagataacg cccaattcac caagagccga agccaccctg 540

gggggttttg gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat 600

ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac 660

attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720

gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780

caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840

aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900

aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat cccggctgaa 960

acactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020

gttccagctc agatggcggt ggacatgcaa actctgaccc cagttgggag gttgataacc 1080

gctaaccccg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac ccaccactgg 1200

cacaggagtg gc 1212

<210> 31
<211> 1211
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 31
tccggtgcat cggcgtgagc aatagagact tcgtggaggg aatgtccgga ggaacctggg 60

tggatgtggt gctggagcac ggcggctgcg tgacagtgat ggcccaggac aagccaaccg 120

tggatatcga gctggtgacc acaaccgtgt ccaacatggc cgaggtgagg tcttactgct 180

atgaggccag catctccgac atggcctctg atagcaggtg tccaacccag ggagaggcat 240

acctggacaa gcagtccgat acacagtacg tgtgcaagcg gaccctggtg gacagaggct 300

ggggcaatgg ctgtggcctg tttggcaagg gctctctggt gacatgcgcc aagttcgcct 360

gtagcaagaa gatgaccggc aagtccatcc agccagagaa cctggagtac cggatcatgc 420 tgtctgtgca cggctcccag cactctggca tgatcgtgaa cgacacaggc cacgagacag 480

atgagaatcg ggccaaggtg gagatcacac ctaactctcc aagagccgag gccaccctgg 540

gaggatttgg ctctctgggc ctggactgcg agcctagaac aggcctggac ttctccgatc 600

tgtactatct gaccatgaac aataagcact ggctggtgca caaggagtgg tttcacgaca 660

tcccactgcc atggcacgca ggagcagata caggaacacc acactggaac aataaggagg 720

ccctggtgga gttcaaggat gcccacgcca agcggcagac agtggtggtg ctgggcagcc 780

aggagggagc agtgcacacc gccctggcag gcgccctgga ggcagagatg gacggagcta 840

agggcagact gtctagcggc cacctgaagt gcaggctgaa gatggataag ctgcgcctga 900

agggcgtgtc ctactctctg tgcacagccg ccttcacctt caccaagatc cctgccgaga 960

cactgcacgg cacagtgacc gtggaggtgc agtatgccgg cacagacgga ccctgtaagg 1020

tgcctgccca gatggccgtg gatatgcaga cactgacacc tgtgggcagg ctgatcaccg 1080

ccaatccagt gatcacagag tctaccgaga acagcaagat gatgctggag ctggacccac 1140

catttggcga tagctatatc gtgatcggcg tgggcgagaa gaagatcaca caccactggc 1200

accgcagcgg c 1211

<210> 32
<211> 404
<212> PRT
<213> Artificial sequence

<220>
<223> E protein of ZIKV truncated at amino acid position 395 (Ed395)

<400> 32

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

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

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

```
Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
    50                  55                  60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65                  70                  75                  80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
                85                  90                  95

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
        115                 120                 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
    130                 135                 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145                 150                 155                 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
                165                 170                 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
            180                 185                 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
        195                 200                 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
    210                 215                 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225                 230                 235                 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
                245                 250                 255
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Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
            260                 265                 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
        275                 280                 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
    290                 295                 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305                 310                 315                 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
                325                 330                 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
            340                 345                 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
        355                 360                 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
    370                 375                 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385                 390                 395                 400

His Arg Ser Gly



<210>  33
<211>  156
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of E stem region of ZIKV

<400>  33
agcaccattg gaaaagcatt tgaagccact gtgagaggtg ccaagagaat ggcagtcttg       60

ggagacacag cctgggactt tggatcagtt ggaggcgctc tcaactcatt gggcaagggc      120
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atccatcaaa tttttggagc agctttcaaa tcattg 156

<210> 34
<211> 156
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E stem region of ZIKV

<400> 34
tccacaatcg gcaaggcctt tgaggcaacc gtgcgcggag caaagagaat ggccgtgctg 60

ggcgacaccg catgggattt cggatctgtg ggaggcgccc tgaacagcct gggcaagggc 120

atccaccaga tcttcggcgc cgcctttaag tccctg 156

<210> 35
<211> 52
<212> PRT
<213> Artificial sequence

<220>
<223> E stem region of ZIKV

<400> 35

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

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
20 25 30

Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
35 40 45

Phe Lys Ser Leu
50

<210> 36
<211> 24
<212> DNA
<213> Artificial sequence

<220>

<223> Native nucleotide sequence of intermediate domain between E stem and E anchor regions of ZIKV

<400> 36
tttggaggaa tgtcctggtt ctca   24

<210> 37
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of intermediate domain between E stem and E anchor regions of ZIKV

<400> 37
ttcggcggca tgagctggtt ctcacagatc ctga   34

<210> 38
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Intermediate domain between E stem and E anchor regions of ZIKV

<400> 38

Phe Gly Gly Met Ser Trp Phe Ser
1   5

<210> 39
<211> 120
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of E anchor region of ZIKV

<400> 39
caaattctca ttggaacgtt gctgatgtgg ttgggtctga acacaaagaa tggatctatt   60

tcccttatgt gcttggcctt agggggagtg ttgatcttct tatccacagc cgtctctgct   120

<210> 40
<211> 110
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of E anchor region of ZIKV

<400> 40
tcggcacact gctgatgtgg ctgggcctga acaccaagaa tggctctatc agcctgatgt   60

gcctggccct gggaggcgtg ctgatcttcc tgtccaccgc cgtgtctgcc   110

<210> 41
<211> 40
<212> PRT
<213> Artificial sequence

<220>
<223> E anchor region of ZIKV

<400> 41

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
1   5   10   15

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
            20   25   30

Phe Leu Ser Thr Ala Val Ser Ala
        35   40

<210> 42
<211> 192
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 42
atgaaaggtt tatcgagcac tagcatagtc tacatcctga ttgcagtgtg tcttggaggg   60

ttgataggga tccccgcttt aatatgttgc tgcagggggc gttgtaacaa aaagggagaa   120

caagttggta tgtcaagacc aggcctaaag cctgatctta cgggaacatc aaaatcctat   180

gtaaggtcgc tc   192

<210> 43

<211> 192
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 43
atgaagggcc tgtcctctac ctctatcgtg tacatcctga tcgccgtgtg cctgggaggc   60

ctgatcggaa tcccagccct gatctgctgt tgcagaggcc gctgcaacaa gaagggagag   120

caagtgggaa tgtctcggcc aggcctgaag ccagacctga caggcacctc caagtcttat   180

gtgagaagcc tg   192

<210> 44
<211> 64
<212> PRT
<213> Artificial sequence

<220>
<223> Transmembrane (TM) and intracytoplasmic tail of MV F protein

<400> 44

Met Lys Gly Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu Ile Ala Val
1   5   10   15

Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg
            20   25   30

Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro Gly
        35   40   45

Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
    50   55   60

<210> 45
<211> 2094
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaprME protein (A1)

<400> 45
atggagaaga agagacgagg cgcagatact agtgtcggaa ttgttggcct cctgctgacc   60

acagctatgg cagcggaggt cactagacgt gggagtgcat actatatgta cttggacaga   120

aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata   180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg   240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt   300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg   360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga   420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg   480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac   540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat   600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga   660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca   720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg   780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact   840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt   900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag   960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac   1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag   1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt   1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac   1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg   1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca   1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc   1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac   1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt   1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg   1560 gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtttgga ggaatgtcct ggttctcaca aattctcatt 1980

ggaacgttgc tgatgtggtt gggtctgaac acaaagaatg gatctatttc ccttatgtgc 2040

ttggccttag ggggagtgtt gatcttctta tccacagccg tctctgcttg atga 2094

<210> 46
<211> 2094
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaprME protein (A1)

<400> 46
atggagaaga agcggagagg agcagacaca agcgtgggaa tcgtgggcct gctgctgacc 60

acagcaatgg cagcagaggt gaccaggaga ggaagcgcct actatatgta cctggacagg 120

aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720 accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

tccatccagc cagagaacct ggagtaccgg atcatgctgt ctgtgcacgg ctcccagcac 1020

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atcacaccta actctccaag agccgaggcc accctgggag gatttggctc tctgggcctg 1140

gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ccaccagatc 1920

ttcggcgccg cctttaagtc cctgttcggc ggcatgagct ggttctcaca gatcctgatc 1980

ggcacactgc tgatgtggct gggcctgaac accaagaatg gctctatcag cctgatgtgc 2040

ctggccctgg gaggcgtgct gatcttcctg tccaccgccg tgtctgcctg atga 2094

<210> 47
<211> 696
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaprME protein (A1)

<400> 47

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

Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser
            20   25   30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35   40   45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50   55   60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65   70   75   80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85   90   95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100   105   110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115   120   125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130   135   140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145   150   155   160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165   170   175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180   185   190

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Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400
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Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605
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Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
                645                 650                 655

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
            660                 665                 670

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
        675                 680                 685

Phe Leu Ser Thr Ala Val Ser Ala
    690                 695


<210>  48
<211>  1950
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of Zikasp_Zika_prME_no_Anchor protein (A2)

<400>  48
atggagaaga agagacgagg cgcagatact agtgtcggaa ttgttggcct cctgctgacc      60

acagctatgg cagcggaggt cactagacgt gggagtgcat actatatgta cttggacaga     120

aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata     180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg     240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt     300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg     360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga     420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg     480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac     540
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ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

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gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtgatga 1950

<210> 49
<211> 1950

<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME_no_Anchor protein (A2)

<400> 49
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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc   180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg   240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg   300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca   360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga   420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca   480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac   540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat   600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc   660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca   720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg   780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca   840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt   900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag   960

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gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat   1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga   1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc   1320 cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

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gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ccaccagatc 1920

ttcggcgccg cctttaagtc cctgtgatga 1950

<210> 50
<211> 648
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME_no_Anchor protein (A2)

<400> 50

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Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser
            20   25   30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35   40   45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50   55   60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65   70   75   80

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Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285
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Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495
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Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510


Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525


Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540


Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560


Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575


Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590


His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605


Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620


Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640


Phe Gly Ala Ala Phe Lys Ser Leu
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<210>  51
<211>  1914
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of Zikasp_Zika_prME411 protein (A3)

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aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata 180

cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

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agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

gattgtgaac cgaggacagg ccttgacttt tcagatttgt attacttgac tatgaataac 1200

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gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ctga 1914

<210> 52
<211> 1914
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME411 protein (A3)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

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accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

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aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

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gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

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atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ctga 1914

<210> 53
<211> 637
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME411 protein (A3)

<400> 53

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

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Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35                  40                  45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240
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Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245   250   255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260   265   270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275   280   285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290   295   300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305   310   315   320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325   330   335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340   345   350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370   375   380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385   390   395   400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405   410   415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420   425   430

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

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Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635
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<210> 54
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_Zika_prME395 protein (A4)

<400> 54
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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg   240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt   300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg   360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga   420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg   480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac   540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat   600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga   660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca   720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg   780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact   840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt   900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag   960

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gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca   1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc   1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac   1440 ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

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ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggctg atga 1794

<210> 55
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_Zika_prME395 protein (A4)

<400> 55
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acagcaatgg cagcagaggt gaccaggaga ggaagcgcct actatatgta cctggacagg 120

aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840 cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

tccatccagc cagagaacct ggagtaccgg atcatgctgt ctgtgcacgg ctcccagcac 1020

tctggcatga tcgtgaacga cacaggccac gagacagatg agaatcgggc caaggtggag 1080

atcacaccta actctccaag agccgaggcc accctgggag gatttggctc tctgggcctg 1140

gactgcgagc ctagaacagg cctggacttc tccgatctgt actatctgac catgaacaat 1200

aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

acagccgcct tcaccttcac caagatccct gccgagacac tgcacggcac agtgaccgtg 1560

gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

atgcagacac tgacacctgt gggcaggctg atcaccgcca atccagtgat cacagagtct 1680

accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctg atga 1794

<210> 56
<211> 596
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_Zika_prME395 protein (A4)

<400> 56

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

Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser
20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser

35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
50 55 60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65 70 75 80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
85 90 95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
100 105 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
115 120 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
130 135 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145 150 155 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
165 170 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
180 185 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
195 200 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
210 215 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225 230 235 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser

245 250 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
260 265 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
275 280 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
290 295 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305 310 315 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
325 330 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
340 345 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
370 375 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385 390 395 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
405 410 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
420 425 430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala

    450   455   460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465   470   475   480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485   490   495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500   505   510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515   520   525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530   535   540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545   550   555   560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565   570   575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580   585   590

His Arg Ser Gly
        595

<210> 57
<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE protein (A5)

<400> 57
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gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg 1440

tttggaggaa tgtcctggtt ctcacaaatt ctcattggaa cgttgctgat gtggttgggt 1500

ctgaacacaa agaatggatc tatttccctt atgtgcttgg ccttaggggg agtgttgatc 1560

ttcttatcca cagccgtctc tgcttgatga 1590

<210> 58

<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE protein (A5)

<400> 58
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc   120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag   180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg   240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc   300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg   360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc   420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag   480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca   540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc   600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg   660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag   720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg   780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg   840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag   900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat   960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag   1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac   1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc   1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg   1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc   1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc   1320 ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc   1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg   1440

ttcggcggca tgagctggtt ctcacagatc ctgatcggca cactgctgat gtggctgggc   1500

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ttcctgtcca ccgccgtgtc tgcctgatga   1590

<210> 59
<211> 528
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE protein (A5)

<400> 59

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Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
            20   25   30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35   40   45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50   55   60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65   70   75   80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85   90   95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100   105   110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115   120   125

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Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335
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Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470                 475                 480

Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu
                485                 490                 495

Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys
            500                 505                 510

Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
        515                 520                 525
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<210> 60
<211> 1446
<212> DNA

<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE_no_Anchor protein (A6)

<400> 60
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca   120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag   180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta   240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca   300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta   360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc   420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag   480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca   540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc   600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt   660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag   720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg   780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg   840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag   900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat   960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag   1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat   1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg   1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg   1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc   1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga   1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc   1380 gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg 1440

tgatga 1446

<210> 61
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE_no_Anchor protein (A6)

<400> 61
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

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aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg 1440

tgatga 1446

<210> 62
<211> 480
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE_no_Anchor protein (A6)

<400> 62

Met Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly
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Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
50 55 60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65 70 75 80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
85 90 95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
100 105 110

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Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320
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Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325   330   335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340   345   350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355   360   365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370   375   380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385   390   395   400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405   410   415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420   425   430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435   440   445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450   455   460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465   470   475   480

<210> 63
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE411 protein (A7)

<400> 63
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acagctatgg caatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca 120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc 1380

gctctcaact cattgggcaa gggcatctga 1410

<210> 64
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE411 protein (A7)

<400> 64
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acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc   120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag   180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg   240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc   300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg   360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc   420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag   480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca   540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc   600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg   660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag   720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg   780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg   840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag   900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat   960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag   1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac   1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc   1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg   1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc   1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc   1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc   1380

gccctgaaca gcctgggcaa gggcatctga   1410

<210> 65
<211> 469
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE411 protein (A7)

<400> 65

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


Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
            20                  25                  30


Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45


Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60


Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80


Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95


Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110


Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125


Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140


Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160


Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
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165 170 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
180 185 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
195 200 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
210 215 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225 230 235 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
245 250 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
260 265 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
275 280 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
290 295 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305 310 315 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
325 330 335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
340 345 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
355 360 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr

370 375 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385 390 395 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
405 410 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
420 425 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
435 440 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
450 455 460

Leu Gly Lys Gly Ile
465

<210> 66
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp_ZikaE395 protein (A8)

<400> 66
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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag 180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta 240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480 taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg 1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggctgatga 1290

<210> 67
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp_ZikaE395 protein (A8)

<400> 67
atggagaaga agcggagagg agcagacaca agcgtgggaa tcgtgggcct gctgctgacc 60

acagcaatgg caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420 gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc 1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctgatga 1290

<210> 68
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp_ZikaE395 protein (A8)

<400> 68

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

Leu Leu Leu Thr Thr Ala Met Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

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Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255
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Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
            420                 425
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<210> 69
<211> 1572
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp'_ZikaE protein (A9)

<400> 69
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tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat   120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac   180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag   240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt   300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga   360

aatggatgtg gactttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc   420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca   480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag   540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctggggggt   600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat   660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca   720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg   780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa   840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga   900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc   960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg   1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca   1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac   1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt   1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg   1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca   1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc   1380

aagggcatcc atcaaatttt tggagcagct ttcaaatcat tgtttggagg aatgtcctgg   1440

ttctcacaaa ttctcattgg aacgttgctg atgtggttgg gtctgaacac aaagaatgga   1500 tctatttccc ttatgtgctt ggccttaggg ggagtgttga tcttcttatc cacagccgtc 1560

tctgcttgat ga 1572

<210> 70
<211> 1572
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE protein (A9)

<400> 70
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tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

gtggagttca aggatgccca cgccaagcgg cagacagtgg tggtgctggg cagccaggag 840

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gtgtcctact ctctgtgcac agccgccttc accttcacca agatccctgc cgagacactg 1020

cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggaccctg taaggtgcct 1080

gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140 ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc 1320

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ttctcacaga tcctgatcgg cacactgctg atgtggctgg gcctgaacac caagaatggc 1500

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tctgcctgat ga 1572

<210> 71
<211> 522
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE protein (A9)

<400> 71

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1   5   10   15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
            20   25   30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
        35   40   45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
    50   55   60

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65   70   75   80

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
                85   90   95

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg

            100   105   110

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115   120   125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130   135   140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145   150   155   160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165   170   175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180   185   190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195   200   205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210   215   220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225   230   235   240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245   250   255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260   265   270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275   280   285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290   295   300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly

```
305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355                 360                 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370                 375                 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385                 390                 395                 400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405                 410                 415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
            420                 425                 430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
        435                 440                 445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
    450                 455                 460

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
465                 470                 475                 480

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
                485                 490                 495

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
            500                 505                 510

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
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515 520

<210> 72
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp'_ZikaE_no_anchor protein (A10)

<400> 72
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tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gactttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctggggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa 840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga 900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc 960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg 1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200 ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca 1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc 1380

aagggcatcc atcaaatttt tggagcagct ttcaaatcat tgtgatga 1428

<210> 73
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp'_ZikaE_no_anchor protein (A10)

<400> 73
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tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat 120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

gtggagttca aggatgccca cgccaagcgg cagacagtgg tggtgctggg cagccaggag 840

ggagcagtgc acaccgccct ggcaggcgcc ctggaggcag agatggacgg agctaagggc 900

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gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc 1320

gtgctgggcg acaccgcatg ggatttcgga tctgtgggag gcgccctgaa cagcctgggc 1380

aagggcatcc accagatctt cggcgccgcc tttaagtccc tgtgatga 1428

<210> 74
<211> 474
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE_no_anchor protein (A10)

<400> 74

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1 5 10 15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
20 25 30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
35 40 45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
50 55 60

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65 70 75 80

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
85 90 95

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
100 105 110

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115   120   125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130   135   140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145   150   155   160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165   170   175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180   185   190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195   200   205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210   215   220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225   230   235   240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245   250   255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260   265   270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275   280   285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290   295   300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305   310   315   320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325   330   335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340   345   350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355   360   365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370   375   380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385   390   395   400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405   410   415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
            420   425   430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
        435   440   445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
    450   455   460

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465   470

<210> 75
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp’_ZikaE411 protein (A11)

<400> 75
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tgcataggag tcagcaatag ggactttgtg gaaggtatgt caggtgggac ttgggttgat 120

gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac 180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag 240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt 300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga 360

aatggatgtg gactttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc 420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca 480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag 540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt 600

tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

gtagagttca aggacgcaca tgccaaaagg caaactgtcg tggttctagg gagtcaagaa 840

ggagcagttc acacggccct tgctggagct ctggaggctg agatggatgg tgcaaaggga 900

aggctgtcct ctggccactt gaaatgtcgc ctgaaaatgg ataaacttag attgaagggc 960

gtgtcatact ccttgtgtac cgcagcgttc acattcacca agatcccggc tgaaacactg 1020

cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggcagca ccattggaaa agcatttgaa gccactgtga gaggtgccaa gagaatggca 1320

gtcttgggag acacagcctg ggactttgga tcagttggag gcgctctcaa ctcattgggc 1380

aagggcatct ga 1392

<210> 76
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp’_ZikaE411 protein (A11)

<400> 76
atgcagaaag tgatctacct ggtcatgatc ctgctgatcg ctcctgccta ttctatccgg   60

tgcatcggcg tgagcaatag agacttcgtg gagggaatgt ccggaggaac ctgggtggat   120

gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat   180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag   240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg   300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc   360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc   420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct   480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag   540

aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga   600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac   660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca   720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg   780

gtggagttca aggatgccca cgccaagcgg cagacagtgg tggtgctggg cagccaggag   840

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agactgtcta gcggccacct gaagtgcagg ctgaagatgg ataagctgcg cctgaagggc   960

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gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat   1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt   1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc   1260

agcggctcca caatcggcaa ggcctttgag gcaaccgtgc gcggagcaaa gagaatggcc   1320

gtgctgggcg acaccgcatg ggatttcgga tctgtgggag gcgccctgaa cagcctgggc   1380

aagggcatct ga   1392

<210> 77
<211> 463
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE411 protein (A11)

<400> 77

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Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
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Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
            20                  25                  30


Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
        35                  40                  45


Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
    50                  55                  60


Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65                  70                  75                  80


Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
                85                  90                  95


Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
            100                 105                 110


Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125


Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140


Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160
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Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165                 170                 175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290                 295                 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355                 360                 365
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Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370   375   380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385   390   395   400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405   410   415

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
            420   425   430

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
        435   440   445

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
    450   455   460

<210> 78
<211> 1266
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of Zikasp’_ZikaE395 protein (A12)

<400> 78
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gttgtcttgg aacatggagg ttgtgtcacc gtaatggcac aggacaaacc gactgtcgac   180

atagagctgg ttacaacaac agtcagcaac atggcggagg taagatccta ctgctatgag   240

gcatcaatat cagacatggc ttcggacagc cgctgcccaa cacaaggtga agcctacctt   300

gacaagcaat cagacactca atatgtctgc aaaagaacgt tagtggacag aggctgggga   360

aatggatgtg gactttttgg caaagggagc ctggtgacat gcgctaagtt tgcatgctcc   420

aagaaaatga ccgggaagag catccagcca gagaatctgg agtaccggat aatgctgtca   480

gttcatggct cccagcacag tgggatgatc gttaatgaca caggacatga aactgatgag   540

aatagagcga aggttgagat aacgcccaat tcaccaagag ccgaagccac cctgggggt   600 tttggaagcc taggacttga ttgtgaaccg aggacaggcc ttgacttttc agatttgtat 660

tacttgacta tgaataacaa gcactggttg gttcacaagg agtggttcca cgacattcca 720

ttaccttggc acgctggggc agacaccgga actccacact ggaacaacaa agaagcactg 780

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cacgggacag tcacagtgga ggtacagtac gcagggacag atggaccttg caaggttcca 1080

gctcagatgg cggtggacat gcaaactctg accccagttg ggaggttgat aaccgctaac 1140

cccgtaatca ctgaaagcac tgagaactct aagatgatgc tggaacttga tccaccattt 1200

ggggactctt acattgtcat aggagtcggg gagaagaaga tcacccacca ctggcacagg 1260

agtggc 1266

<210> 79
<211> 1272
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of Zikasp’_ZikaE395 protein (A12)

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gtggtgctgg agcacggcgg ctgcgtgaca gtgatggccc aggacaagcc aaccgtggat 180

atcgagctgg tgaccacaac cgtgtccaac atggccgagg tgaggtctta ctgctatgag 240

gccagcatct ccgacatggc ctctgatagc aggtgtccaa cccagggaga ggcatacctg 300

gacaagcagt ccgatacaca gtacgtgtgc aagcggaccc tggtggacag aggctggggc 360

aatggctgtg gcctgtttgg caagggctct ctggtgacat gcgccaagtt cgcctgtagc 420

aagaagatga ccggcaagtc catccagcca gagaacctgg agtaccggat catgctgtct 480

gtgcacggct cccagcactc tggcatgatc gtgaacgaca caggccacga gacagatgag 540 aatcgggcca aggtggagat cacacctaac tctccaagag ccgaggccac cctgggagga 600

tttggctctc tgggcctgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac 660

tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca 720

ctgccatggc acgcaggagc agatacagga acaccacact ggaacaataa ggaggccctg 780

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agactgtcta gcggccacct gaagtgcagg ctgaagatgg ataagctgcg cctgaagggc 960

gtgtcctact ctctgtgcac agccgccttc accttcacca agatccctgc cgagacactg 1020

cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggaccctg taaggtgcct 1080

gcccagatgg ccgtggatat gcagacactg acacctgtgg gcaggctgat caccgccaat 1140

ccagtgatca cagagtctac cgagaacagc aagatgatgc tggagctgga cccaccattt 1200

ggcgatagct atatcgtgat cggcgtgggc gagaagaaga tcacacacca ctggcaccgc 1260

agcggctgat ga 1272

<210> 80
<211> 422
<212> PRT
<213> Artificial sequence

<220>
<223> Zikasp'_ZikaE395 protein (A12)

<400> 80

Met Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
1   5   10   15

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
            20   25   30

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
        35   40   45

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
    50   55   60

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Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
65                  70                  75                  80

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
                85                  90                  95

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
            100                 105                 110

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
        115                 120                 125

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
    130                 135                 140

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
145                 150                 155                 160

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
                165                 170                 175

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
            180                 185                 190

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
        195                 200                 205

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
    210                 215                 220

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
225                 230                 235                 240

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
                245                 250                 255

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
            260                 265                 270
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Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
        275                 280                 285

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
    290                 295                 300

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
305                 310                 315                 320

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
                325                 330                 335

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
            340                 345                 350

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
        355                 360                 365

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
    370                 375                 380

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
385                 390                 395                 400

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
                405                 410                 415

His Trp His Arg Ser Gly
            420


<210>  81
<211>  2094
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of JEVsp_ZikaprME protein (B1)

<400>  81
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aacgatgctg gggaggccat atcttttcca accacattgg ggatgaataa gtgttatata      180
cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg      240
gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt      300
gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg      360
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cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac     1440
ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt     1500
accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg     1560
gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac     1620
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actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtttgga ggaatgtcct ggttctcaca aattctcatt 1980

ggaacgttgc tgatgtggtt gggtctgaac acaaagaatg gatctatttc ccttatgtgc 2040

ttggccttag gggagtgttt gatcttctta tccacagccg tctctgcttg atga 2094

<210> 82
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<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaprME protein (B1)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

ctggtcatga tcctgctgat cgctcctgcc tattctatcc ggtgcatcgg cgtgagcaat 600

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ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780 gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

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aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

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gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

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accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ccaccagatc 1920

ttcggcgccg cctttaagtc cctgttcggc ggcatgagct ggttctcaca gatcctgatc 1980

ggcacactgc tgatgtggct gggcctgaac accaagaatg gctctatcag cctgatgtgc 2040

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<210> 83
<211> 696
<212> PRT
<213> Artificial sequence

<220>

<223> JEVsp_ZikaprME protein (B1)

<400> 83

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            20                  25                  30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
        35                  40                  45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190
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Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400
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Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405   410   415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420   425   430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450   455   460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465   470   475   480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485   490   495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500   505   510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515   520   525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530   535   540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545   550   555   560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565   570   575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580   585   590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595   600   605

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Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620


Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625                 630                 635                 640


Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
                645                 650                 655


Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
            660                 665                 670


Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
        675                 680                 685


Phe Leu Ser Thr Ala Val Ser Ala
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<210>  84
<211>  1950
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of JEVsp_Zika_prME_no_Anchor protein (B2)

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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg      240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt      300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg      360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga      420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg      480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac      540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat      600
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agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

agcatccagc cagagaatct ggagtaccgg ataatgctgt cagttcatgg ctcccagcac 1020

agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

ataacgccca attcaccaag agccgaagcc accctggggg gttttggaag cctaggactt 1140

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gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

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actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ccatcaaatt 1920

tttggagcag ctttcaaatc attgtgatga 1950

<210> 85
<211> 1950
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME_no_Anchor protein (B2)

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ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga   420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca   480

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accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg   780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca   840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt   900

ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag   960

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aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga   1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc   1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc   1380 ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

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accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

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ttcggcgccg cctttaagtc cctgtgatga 1950

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<211> 648
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_Zika_prME_no_Anchor protein (B2)

<400> 86

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20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
50 55 60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65 70 75 80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr

                85   90   95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100   105   110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115   120   125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130   135   140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145   150   155   160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165   170   175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180   185   190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195   200   205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210   215   220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225   230   235   240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245   250   255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260   265   270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275   280   285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser

290 295 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305 310 315 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
325 330 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
340 345 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
370 375 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385 390 395 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
405 410 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
420 425 430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
450 455 460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465 470 475 480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
485 490 495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu

            500   505   510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515   520   525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530   535   540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545   550   555   560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565   570   575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580   585   590

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595   600   605

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610   615   620

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
625   630   635   640

Phe Gly Ala Ala Phe Lys Ser Leu
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<211> 1914
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<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_Zika_prME411 protein (B3)

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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg 240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt 300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg 360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga 420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg 480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac 540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat 600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga 660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca 720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg 780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact 840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt 900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag 960

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agtgggatga tcgttaatga cacaggacat gaaactgatg agaatagagc gaaggttgag 1080

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aagcactggt tggttcacaa ggagtggttc cacgacattc cattaccttg gcacgctggg 1260

gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca 1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc 1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac 1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt 1500

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gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

atgcaaactc tgaccccagt tgggaggttg ataaccgcta accccgtaat cactgaaagc 1680

actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg gggagaagaa gatcacccac cactggcaca ggagtggcag caccattgga 1800

aaagcatttg aagccactgt gagaggtgcc aagagaatgg cagtcttggg agacacagcc 1860

tgggactttg gatcagttgg aggcgctctc aactcattgg gcaagggcat ctga 1914

<210> 88
<211> 1914
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME411 protein (B3)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

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ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

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ggcaagggct ctctggtgac atgcgccaag ttcgcctgta gcaagaagat gaccggcaag 960

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aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

gcagatacag gaacaccaca ctggaacaat aaggaggccc tggtggagtt caaggatgcc 1320

cacgccaagc ggcagacagt ggtggtgctg ggcagccagg agggagcagt gcacaccgcc 1380

ctggcaggcg ccctggaggc agagatggac ggagctaagg gcagactgtc tagcggccac 1440

ctgaagtgca ggctgaagat ggataagctg cgcctgaagg gcgtgtccta ctctctgtgc 1500

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gaggtgcagt atgccggcac agacggaccc tgtaaggtgc ctgcccagat ggccgtggat 1620

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accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctc cacaatcggc 1800

aaggcctttg aggcaaccgt gcgcggagca aagagaatgg ccgtgctggg cgacaccgca 1860

tgggatttcg gatctgtggg aggcgccctg aacagcctgg gcaagggcat ctga 1914

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<211> 637
<212> PRT
<213> Artificial sequence

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<400> 89

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Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

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Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp
    50                  55                  60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65                  70                  75                  80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85                  90                  95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100                 105                 110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115                 120                 125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130                 135                 140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145                 150                 155                 160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165                 170                 175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180                 185                 190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195                 200                 205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210                 215                 220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225                 230                 235                 240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245                 250                 255
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Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
            260                 265                 270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275                 280                 285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290                 295                 300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305                 310                 315                 320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325                 330                 335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340                 345                 350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370                 375                 380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385                 390                 395                 400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405                 410                 415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420                 425                 430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450                 455                 460
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Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
465                 470                 475                 480


Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485                 490                 495


Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500                 505                 510


Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515                 520                 525


Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530                 535                 540


Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545                 550                 555                 560


Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565                 570                 575


Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580                 585                 590


His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
        595                 600                 605


Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
    610                 615                 620


Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635


<210>  90
<211>  1794
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of JEVsp_Zika_prME395 protein (B4)
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cagatcatgg atcttggaca catgtgtgat gccaccatga gctatgaatg ccctatgctg   240

gatgaggggg tggaaccaga tgacgtcgat tgttggtgca acacgacgtc aacttgggtt   300

gtgtacggaa cctgccatca caaaaaaggt gaagcacgga gatctagaag agctgtgacg   360

ctcccctccc attccactag gaagctgcaa acgcggtcgc aaacctggtt ggaatcaaga   420

gaatacacaa agcacttgat tagagtcgaa aattggatat tcaggaaccc tggcttcgcg   480

ttagcagcag ctgccatcgc ttggcttttg ggaagctcaa cgagccaaaa agtcatatac   540

ttggtcatga tactgctgat tgccccggca tacagcatca ggtgcatagg agtcagcaat   600

agggactttg tggaaggtat gtcaggtggg acttgggttg atgttgtctt ggaacatgga   660

ggttgtgtca ccgtaatggc acaggacaaa ccgactgtcg acatagagct ggttacaaca   720

acagtcagca acatggcgga ggtaagatcc tactgctatg aggcatcaat atcagacatg   780

gcttcggaca gccgctgccc aacacaaggt gaagcctacc ttgacaagca atcagacact   840

caatatgtct gcaaaagaac gttagtggac agaggctggg gaaatggatg tggacttttt   900

ggcaaaggga gcctggtgac atgcgctaag tttgcatgct ccaagaaaat gaccgggaag   960

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gcagacaccg gaactccaca ctggaacaac aaagaagcac tggtagagtt caaggacgca   1320

catgccaaaa ggcaaactgt cgtggttcta gggagtcaag aaggagcagt tcacacggcc   1380

cttgctggag ctctggaggc tgagatggat ggtgcaaagg gaaggctgtc ctctggccac   1440

ttgaaatgtc gcctgaaaat ggataaactt agattgaagg gcgtgtcata ctccttgtgt   1500 accgcagcgt tcacattcac caagatcccg gctgaaacac tgcacgggac agtcacagtg 1560

gaggtacagt acgcagggac agatggacct tgcaaggttc cagctcagat ggcggtggac 1620

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actgagaact ctaagatgat gctggaactt gatccaccat ttggggactc ttacattgtc 1740

ataggagtcg ggagaagaa gatcacccac cactggcaca ggagtggctg atga 1794

<210> 91
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_Zika_prME395 protein (B4)

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aatgatgccg gcgaggccat ctccttccca accacactgg gcatgaacaa gtgctacatc 180

cagatcatgg acctgggcca catgtgcgat gccaccatgt cctatgagtg tccaatgctg 240

gacgagggcg tggagcccga cgatgtggat tgctggtgta ataccacatc tacatgggtg 300

gtgtacggca cctgtcacca caagaaggga gaggcccggc ggagccggcg ggccgtgaca 360

ctgccttccc actctaccag gaagctgcag acacgcagcc agacctggct ggagtccaga 420

gagtatacca agcacctgat cagggtggag aactggatct ttcgcaatcc aggattcgca 480

ctggcagcag cagcaatcgc atggctgctg ggaagctcca ccagccagaa agtgatctac 540

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agagacttcg tggagggaat gtccggagga acctgggtgg atgtggtgct ggagcacggc 660

ggctgcgtga cagtgatggc ccaggacaag ccaaccgtgg atatcgagct ggtgaccaca 720

accgtgtcca acatggccga ggtgaggtct tactgctatg aggccagcat ctccgacatg 780

gcctctgata gcaggtgtcc aacccaggga gaggcatacc tggacaagca gtccgataca 840

cagtacgtgt gcaagcggac cctggtggac agaggctggg gcaatggctg tggcctgttt 900

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aagcactggc tggtgcacaa ggagtggttt cacgacatcc cactgccatg gcacgcagga 1260

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accgagaaca gcaagatgat gctggagctg gacccaccat ttggcgatag ctatatcgtg 1740

atcggcgtgg gcgagaagaa gatcacacac cactggcacc gcagcggctg atga 1794

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<211> 596
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_Zika_prME395 protein (B4)

<400> 92

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Val Val Ile Ala Cys Ala Gly Ala Ala Glu Val Thr Arg Arg Gly Ser
20 25 30

Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser
35 40 45

Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp

    50   55   60

Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu
65   70   75   80

Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr
                85   90   95

Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala
            100   105   110

Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys
        115   120   125

Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys
    130   135   140

His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala
145   150   155   160

Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln
                165   170   175

Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser
            180   185   190

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
        195   200   205

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
    210   215   220

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
225   230   235   240

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
                245   250   255

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala

            260   265   270

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
        275   280   285

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
    290   295   300

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
305   310   315   320

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
                325   330   335

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
            340   345   350

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

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
    370   375   380

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
385   390   395   400

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
                405   410   415

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
            420   425   430

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
    450   455   460

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His

465   470   475   480

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
                485   490   495

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
            500   505   510

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
        515   520   525

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
    530   535   540

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
545   550   555   560

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
                565   570   575

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
            580   585   590

His Arg Ser Gly
        595

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<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE protein (B5)

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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag   180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta   240 agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

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gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

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aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

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aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

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<210> 94
<211> 1590
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE protein (B5)

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gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg   660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag   720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg   780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg   840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag   900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat   960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag   1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac   1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc   1140

aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg   1200

gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc   1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc   1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc   1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg   1440 ttcggcggca tgagctggtt ctcacagatc ctgatcggca cactgctgat gtggctgggc 1500

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ttcctgtcca ccgccgtgtc tgcctgatga 1590

<210> 95
<211> 528
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE protein (B5)

<400> 95

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1   5   10   15

Val Val Ile Ala Cys Ala Gly Ala Ile Arg Cys Ile Gly Val Ser Asn
            20   25   30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35   40   45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50   55   60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65   70   75   80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85   90   95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100   105   110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115   120   125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130   135   140

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Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350
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Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405                 410                 415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420                 425                 430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435                 440                 445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450                 455                 460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465                 470                 475                 480

Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu
                485                 490                 495

Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys
            500                 505                 510

Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
        515                 520                 525
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<210> 96
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE_no_Anchor protein (B6)

<400> 96
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tgtgcaggag ccatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca   120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag   180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta   240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca   300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta   360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc   420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag   480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca   540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc   600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt   660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag   720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg   780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg   840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag   900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat   960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag   1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat   1080

ggaccttgca aggttccagc tcagatggcg gtggacatgc aaactctgac cccagttggg   1140

aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg   1200

gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc   1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga   1320

ggtgccaaga gaatggcagt cttgggagac acagcctggg actttggatc agttggaggc   1380

gctctcaact cattgggcaa gggcatccat caaatttttg gagcagcttt caaatcattg   1440

tgatga   1446

<210> 97
<211> 1446
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE_no_Anchor protein (B6)

<400> 97
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tgtgcaggag caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc   120

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gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg   240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc   300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg   360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc   420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag   480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca   540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc   600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg   660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag   720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg   780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg   840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag   900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat   960

aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag   1020

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc   1260 acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatccac cagatcttcg gcgccgcctt taagtccctg 1440

tgatga 1446

<210> 98
<211> 480
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE_no_Anchor protein (B6)

<400> 98

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Ile Arg Cys Ile Gly Val Ser Asn
20 25 30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
35 40 45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
50 55 60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65 70 75 80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
85 90 95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
100 105 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
115 120 125

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Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335
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Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340   345   350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355   360   365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370   375   380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385   390   395   400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405   410   415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420   425   430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435   440   445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450   455   460

Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
465   470   475   480

<210> 99
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE411 protein (B7)

<400> 99
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tgtgcaggag ccatcaggtg cataggagtc agcaataggg actttgtgga aggtatgtca   120

ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag   180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta   240 agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca 300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta 360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc 420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag 480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca 540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc 600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt 660

gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

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gaacttgatc caccatttgg ggactcttac attgtcatag gagtcgggga gaagaagatc 1260

acccaccact ggcacaggag tggcagcacc attggaaaag catttgaagc cactgtgaga 1320

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gctctcaact cattgggcaa gggcatctga 1410

<210> 100
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE411 protein (B7)

<400> 100
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tgtgcaggag caatccggtg catcggcgtg agcaatagag acttcgtgga gggaatgtcc 120

ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

gtggacagag gctggggcaa tggctgtggc ctgtttggca agggctctct ggtgacatgc 420

gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

taccggatca tgctgtctgt gcacggctcc cagcactctg gcatgatcgt gaacgacaca 540

ggccacgaga cagatgagaa tcgggccaag gtggagatca cacctaactc tccaagagcc 600

gaggccaccc tgggaggatt tggctctctg ggcctggact gcgagcctag aacaggcctg 660

gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

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aagctgcgcc tgaagggcgt gtcctactct ctgtgcacag ccgccttcac cttcaccaag 1020

atccctgccg agacactgca cggcacagtg accgtggagg tgcagtatgc cggcacagac 1080

ggaccctgta aggtgcctgc ccagatggcc gtggatatgc agacactgac acctgtgggc 1140

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gagctggacc caccatttgg cgatagctat atcgtgatcg gcgtgggcga gaagaagatc 1260

acacaccact ggcaccgcag cggctccaca atcggcaagg cctttgaggc aaccgtgcgc 1320

ggagcaaaga gaatggccgt gctgggcgac accgcatggg atttcggatc tgtgggaggc 1380

gccctgaaca gcctgggcaa gggcatctga 1410

<210> 101
<211> 469
<212> PRT
<213> Artificial sequence

<220>
<223> JEVsp_ZikaE411 protein (B7)

<400> 101

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1               5                   10                  15

Val Val Ile Ala Cys Ala Gly Ala Ile Arg Cys Ile Gly Val Ser Asn
            20                  25                  30

Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35                  40                  45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50                  55                  60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65                  70                  75                  80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85                  90                  95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100                 105                 110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115                 120                 125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130                 135                 140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145                 150                 155                 160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165                 170                 175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180                 185                 190
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Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195                 200                 205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210                 215                 220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225                 230                 235                 240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245                 250                 255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260                 265                 270

His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400
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Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
                405   410   415

Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly
            420   425   430

Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu
        435   440   445

Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser
    450   455   460

Leu Gly Lys Gly Ile
465

<210> 102
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of JEVsp_ZikaE395 protein (B8)

<400> 102
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ggtgggactt gggttgatgt tgtcttggaa catggaggtt gtgtcaccgt aatggcacag   180

gacaaaccga ctgtcgacat agagctggtt acaacaacag tcagcaacat ggcggaggta   240

agatcctact gctatgaggc atcaatatca gacatggctt cggacagccg ctgcccaaca   300

caaggtgaag cctaccttga caagcaatca gacactcaat atgtctgcaa aagaacgtta   360

gtggacagag gctggggaaa tggatgtgga ctttttggca aagggagcct ggtgacatgc   420

gctaagtttg catgctccaa gaaaatgacc gggaagagca tccagccaga gaatctggag   480

taccggataa tgctgtcagt tcatggctcc cagcacagtg ggatgatcgt taatgacaca   540

ggacatgaaa ctgatgagaa tagagcgaag gttgagataa cgcccaattc accaagagcc   600

gaagccaccc tgggggggttt tggaagccta ggacttgatt gtgaaccgag gacaggcctt   660 gacttttcag atttgtatta cttgactatg aataacaagc actggttggt tcacaaggag 720

tggttccacg acattccatt accttggcac gctggggcag acaccggaac tccacactgg 780

aacaacaaag aagcactggt agagttcaag gacgcacatg ccaaaaggca aactgtcgtg 840

gttctaggga gtcaagaagg agcagttcac acggcccttg ctggagctct ggaggctgag 900

atggatggtg caaagggaag gctgtcctct ggccacttga aatgtcgcct gaaaatggat 960

aaacttagat tgaagggcgt gtcatactcc ttgtgtaccg cagcgttcac attcaccaag 1020

atcccggctg aaacactgca cgggacagtc acagtggagg tacagtacgc agggacagat 1080

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aggttgataa ccgctaaccc cgtaatcact gaaagcactg agaactctaa gatgatgctg 1200

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acccaccact ggcacaggag tggctgatga 1290

<210> 103
<211> 1290
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of JEVsp_ZikaE395 protein (B8)

<400> 103
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ggaggaacct gggtggatgt ggtgctggag cacggcggct gcgtgacagt gatggcccag 180

gacaagccaa ccgtggatat cgagctggtg accacaaccg tgtccaacat ggccgaggtg 240

aggtcttact gctatgaggc cagcatctcc gacatggcct ctgatagcag gtgtccaacc 300

cagggagagg catacctgga caagcagtcc gatacacagt acgtgtgcaa gcggaccctg 360

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gccaagttcg cctgtagcaa gaagatgacc ggcaagtcca tccagccaga gaacctggag 480

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gacttctccg atctgtacta tctgaccatg aacaataagc actggctggt gcacaaggag 720

tggtttcacg acatcccact gccatggcac gcaggagcag atacaggaac accacactgg 780

aacaataagg aggccctggt ggagttcaag gatgcccacg ccaagcggca gacagtggtg 840

gtgctgggca gccaggaggg agcagtgcac accgccctgg caggcgccct ggaggcagag 900

atggacggag ctaagggcag actgtctagc ggccacctga agtgcaggct gaagatggat 960

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aggctgatca ccgccaatcc agtgatcaca gagtctaccg agaacagcaa gatgatgctg 1200

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<211> 428
<212> PRT
<213> Artificial sequence

<220>
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<400> 104

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Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val
        35   40   45

Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr
    50   55   60

Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val
65   70   75   80

Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser
                85   90   95

Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr
            100   105   110

Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly
        115   120   125

Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala
    130   135   140

Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu
145   150   155   160

Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile
                165   170   175

Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu
            180   185   190

Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly
        195   200   205

Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp
    210   215   220

Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu
225   230   235   240

Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly
                245   250   255

Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala
            260   265   270

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His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala
        275                 280                 285

Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala
    290                 295                 300

Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp
305                 310                 315                 320

Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe
                325                 330                 335

Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val
            340                 345                 350

Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln
        355                 360                 365

Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr
    370                 375                 380

Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu
385                 390                 395                 400

Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly
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Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
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<210>  105
<211>  2106
<212>  DNA
<213>  Artificial sequence

<220>
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gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg 300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct 360

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tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

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gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

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catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggtttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

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gcttga 2106

<210> 106
<211> 2106
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaprME (C1)

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aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

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aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

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gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

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ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

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ggcatccacc agatcttcgg cgccgccttt aagtccctgt tcggcggcat gagctggttc 1980

tcacagatcc tgatcggcac actgctgatg tggctgggcc tgaacaccaa gaatggctct 2040

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gcctga 2106

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<211> 701
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaprME (C1)

<400> 107

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Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
            20   25   30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35   40   45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50   55   60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65   70   75   80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85   90   95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100   105   110

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

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130   135   140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145   150   155   160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165   170   175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180   185   190

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Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355                 360                 365

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400
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Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg
465                 470                 475                 480

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605
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Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610   615   620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625   630   635   640

Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly
                645   650   655

Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu
            660   665   670

Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu
        675   680   685

Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
    690   695   700

<210> 108
<211> 1962
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_prME_no_anchor (C2)

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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg   180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat   240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg   300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct   360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc   420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg   480

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gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

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agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

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gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

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gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

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gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatccatc aaatttttgg agcagctttc aaatcattgt ga 1962

<210> 109
<211> 1962

<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME_no_anchor (C2)

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gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc   300

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cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc   420

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cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc   600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg   660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc   720

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<211> 653
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME_no_anchor (C2)

<400> 110

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20 25 30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
35 40 45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
50 55 60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65 70 75 80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85   90   95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100   105   110

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

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130   135   140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145   150   155   160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165   170   175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180   185   190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195   200   205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210   215   220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225   230   235   240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245   250   255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260   265   270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275   280   285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290   295   300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305   310   315   320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325   330   335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340   345   350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355   360   365

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370   375   380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385   390   395   400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405   410   415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420   425   430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435   440   445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450   455   460

Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg
465   470   475   480

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485   490   495

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Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510


Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525


Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540


Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560


Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575


Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590


Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605


Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620


Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640


Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
                645                 650


<210>  111
<211>  1932
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of MVsp_Zika_prME411 (C3)

<400>  111
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ctccaaacac ccaccggtca aatccatgcg gaggtcacta gacgtgggag tgcatactat      120
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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg 180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat 240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg 300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct 360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc 420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg 480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc 540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc 600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt 660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata 720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca 780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac 840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat 900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag 960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680 gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatctgat ga 1932

<210> 112
<211> 1932
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME411 (C3)

<400> 112
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ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat 120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg 180

aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc 360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc 420

tggctggagt ccagagagta taccaagcac ctgatcaggg tggagaactg gatctttcgc 480

aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg 660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc 720

gagctggtga ccacaaccgt gtccaacatg gccgaggtga ggtcttactg ctatgaggcc 780

agcatctccg acatggcctc tgatagcagg tgtccaaccc agggagaggc atacctggac 840

aagcagtccg atacacagta cgtgtgcaag cggaccctgg tggacagagg ctggggcaat 900

ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960 aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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ctgaccatga acaataagca ctggctggtg cacaaggagt ggtttcacga catcccactg 1260

ccatggcacg caggagcaga tacaggaaca ccacactgga acaataagga ggccctggtg 1320

gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga 1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatctgat ga 1932

<210> 113
<211> 642
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME411 (C3)

<400> 113

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
            20   25   30

```
Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35                  40                  45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50                  55                  60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65                  70                  75                  80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

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

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

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

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355                 360                 365

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445
```

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450   455   460

Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg
465   470   475   480

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485   490   495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500   505   510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515   520   525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530   535   540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545   550   555   560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565   570   575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580   585   590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595   600   605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610   615   620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625   630   635   640

Gly Ile

<210> 114
<211> 1806
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_prME395 (C4)

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atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg   180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat   240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg   300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct   360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc   420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg   480

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ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt   660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata   720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca   780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac   840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat   900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag   960

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt   1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat   1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggtttt   1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac   1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta   1260 ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggctga 1806

<210> 115
<211> 1806
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_prME395 (C4)

<400> 115
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aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat 240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc 300

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aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc 540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc 600

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aagcagtccg atacacagta cgtgtgcaag cggaccctgg tggacagagg ctggggcaat 900

ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag 960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg 1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat 1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt 1140

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gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga 1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga 1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg 1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac 1560

ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctga 1806

<210> 116
<211> 601
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_prME395 (C4)

<400> 116

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Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
            20                  25                  30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35                  40                  45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50                  55                  60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65                  70                  75                  80

Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

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

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205
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Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285

Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355                 360                 365

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415
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Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg
465                 470                 475                 480

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495

Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly
        595                 600
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<210> 117
<211> 1602
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE (C5)

<400> 117
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact   60

ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt   120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc   180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc   240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac   300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc   360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg   420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag   480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg   540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc   600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa   660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg   720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc   780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa   840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga   900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt   960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg   1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag   1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact   1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac   1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc   1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt   1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt   1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca   1440 gctttcaaat cattgtttgg aggaatgtcc tggttctcac aaattctcat tggaacgttg 1500

ctgatgtggt tgggtctgaa cacaaagaat ggatctattt cccttatgtg cttggcctta 1560

gggggagtgt tgatcttctt atccacagcc gtctctgctt ga 1602

<210> 118
<211> 1602
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE (C5)

<400> 118
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080 tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgttcgg cggcatgagc tggttctcac agatcctgat cggcacactg 1500

ctgatgtggc tgggcctgaa caccaagaat ggctctatca gcctgatgtg cctggccctg 1560

ggaggcgtgc tgatcttcct gtccaccgcc gtgtctgcct ga 1602

<210> 119
<211> 533
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE (C5)

<400> 119

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20   25   30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35   40   45

Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala
    50   55   60

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

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85   90   95

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Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100                 105                 110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140

Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300
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Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465                 470                 475                 480

Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu
                485                 490                 495

Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser
            500                 505                 510
```

Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser
        515   520   525

Thr Ala Val Ser Ala
    530

<210> 120
<211> 1458
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE_no_anchor (C6)

<400> 120
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ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt   120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc   180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc   240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac   300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc   360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg   420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag   480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg   540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc   600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa   660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg   720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc   780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa   840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga   900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt   960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg   1020 ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca 1440

gctttcaaat cattgtga 1458

<210> 121
<211> 1458
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE_no_anchor (C6)

<400> 121
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780 ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgtga 1458

<210> 122
<211> 485
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE_no_anchor (C6)

<400> 122

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20   25   30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35   40   45

Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala
    50   55   60

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


Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85                  90                  95


Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100                 105                 110


Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125


Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140


Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160


Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175


His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190


Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205


Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220


Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240


Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255


Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270
```

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Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465                 470                 475                 480
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Ala Phe Lys Ser Leu
                485

<210> 123
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaE411 (C7)

<400> 123
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact   60

ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt   120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc   180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc   240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac   300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc   360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg   420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag   480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg   540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc   600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa   660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg   720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc   780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa   840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga   900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt   960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg   1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag   1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact   1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac   1200 tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tctgatga 1428

<210> 124
<211> 1428
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE411 (C7)

<400> 124
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc 120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020 ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tctgatga 1428

<210> 125
<211> 474
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaE411 (C7)

<400> 125

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
20 25 30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
35 40 45

Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala
50 55 60

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

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
85 90 95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
100 105 110

```
Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140

Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320
```

```
Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405                 410                 415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420                 425                 430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435                 440                 445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450                 455                 460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
465                 470


<210>  126
<211>  1302
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of MVsp_ZikaE395 (C8)

<400>  126
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact       60
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ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt 120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc 180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc 240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac 300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc 360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg 420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag 480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg 540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc 600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa 660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg 720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc 780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa 840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga 900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt 960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg 1020

ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggct ga 1302

<210> 127
<211> 1302
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaE395 (C8)

<400> 127
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc   60

ctgcagacac caacaggcca gatccacatc cggtgcatcg gcgtgagcaa tagagacttc   120

gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg   180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc   240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat   300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg   360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc   420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag   480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg   540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct   600

aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag   660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg   720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca   780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag   840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc   900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc   960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc   1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag   1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca   1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac   1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg   1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ga   1302

<210> 128
<211> 433
<212> PRT
<213> Artificial sequence

<220>

<223> MVsp_ZikaE395 (C8)

<400> 128

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Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20                  25                  30


Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35                  40                  45


Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala
    50                  55                  60


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


Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85                  90                  95


Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100                 105                 110


Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115                 120                 125


Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130                 135                 140


Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145                 150                 155                 160


Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165                 170                 175


His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180                 185                 190
```

```
Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195                 200                 205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210                 215                 220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225                 230                 235                 240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245                 250                 255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260                 265                 270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275                 280                 285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290                 295                 300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305                 310                 315                 320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325                 330                 335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340                 345                 350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355                 360                 365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370                 375                 380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385                 390                 395                 400
```

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405   410   415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420   425   430

Gly

<210> 129
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_ZikaprME_MVTMintracyto (C9)

<400> 129
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ctccaaacac ccaccggtca aatccatgcg gaggtcacta gacgtgggag tgcatactat   120

atgtacttgg acagaaacga tgctggggag gccatatctt ttccaaccac attggggatg   180

aataagtgtt atatacagat catggatctt ggacacatgt gtgatgccac catgagctat   240

gaatgcccta tgctggatga gggggtggaa ccagatgacg tcgattgttg gtgcaacacg   300

acgtcaactt gggttgtgta cggaacctgc catcacaaaa aaggtgaagc acggagatct   360

agaagagctg tgacgctccc ctcccattcc actaggaagc tgcaaacgcg gtcgcaaacc   420

tggttggaat caagagaata cacaaagcac ttgattagag tcgaaaattg gatattcagg   480

aaccctggct tcgcgttagc agcagctgcc atcgcttggc ttttgggaag ctcaacgagc   540

caaaaagtca tatacttggt catgatactg ctgattgccc cggcatacag catcaggtgc   600

ataggagtca gcaataggga ctttgtggaa ggtatgtcag gtgggacttg ggttgatgtt   660

gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata   720

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca   780

tcaatatcag acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac   840

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat   900

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag   960 aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt 1020

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat 1080

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggctttt 1140

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac 1200

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta 1260

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta 1320

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga 1380

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg 1440

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg 1500

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac 1560

gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1620

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1680

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1740

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1800

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1860

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1920

ggcatccatc aaatttttgg agcagctttc aaatcattgt ttggaggaat gtcctggttc 1980

tcaatgaaag gtttatcgag cactagcata gtctacatcc tgattgcagt gtgtcttgga 2040

gggttgatag ggatccccgc tttaatatgt tgctgcaggg ggcgttgtaa caaaaaggga 2100

gaacaagttg gtatgtcaag accaggccta aagcctgatc ttacgggaac atcaaaatcc 2160

tatgtaaggt cgctctga 2178

<210> 130
<211> 2178
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_ZikaprME_MVTMintracyto (C9)

<400> 130
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ctgcagacac caacaggcca gatccacgca gaggtgacca ggagaggaag cgcctactat   120

atgtacctgg acaggaatga tgccggcgag gccatctcct tcccaaccac actgggcatg   180

aacaagtgct acatccagat catggacctg ggccacatgt gcgatgccac catgtcctat   240

gagtgtccaa tgctggacga gggcgtggag cccgacgatg tggattgctg gtgtaatacc   300

acatctacat gggtggtgta cggcacctgt caccacaaga agggagaggc ccggcggagc   360

cggcgggccg tgacactgcc ttcccactct accaggaagc tgcagacacg cagccagacc   420

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aatccaggat tcgcactggc agcagcagca atcgcatggc tgctgggaag ctccaccagc   540

cagaaagtga tctacctggt catgatcctg ctgatcgctc ctgcctattc tatccggtgc   600

atcggcgtga gcaatagaga cttcgtggag ggaatgtccg gaggaacctg ggtggatgtg   660

gtgctggagc acggcggctg cgtgacagtg atggcccagg acaagccaac cgtggatatc   720

gagctggtga ccacaaccgt gtccaacatg gccgaggtga ggtcttactg ctatgaggcc   780

agcatctccg acatggcctc tgatagcagg tgtccaaccc agggagaggc atacctggac   840

aagcagtccg atacacagta cgtgtgcaag cggaccctgg tggacagagg ctggggcaat   900

ggctgtggcc tgtttggcaa gggctctctg gtgacatgcg ccaagttcgc ctgtagcaag   960

aagatgaccg gcaagtccat ccagccagag aacctggagt accggatcat gctgtctgtg   1020

cacggctccc agcactctgg catgatcgtg aacgacacag gccacgagac agatgagaat   1080

cgggccaagg tggagatcac acctaactct ccaagagccg aggccaccct gggaggattt   1140

ggctctctgg gcctggactg cgagcctaga acaggcctgg acttctccga tctgtactat   1200

ctgaccatga acaataagca ctggctggtg cacaaggagt ggtttcacga catcccactg   1260

ccatggcacg caggagcaga tacaggaaca ccacactgga acaataagga ggccctggtg   1320

gagttcaagg atgcccacgc caagcggcag acagtggtgg tgctgggcag ccaggaggga   1380

gcagtgcaca ccgccctggc aggcgccctg gaggcagaga tggacggagc taagggcaga   1440

ctgtctagcg gccacctgaa gtgcaggctg aagatggata agctgcgcct gaagggcgtg   1500

tcctactctc tgtgcacagc cgccttcacc ttcaccaaga tccctgccga gacactgcac   1560 ggcacagtga ccgtggaggt gcagtatgcc ggcacagacg gaccctgtaa ggtgcctgcc 1620

cagatggccg tggatatgca gacactgaca cctgtgggca ggctgatcac cgccaatcca 1680

gtgatcacag agtctaccga gaacagcaag atgatgctgg agctggaccc accatttggc 1740

gatagctata tcgtgatcgg cgtgggcgag aagaagatca cacaccactg gcaccgcagc 1800

ggctccacaa tcggcaaggc ctttgaggca accgtgcgcg gagcaaagag aatggccgtg 1860

ctgggcgaca ccgcatggga tttcggatct gtgggaggcg ccctgaacag cctgggcaag 1920

ggcatccacc agatcttcgg cgccgccttt aagtccctgt tcggcggcat gagctggttc 1980

tcaatgaagg gcctgtcctc tacctctatc gtgtacatcc tgatcgccgt gtgcctggga 2040

ggcctgatcg gaatcccagc cctgatctgc tgttgcagag gccgctgcaa caagaaggga 2100

gagcaagtgg gaatgtctcg gccaggcctg aagccagacc tgacaggcac ctccaagtct 2160

tatgtgagaa gcctgtga 2178

<210> 131
<211> 725
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_ZikaprME_MVTMintracyto (C9)

<400> 131

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ala Glu Val
            20   25   30

Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala
        35   40   45

Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr
    50   55   60

Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr
65   70   75   80

```
Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys
                85                  90                  95

Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His
            100                 105                 110

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

His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser
    130                 135                 140

Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg
145                 150                 155                 160

Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly
                165                 170                 175

Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile
            180                 185                 190

Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe
        195                 200                 205

Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His
    210                 215                 220

Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile
225                 230                 235                 240

Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr
                245                 250                 255

Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro
            260                 265                 270

Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val
        275                 280                 285
```

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Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
    290                 295                 300

Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys
305                 310                 315                 320

Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile
                325                 330                 335

Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp
            340                 345                 350

Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro
        355                 360                 365

Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly
    370                 375                 380

Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr
385                 390                 395                 400

Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His
                405                 410                 415

Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His
            420                 425                 430

Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys
        435                 440                 445

Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr
    450                 455                 460

Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg
465                 470                 475                 480

Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg
                485                 490                 495
```

```
Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr
            500                 505                 510

Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln
        515                 520                 525

Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val
    530                 535                 540

Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro
545                 550                 555                 560

Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp
                565                 570                 575

Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys
            580                 585                 590

Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe
        595                 600                 605

Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr
    610                 615                 620

Ala Trp Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys
625                 630                 635                 640

Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly
                645                 650                 655

Met Ser Trp Phe Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val Tyr
            660                 665                 670

Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu
        675                 680                 685

Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly
    690                 695                 700
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Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser
705   710   715   720

Tyr Val Arg Ser Leu
                725

<210> 132
<211> 1674
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp_Zika_MVTMintracytoE (C10)

<400> 132
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ctccaaacac ccaccggtca aatccatatc aggtgcatag gagtcagcaa tagggacttt   120

gtggaaggta tgtcaggtgg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc   180

accgtaatgg cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc   240

aacatggcgg aggtaagatc ctactgctat gaggcatcaa tatcagacat ggcttcggac   300

agccgctgcc caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc   360

tgcaaaagaa cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg   420

agcctggtga catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag   480

ccagagaatc tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg   540

atcgttaatg acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc   600

aattcaccaa gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa   660

ccgaggacag gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg   720

ttggttcaca aggagtggtt ccacgacatt ccattacctt ggcacgctgg ggcagacacc   780

ggaactccac actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa   840

aggcaaactg tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga   900

gctctggagg ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt   960

cgcctgaaaa tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg   1020 ttcacattca ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag 1080

tacgcaggga cagatggacc ttgcaaggtt ccagctcaga tggcggtgga catgcaaact 1140

ctgaccccag ttgggaggtt gataaccgct aaccccgtaa tcactgaaag cactgagaac 1200

tctaagatga tgctggaact tgatccacca tttggggact cttacattgt cataggagtc 1260

ggggagaaga agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt 1320

gaagccactg tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt 1380

ggatcagttg gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca 1440

gctttcaaat cattgtttgg aggaatgtcc tggttctcaa tgaaaggttt atcgagcact 1500

agcatagtct acatcctgat tgcagtgtgt cttggagggt tgatagggat ccccgcttta 1560

atatgttgct gcagggggcg ttgtaacaaa aagggagaac aagttggtat gtcaagacca 1620

ggcctaaagc ctgatcttac gggaacatca aaatcctatg taaggtcgct ctga 1674

<210> 133
<211> 1674
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp_Zika_MVTMintracytoE (C10)

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gtggagggaa tgtccggagg aacctgggtg gatgtggtgc tggagcacgg cggctgcgtg 180

acagtgatgg cccaggacaa gccaaccgtg gatatcgagc tggtgaccac aaccgtgtcc 240

aacatggccg aggtgaggtc ttactgctat gaggccagca tctccgacat ggcctctgat 300

agcaggtgtc caacccaggg agaggcatac ctggacaagc agtccgatac acagtacgtg 360

tgcaagcgga ccctggtgga cagaggctgg ggcaatggct gtggcctgtt tggcaagggc 420

tctctggtga catgcgccaa gttcgcctgt agcaagaaga tgaccggcaa gtccatccag 480

ccagagaacc tggagtaccg gatcatgctg tctgtgcacg gctcccagca ctctggcatg 540

atcgtgaacg acacaggcca cgagacagat gagaatcggg ccaaggtgga gatcacacct 600 aactctccaa gagccgaggc caccctggga ggatttggct ctctgggcct ggactgcgag 660

cctagaacag gcctggactt ctccgatctg tactatctga ccatgaacaa taagcactgg 720

ctggtgcaca aggagtggtt tcacgacatc ccactgccat ggcacgcagg agcagataca 780

ggaacaccac actggaacaa taaggaggcc ctggtggagt tcaaggatgc ccacgccaag 840

cggcagacag tggtggtgct gggcagccag gagggagcag tgcacaccgc cctggcaggc 900

gccctggagg cagagatgga cggagctaag ggcagactgt ctagcggcca cctgaagtgc 960

aggctgaaga tggataagct gcgcctgaag ggcgtgtcct actctctgtg cacagccgcc 1020

ttcaccttca ccaagatccc tgccgagaca ctgcacggca cagtgaccgt ggaggtgcag 1080

tatgccggca cagacggacc ctgtaaggtg cctgcccaga tggccgtgga tatgcagaca 1140

ctgacacctg tgggcaggct gatcaccgcc aatccagtga tcacagagtc taccgagaac 1200

agcaagatga tgctggagct ggacccacca tttggcgata gctatatcgt gatcggcgtg 1260

ggcgagaaga agatcacaca ccactggcac cgcagcggct ccacaatcgg caaggccttt 1320

gaggcaaccg tgcgcggagc aaagagaatg gccgtgctgg gcgacaccgc atgggatttc 1380

ggatctgtgg gaggcgccct gaacagcctg ggcaagggca tccaccagat cttcggcgcc 1440

gcctttaagt ccctgttcgg cggcatgagc tggttctcaa tgaagggcct gtcctctacc 1500

tctatcgtgt acatcctgat cgccgtgtgc ctgggaggcc tgatcggaat cccagccctg 1560

atctgctgtt gcagaggccg ctgcaacaag aagggagagc aagtgggaat gtctcggcca 1620

ggcctgaagc cagacctgac aggcacctcc aagtcttatg tgagaagcct gtga 1674

<210> 134
<211> 557
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp_Zika_MVTMintracytoE (C10)

<400> 134

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1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Ile Arg Cys
            20   25   30

Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr
        35   40   45

Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala
    50   55   60

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

Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp
                85   90   95

Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp
            100   105   110

Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg
        115   120   125

Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr
    130   135   140

Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln
145   150   155   160

Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln
                165   170   175

His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn
            180   185   190

Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr
        195   200   205

Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly
    210   215   220

Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp
225   230   235   240

Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala
                245   250   255

Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val
            260   265   270

Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly
        275   280   285

Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala
    290   295   300

Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys
305   310   315   320

Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu
                325   330   335

Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His
            340   345   350

Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys
        355   360   365

Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val
    370   375   380

Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn
385   390   395   400

Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile
                405   410   415

Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
            420   425   430

Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys
        435   440   445

Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
    450   455   460

Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala
465   470   475   480

Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Met Lys Gly
                485   490   495

Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly
            500   505   510

Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys
        515   520   525

Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro Gly Leu Lys Pro
    530   535   540

Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser Leu
545   550   555

<210> 135
<211> 2100
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaprME (D1)

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ttggacagaa acgatgctgg ggaggccata tcttttccaa ccacattggg gatgaataag   180

tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc   240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca   300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga   360 gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggactttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

tcccagcaca gtgggatgat cgttaatgac acaggacatg aaactgatga gaatagagcg 1080

aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

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tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920 catcaaattt ttggagcagc tttcaaatca ttgtttggag gaatgtcctg gttctcacaa 1980

attctcattg gaacgttgct gatgtggttg ggtctgaaca caaagaatgg atctatttcc 2040

cttatgtgct tggccttagg gggagtgttg atcttcttat ccacagccgt ctctgcttga 2100

<210> 136
<211> 2100
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp'_ZikaprME (D1)

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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc 780

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tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080 aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

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atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

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<210> 137
<211> 699
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaprME (D1)

<400> 137

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            20   25   30

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Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
        35                  40                  45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
    50                  55                  60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65                  70                  75                  80

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

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

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240
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Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445
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Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465                 470                 475                 480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500                 505                 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515                 520                 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530                 535                 540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635                 640

His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser
                645                 650                 655
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Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu
660 665 670

Asn Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly
675 680 685

Val Leu Ile Phe Leu Ser Thr Ala Val Ser Ala
690 695

<210> 138
<211> 1956
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_Zika_prME_no_anchor (D2)

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tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

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accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

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aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

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aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

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tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

catcaaattt ttggagcagc tttcaaatca ttgtga 1956

<210> 139
<211> 1956
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp'_Zika_prME_no_anchor (D2)

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tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240
ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300
acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360
gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420
gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480
ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540
gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600
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gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720
gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc 780
tccgacatgg cctctgatag caggtgtcca acccagggag aggcatacct ggacaagcag 840
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ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960
accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020
tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080
aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140
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aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380
cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440
agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500
tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560
gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620
gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680
acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

tatatcgtga tcggcgtggg cgagaagaag atcacacacc actggcaccg cagcggctcc 1800

acaatcggca aggcctttga ggcaaccgtg cgcggagcaa agagaatggc cgtgctgggc 1860

gacaccgcat gggatttcgg atctgtggga ggcgccctga acagcctggg caagggcatc 1920

caccagatct tcggcgccgc ctttaagtcc ctgtga 1956

<210> 140
<211> 651
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_Zika_prME_no_anchor (D2)

<400> 140

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

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

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
35 40 45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
50 55 60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65 70 75 80

Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
85 90 95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
100 105 110

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

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130   135   140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145   150   155   160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165   170   175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180   185   190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195   200   205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210   215   220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225   230   235   240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245   250   255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260   265   270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275   280   285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290   295   300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305   310   315   320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325   330   335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
340 345 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
370 375 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385 390 395 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
405 410 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
420 425 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
435 440 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
450 455 460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465 470 475 480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
485 490 495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
500 505 510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
515 520 525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
530 535 540

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Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545                 550                 555                 560


Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565                 570                 575


Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580                 585                 590


His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595                 600                 605


Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610                 615                 620


Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625                 630                 635                 640


His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu
                645                 650


<210>  141
<211>  1926
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Native nucleotide sequence of MVsp'_Zika_prME411 (D3)

<400>  141
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ctccaaacac ccaccggtca agcggaggtc actagacgtg ggagtgcata ctatatgtac       120

ttggacagaa acgatgctgg ggaggccata tcttttccaa ccacattggg gatgaataag       180

tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc       240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca       300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga       360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg       420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct       480
```

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540
gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600
gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660
gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720
gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780
tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840
tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900
ggactttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960
accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020
tcccagcaca gtgggatgat cgttaatgac acaggacatg aaactgatga gaatagagcg 1080
aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140
ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200
atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260
cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320
aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380
cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440
tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500
tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560
gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620
gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680
actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740
tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800
accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860
gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920
tgatga 1926

<210> 142
<211> 1926
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_Zika_prME411 (D3)

<400> 142
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ctgcagacac caacaggcca ggcagaggtg accaggagag gaagcgccta ctatatgtac   120

ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag   180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt   240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct   300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg   360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg   420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca   480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa   540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc   600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg   660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg   720

gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc   780

tccgacatgg cctctgatag caggtgtcca acccagggag aggcatacct ggacaagcag   840

tccgatacac agtacgtgtg caagcggacc ctggtggaca gaggctgggg caatggctgt   900

ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg   960

accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc   1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc   1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct   1140

ctgggcctgg actgcgagcc tagaacaggc ctggacttct ccgatctgta ctatctgacc   1200

atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg   1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc   1320 aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

tatatcgtga tcggcgtggg cgagaagaag atcacacacc actggcaccg cagcggctcc 1800

acaatcggca aggcctttga ggcaaccgtg cgcggagcaa agagaatggc cgtgctgggc 1860

gacaccgcat gggatttcgg atctgtggga ggcgccctga acagcctggg caagggcatc 1920

tgatga 1926

<210> 143
<211> 640
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_Zika_prME411 (D3)

<400> 143

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

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

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
35 40 45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
50 55 60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65 70 75 80

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Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

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

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285
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Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290                 295                 300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305                 310                 315                 320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325                 330                 335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340                 345                 350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370                 375                 380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385                 390                 395                 400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405                 410                 415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420                 425                 430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435                 440                 445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450                 455                 460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465                 470                 475                 480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485                 490                 495
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Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500   505   510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515   520   525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530   535   540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545   550   555   560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565   570   575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580   585   590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
        595   600   605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
    610   615   620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625   630   635   640

<210> 144
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_Zika_prME395 (D4)

<400> 144
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ctccaaacac ccaccggtca agcggaggtc actagacgtg ggagtgcata ctatatgtac   120

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cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggactttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

tcccagcaca gtgggatgat cgttaatgac acaggacatg aaactgatga gaatagagcg 1080

aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620

gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

actgaaagca ctgagaactc taagatgatg ctggaacttg atccaccatt tggggactct 1740 tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggctga 1800

<210> 145
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp'_Zika_prME395 (D4)

<400> 145
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ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660

gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

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tccgatacac agtacgtgtg caagcggacc ctggtggaca gaggctgggg caatggctgt 900

ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960

accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

ctgggcctgg actgcgagcc tagaacaggc ctggacttct ccgatctgta ctatctgacc 1200 atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

tatatcgtga tcggcgtggg cgagaagaag atcacacacc actggcaccg cagcggctga 1800

<210> 146
<211> 599
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_Zika_prME395 (D4)

<400> 146

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

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

Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
        35   40   45

Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
    50   55   60

Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65   70   75   80

```
Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95

Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110

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

Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140

Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160

Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
                165                 170                 175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180                 185                 190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195                 200                 205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210                 215                 220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225                 230                 235                 240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245                 250                 255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260                 265                 270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275                 280                 285
```

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290   295   300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305   310   315   320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325   330   335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340   345   350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp
    370   375   380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385   390   395   400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405   410   415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420   425   430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435   440   445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450   455   460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465   470   475   480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485   490   495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500   505   510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515   520   525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530   535   540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545   550   555   560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565   570   575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr
            580   585   590

His His Trp His Arg Ser Gly
        595

<210> 147
<211> 1596
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_ZikaE (D5)

<400> 147
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ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa   120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta   180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg   240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc   300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa   360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg   420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag   480 aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct ggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatccatc aaatttttgg agcagctttc 1440

aaatcattgt ttggaggaat gtcctggttc tcacaaattc tcattggaac gttgctgatg 1500

tggttgggtc tgaacacaaa gaatggatct atttccctta tgtgcttggc cttaggggga 1560

gtgttgatct tcttatccac agccgtctct gcttga 1596

<210> 148
<211> 1596
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE (D5)

<400> 148
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120 ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatccacc agatcttcgg cgccgccttt 1440

aagtccctgt tcggcggcat gagctggttc tcacagatcc tgatcggcac actgctgatg 1500

tggctgggcc tgaacaccaa gaatggctct atcagcctga tgtgcctggc cctgggaggc 1560

gtgctgatct tcctgtccac cgccgtgtct gcctga 1596

<210> 149
<211> 531
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaE (D5)

<400> 149

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1   5   10   15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20   25   30

Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35   40   45

Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp
    50   55   60

Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65   70   75   80

Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85   90   95

Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100   105   110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115   120   125

Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130   135   140

Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145   150   155   160

Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165   170   175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180   185   190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195   200   205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210   215   220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225   230   235   240

His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala
                245   250   255

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260   265   270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275   280   285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290   295   300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305   310   315   320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325   330   335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340   345   350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355   360   365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370   375   380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385 390 395 400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
405 410 415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
420 425 430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
435 440 445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
450 455 460

Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
465 470 475 480

Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly
485 490 495

Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser
500 505 510

Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala
515 520 525

Val Ser Ala
530

<210> 150
<211> 1452
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaE_no_anchor (D6)

<400> 150
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact 60

ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa 120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta 180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg 240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc 300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa 360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct gggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatccatc aaatttttgg agcagctttc 1440

aaatcattgt ga 1452

<210> 151
<211> 1452

<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp'_ZikaE_no_anchor (D6)

<400> 151
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380 gtgggaggcg ccctgaacag cctgggcaag ggcatccacc agatcttcgg cgccgccttt 1440

aagtccctgt ga 1452

<210> 152
<211> 483
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaE_no_anchor (D6)

<400> 152

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
20 25 30

Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
35 40 45

Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp
50 55 60

Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65 70 75 80

Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
85 90 95

Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
100 105 110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
115 120 125

Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
130 135 140

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Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160

Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195                 200                 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210                 215                 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225                 230                 235                 240

His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala
                245                 250                 255

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260                 265                 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275                 280                 285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290                 295                 300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305                 310                 315                 320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325                 330                 335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340                 345                 350
```

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355   360   365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370   375   380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385   390   395   400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405   410   415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420   425   430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435   440   445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450   455   460

Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
465   470   475   480

Lys Ser Leu

<210> 153
<211> 1422
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaE411 (D7)

<400> 153
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact   60

ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa   120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta   180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg   240 gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc 300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa 360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg 420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag 480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt 540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca 600

ccaagagccg aagccaccct gggggggtttt ggaagcctag gacttgattg tgaaccgagg 660

acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggcagcacca ttggaaaagc atttgaagcc 1320

actgtgagag gtgccaagag aatggcagtc ttgggagaca cagcctggga ctttggatca 1380

gttggaggcg ctctcaactc attgggcaag ggcatctgat ga 1422

<210> 154
<211> 1422
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE411 (D7)

<400> 154
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600

ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctccacaa tcggcaaggc ctttgaggca 1320

accgtgcgcg gagcaaagag aatggccgtg ctgggcgaca ccgcatggga tttcggatct 1380

gtgggaggcg ccctgaacag cctgggcaag ggcatctgat ga 1422

<210> 155
<211> 472
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp’_ZikaE411 (D7)

<400> 155

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1               5                   10                  15


Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
            20                  25                  30


Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
        35                  40                  45


Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp
    50                  55                  60


Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65                  70                  75                  80


Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
                85                  90                  95


Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
            100                 105                 110


Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
        115                 120                 125


Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
    130                 135                 140


Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145                 150                 155                 160


Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
                165                 170                 175


Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
            180                 185                 190
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Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
        195   200   205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
    210   215   220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225   230   235   240

His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala
                245   250   255

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
            260   265   270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275   280   285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290   295   300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305   310   315   320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325   330   335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340   345   350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355   360   365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370   375   380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385   390   395   400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405   410   415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser
            420   425   430

Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
        435   440   445

Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Ala
    450   455   460

Leu Asn Ser Leu Gly Lys Gly Ile
465   470

<210> 156
<211> 1296
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp'_ZikaE395 (D8)

<400> 156
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ctccaaacac ccaccggtca aatcaggtgc ataggagtca gcaataggga ctttgtggaa   120

ggtatgtcag gtgggacttg ggttgatgtt gtcttggaac atggaggttg tgtcaccgta   180

atggcacagg acaaaccgac tgtcgacata gagctggtta caacaacagt cagcaacatg   240

gcggaggtaa gatcctactg ctatgaggca tcaatatcag acatggcttc ggacagccgc   300

tgcccaacac aaggtgaagc ctaccttgac aagcaatcag acactcaata tgtctgcaaa   360

agaacgttag tggacagagg ctggggaaat ggatgtggac tttttggcaa agggagcctg   420

gtgacatgcg ctaagtttgc atgctccaag aaaatgaccg ggaagagcat ccagccagag   480

aatctggagt accggataat gctgtcagtt catggctccc agcacagtgg gatgatcgtt   540

aatgacacag gacatgaaac tgatgagaat agagcgaagg ttgagataac gcccaattca   600

ccaagagccg aagccaccct gggggggttt ggaagcctag gacttgattg tgaaccgagg   660 acaggccttg acttttcaga tttgtattac ttgactatga ataacaagca ctggttggtt 720

cacaaggagt ggttccacga cattccatta ccttggcacg ctggggcaga caccggaact 780

ccacactgga acaacaaaga agcactggta gagttcaagg acgcacatgc caaaaggcaa 840

actgtcgtgg ttctagggag tcaagaagga gcagttcaca cggcccttgc tggagctctg 900

gaggctgaga tggatggtgc aaagggaagg ctgtcctctg gccacttgaa atgtcgcctg 960

aaaatggata aacttagatt gaagggcgtg tcatactcct tgtgtaccgc agcgttcaca 1020

ttcaccaaga tcccggctga aacactgcac gggacagtca cagtggaggt acagtacgca 1080

gggacagatg gaccttgcaa ggttccagct cagatggcgg tggacatgca aactctgacc 1140

ccagttggga ggttgataac cgctaacccc gtaatcactg aaagcactga gaactctaag 1200

atgatgctgg aacttgatcc accatttggg gactcttaca ttgtcatagg agtcggggag 1260

aagaagatca cccaccactg gcacaggagt ggctga 1296

<210> 157
<211> 1296
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaE395 (D8)

<400> 157
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ctgcagacac caacaggcca gatccggtgc atcggcgtga gcaatagaga cttcgtggag 120

ggaatgtccg gaggaacctg ggtggatgtg gtgctggagc acggcggctg cgtgacagtg 180

atggcccagg acaagccaac cgtggatatc gagctggtga ccacaaccgt gtccaacatg 240

gccgaggtga ggtcttactg ctatgaggcc agcatctccg acatggcctc tgatagcagg 300

tgtccaaccc agggagaggc atacctggac aagcagtccg atacacagta cgtgtgcaag 360

cggaccctgg tggacagagg ctggggcaat ggctgtggcc tgtttggcaa gggctctctg 420

gtgacatgcg ccaagttcgc ctgtagcaag aagatgaccg gcaagtccat ccagccagag 480

aacctggagt accggatcat gctgtctgtg cacggctccc agcactctgg catgatcgtg 540

aacgacacag gccacgagac agatgagaat cgggccaagg tggagatcac acctaactct 600 ccaagagccg aggccaccct gggaggattt ggctctctgg gcctggactg cgagcctaga 660

acaggcctgg acttctccga tctgtactat ctgaccatga acaataagca ctggctggtg 720

cacaaggagt ggtttcacga catcccactg ccatggcacg caggagcaga tacaggaaca 780

ccacactgga acaataagga ggccctggtg gagttcaagg atgcccacgc caagcggcag 840

acagtggtgg tgctgggcag ccaggaggga gcagtgcaca ccgccctggc aggcgccctg 900

gaggcagaga tggacggagc taagggcaga ctgtctagcg gccacctgaa gtgcaggctg 960

aagatggata agctgcgcct gaagggcgtg tcctactctc tgtgcacagc cgccttcacc 1020

ttcaccaaga tccctgccga gacactgcac ggcacagtga ccgtggaggt gcagtatgcc 1080

ggcacagacg gaccctgtaa ggtgcctgcc cagatggccg tggatatgca gacactgaca 1140

cctgtgggca ggctgatcac cgccaatcca gtgatcacag agtctaccga gaacagcaag 1200

atgatgctgg agctggaccc accatttggc gatagctata tcgtgatcgg cgtgggcgag 1260

aagaagatca cacaccactg gcaccgcagc ggctga 1296

<210> 158
<211> 431
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaE395 (D8)

<400> 158

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile Arg Cys Ile Gly
20 25 30

Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val
35 40 45

Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp
50 55 60

Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
65 70 75 80

Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
85 90 95

Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
100 105 110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
115 120 125

Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
130 135 140

Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
145 150 155 160

Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
165 170 175

Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
180 185 190

Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
195 200 205

Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
210 215 220

Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
225 230 235 240

His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala
245 250 255

Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
260 265 270

Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
        275   280   285

Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
    290   295   300

Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
305   310   315   320

Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr
                325   330   335

Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr
            340   345   350

Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
        355   360   365

Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
    370   375   380

Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
385   390   395   400

Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
                405   410   415

Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
            420   425   430

<210> 159
<211> 2172
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_ZikaprME_MVTMintracyto (D9)

<400> 159
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ttggacagaa acgatgctgg ggaggccata tcttttccaa ccacattggg gatgaataag 180

tgttatatac agatcatgga tcttggacac atgtgtgatg ccaccatgag ctatgaatgc 240

cctatgctgg atgagggggt ggaaccagat gacgtcgatt gttggtgcaa cacgacgtca 300

acttgggttg tgtacggaac ctgccatcac aaaaaaggtg aagcacggag atctagaaga 360

gctgtgacgc tcccctccca ttccactagg aagctgcaaa cgcggtcgca aacctggttg 420

gaatcaagag aatacacaaa gcacttgatt agagtcgaaa attggatatt caggaaccct 480

ggcttcgcgt tagcagcagc tgccatcgct tggcttttgg gaagctcaac gagccaaaaa 540

gtcatatact tggtcatgat actgctgatt gccccggcat acagcatcag gtgcatagga 600

gtcagcaata gggactttgt ggaaggtatg tcaggtggga cttgggttga tgttgtcttg 660

gaacatggag gttgtgtcac cgtaatggca caggacaaac cgactgtcga catagagctg 720

gttacaacaa cagtcagcaa catggcggag gtaagatcct actgctatga ggcatcaata 780

tcagacatgg cttcggacag ccgctgccca acacaaggtg aagcctacct tgacaagcaa 840

tcagacactc aatatgtctg caaaagaacg ttagtggaca gaggctgggg aaatggatgt 900

ggactttttg gcaaagggag cctggtgaca tgcgctaagt ttgcatgctc caagaaaatg 960

accgggaaga gcatccagcc agagaatctg gagtaccgga taatgctgtc agttcatggc 1020

tcccagcaca gtgggatgat cgttaatgac acaggacatg aaactgatga gaatagagcg 1080

aaggttgaga taacgcccaa ttcaccaaga gccgaagcca ccctgggggg ttttggaagc 1140

ctaggacttg attgtgaacc gaggacaggc cttgactttt cagatttgta ttacttgact 1200

atgaataaca agcactggtt ggttcacaag gagtggttcc acgacattcc attaccttgg 1260

cacgctgggg cagacaccgg aactccacac tggaacaaca aagaagcact ggtagagttc 1320

aaggacgcac atgccaaaag gcaaactgtc gtggttctag ggagtcaaga aggagcagtt 1380

cacacggccc ttgctggagc tctggaggct gagatggatg gtgcaaaggg aaggctgtcc 1440

tctggccact tgaaatgtcg cctgaaaatg gataaactta gattgaaggg cgtgtcatac 1500

tccttgtgta ccgcagcgtt cacattcacc aagatcccgg ctgaaacact gcacgggaca 1560

gtcacagtgg aggtacagta cgcagggaca gatggacctt gcaaggttcc agctcagatg 1620 gcggtggaca tgcaaactct gaccccagtt gggaggttga taaccgctaa ccccgtaatc 1680

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tacattgtca taggagtcgg ggagaagaag atcacccacc actggcacag gagtggcagc 1800

accattggaa aagcatttga agccactgtg agaggtgcca agagaatggc agtcttggga 1860

gacacagcct gggactttgg atcagttgga ggcgctctca actcattggg caagggcatc 1920

catcaaattt ttggagcagc tttcaaatca ttgtttggag gaatgtcctg gttctcaatg 1980

aaaggtttat cgagcactag catagtctac atcctgattg cagtgtgtct tggagggttg 2040

atagggatcc ccgctttaat atgttgctgc agggggcgtt gtaacaaaaa gggagaacaa 2100

gttggtatgt caagaccagg cctaaagcct gatcttacgg gaacatcaaa atcctatgta 2160

aggtcgctct ga 2172

<210> 160
<211> 2172
<212> DNA
<213> Artificial sequence

<220>
<223> Codon-optimized nucleotide sequence of MVsp’_ZikaprME_MVTMintracyto (D9)

<400> 160
atgagcatca tgggcctgaa ggtgaacgtg tccgccatct tcatggccgt gctgctgacc 60

ctgcagacac caacaggcca ggcagaggtg accaggagag gaagcgccta ctatatgtac 120

ctggacagga atgatgccgg cgaggccatc tccttcccaa ccacactggg catgaacaag 180

tgctacatcc agatcatgga cctgggccac atgtgcgatg ccaccatgtc ctatgagtgt 240

ccaatgctgg acgagggcgt ggagcccgac gatgtggatt gctggtgtaa taccacatct 300

acatgggtgg tgtacggcac ctgtcaccac aagaagggag aggcccggcg gagccggcgg 360

gccgtgacac tgccttccca ctctaccagg aagctgcaga cacgcagcca gacctggctg 420

gagtccagag agtataccaa gcacctgatc agggtggaga actggatctt tcgcaatcca 480

ggattcgcac tggcagcagc agcaatcgca tggctgctgg gaagctccac cagccagaaa 540

gtgatctacc tggtcatgat cctgctgatc gctcctgcct attctatccg gtgcatcggc 600

gtgagcaata gagacttcgt ggagggaatg tccggaggaa cctgggtgga tgtggtgctg 660 gagcacggcg gctgcgtgac agtgatggcc caggacaagc caaccgtgga tatcgagctg 720

gtgaccacaa ccgtgtccaa catggccgag gtgaggtctt actgctatga ggccagcatc 780

tccgacatgg cctctgatag caggtgtcca acccagggag aggcatacct ggacaagcag 840

tccgatacac agtacgtgtg caagcggacc ctggtggaca gaggctgggg caatggctgt 900

ggcctgtttg gcaagggctc tctggtgaca tgcgccaagt tcgcctgtag caagaagatg 960

accggcaagt ccatccagcc agagaacctg gagtaccgga tcatgctgtc tgtgcacggc 1020

tcccagcact ctggcatgat cgtgaacgac acaggccacg agacagatga gaatcgggcc 1080

aaggtggaga tcacacctaa ctctccaaga gccgaggcca ccctgggagg atttggctct 1140

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atgaacaata agcactggct ggtgcacaag gagtggtttc acgacatccc actgccatgg 1260

cacgcaggag cagatacagg aacaccacac tggaacaata aggaggccct ggtggagttc 1320

aaggatgccc acgccaagcg gcagacagtg gtggtgctgg gcagccagga gggagcagtg 1380

cacaccgccc tggcaggcgc cctggaggca gagatggacg gagctaaggg cagactgtct 1440

agcggccacc tgaagtgcag gctgaagatg gataagctgc gcctgaaggg cgtgtcctac 1500

tctctgtgca cagccgcctt caccttcacc aagatccctg ccgagacact gcacggcaca 1560

gtgaccgtgg aggtgcagta tgccggcaca gacggaccct gtaaggtgcc tgcccagatg 1620

gccgtggata tgcagacact gacacctgtg ggcaggctga tcaccgccaa tccagtgatc 1680

acagagtcta ccgagaacag caagatgatg ctggagctgg acccaccatt tggcgatagc 1740

tatatcgtga tcggcgtggg cgagaagaag atcacacacc actggcaccg cagcggctcc 1800

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caccagatct tcggcgccgc ctttaagtcc ctgttcggcg gcatgagctg gttctcaatg 1980

aagggcctgt cctctacctc tatcgtgtac atcctgatcg ccgtgtgcct gggaggcctg 2040

atcggaatcc cagccctgat ctgctgttgc agaggccgct gcaacaagaa gggagagcaa 2100

gtgggaatgt ctcggccagg cctgaagcca gacctgacag gcacctccaa gtcttatgtg 2160

agaagcctgt ga 2172

<210> 161
<211> 723
<212> PRT
<213> Artificial sequence

<220>
<223> MVsp'_ZikaprME_MVTMintracyto (D9)

<400> 161

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1               5                   10                  15


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


Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu
        35                  40                  45


Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln
    50                  55                  60


Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys
65                  70                  75                  80


Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys
                85                  90                  95


Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys
            100                 105                 110


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


Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu
    130                 135                 140


Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro
145                 150                 155                 160


Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser
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                165   170   175

Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro
            180   185   190

Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu
        195   200   205

Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly
    210   215   220

Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu
225   230   235   240

Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr
                245   250   255

Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln
            260   265   270

Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys
        275   280   285

Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly
    290   295   300

Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met
305   310   315   320

Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu
                325   330   335

Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly
            340   345   350

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

Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp

    370   375   380

Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr
385   390   395   400

Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile
                405   410   415

Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn
            420   425   430

Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln
        435   440   445

Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu
    450   455   460

Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser
465   470   475   480

Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys
                485   490   495

Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile
            500   505   510

Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala
        515   520   525

Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met
    530   535   540

Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile
545   550   555   560

Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro
                565   570   575

Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr

580 585 590

His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala
595 600 605

Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp
610 615 620

Asp Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
625 630 635 640

His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser
645 650 655

Trp Phe Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu
660 665 670

Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys
675 680 685

Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser
690 695 700

Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val
705 710 715 720

Arg Ser Leu

<210> 162
<211> 1668
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of MVsp’_Zika_MVTMintracytoE (D10)

<400> 162
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Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp
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Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met
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Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala
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Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln
100 105 110

Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp
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Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala
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Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu
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Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser
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Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala
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Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly
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Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp
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Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val
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His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala
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Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe
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Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln
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Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met
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Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu
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Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val
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Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg
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Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys
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Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile
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Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met
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Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe
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Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Met Lys Gly Leu Ser
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Ser Thr Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu
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Ile Gly Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys
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cacccaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga gcaaaaacag 19740

gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg gaaatgttga atactcatac 19800

tcttcctttt tcaatattat tgaagcattt atcagggtta ttgtctcatg agcggataca 19860

tatttgaatg tatttagaaa aataaacaaa taggggttcc gcgcacattt ccccgaaaag 19920

tgccacctga aattgtaaac gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa 19980

tcagctcatt ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat 20040

agaccgagat agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg 20100

tggactccaa cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac 20160

catcacccta atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta 20220

aagggagccc ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag 20280

ggaagaaagc gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg 20340

taaccaccac acccgccgcg cttaatgcgc cgctacaggg cgcgtcccat tcgccattca 20400

ggctgcgcaa ctgttgggaa gggcgatcgg tgcgggcctc ttcgctatta cgccagccac 20460

cgcggtg 20467

<210> 168
<211> 1764
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of insert 4

<400> 168
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ccaaccacat tggggatgaa taagtgttat atacagatca tggatcttgg acacatgtgt 180

gatgccacca tgagctatga atgccctatg ctggatgagg gggtggaacc agatgacgtc 240

gattgttggt gcaacacgac gtcaacttgg gttgtgtacg gaacctgcca tcacaaaaaa 300

ggtgaagcac ggagatctag aagagctgtg acgctcccct cccattccac taggaagctg 360

caaacgcggt cgcaaacctg gttggaatca agagaataca caaagcactt gattagagtc 420

gaaaattgga tattcaggaa ccctggcttc gcgttagcag cagctgccat cgcttggctt 480

ttgggaagct caacgagcca aaaagtcata tacttggtca tgatactgct gattgccccg 540

gcatacagca tcaggtgcat aggagtcagc aatagggact ttgtggaagg tatgtcaggt 600

gggacttggg ttgatgttgt cttggaacat ggaggttgtg tcaccgtaat ggcacaggac 660

aaaccgactg tcgacataga gctggttaca acaacagtca gcaacatggc ggaggtaaga 720

tcctactgct atgaggcatc aatatcggac atggcttcgg acagccgctg cccaacacaa 780

ggtgaagcct accttgacaa gcaatcagac actcaatatg tctgcaaaag aacgttagtg 840

gacagaggct ggggaaatgg atgtggactt tttggcaaag ggagcctggt gacatgcgct 900

aagtttgcat gctccaagaa aatgaccggg aagagcatcc agccagagaa tctggagtac 960

cggataatgc tgtcagttca tggctcccag cacagtggga tgatcgttaa tgacacagga 1020

catgaaactg atgagaatag agcgaaggtt gagataacgc ccaattcacc aagagccgaa 1080

gccaccctgg ggggttttgg aagcctagga cttgattgtg aaccgaggac aggccttgac 1140

ttttcagatt tgtattactt gactatgaat aacaagcact ggttggttca caaggagtgg 1200

ttccacgaca ttccattacc ttggcacgct ggggcagaca ccggaactcc acactggaac 1260

aacaaagaag cactggtaga gttcaaggac gcacatgcca aaaggcaaac tgtcgtggtt 1320

ctagggagtc aagaaggagc agttcacacg gcccttgctg gagctctgga ggctgagatg 1380

gatggtgcaa agggaaggct gtcctctggc cacttgaaat gtcgcctgaa aatggataaa 1440

cttagattga agggcgtgtc atactccttg tgtaccgcag cgttcacatt caccaagatc 1500

ccggctgaaa cactgcacgg gacagtcaca gtggaggtac agtacgcagg gacagatgga 1560

ccttgcaagg ttccagctca gatggcggtg gacatgcaaa ctctgacccc agttgggagg 1620 ttgataaccg ctaaccccgt aatcactgaa agcactgaga actctaagat gatgctggaa 1680

cttgatccac catttgggga ctcttacatt gtcataggag tcggggagaa gaagatcacc 1740

caccactggc acaggagtgg ctaa 1764

<210> 169
<211> 587
<212> PRT
<213> Artificial sequence

<220>
<223> Insert 4

<400> 169

Met Gly Val Gly Ile Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala
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Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn
            20   25   30

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

Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met
    50   55   60

Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val
65   70   75   80

Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys
                85   90   95

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

Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu
        115   120   125

Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile
    130   135   140

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Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu
145                 150                 155                 160

Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu
                165                 170                 175

Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg
            180                 185                 190

Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu
        195                 200                 205

Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val
    210                 215                 220

Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg
225                 230                 235                 240

Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg
                245                 250                 255

Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln
            260                 265                 270

Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys
        275                 280                 285

Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys
    290                 295                 300

Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr
305                 310                 315                 320

Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val
                325                 330                 335

Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile
            340                 345                 350
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Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser
        355                 360                 365

Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu
    370                 375                 380

Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp
385                 390                 395                 400

Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr
                405                 410                 415

Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His
            420                 425                 430

Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val
        435                 440                 445

His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys
    450                 455                 460

Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys
465                 470                 475                 480

Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr
                485                 490                 495

Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu
            500                 505                 510

Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met
        515                 520                 525

Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala
    530                 535                 540

Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu
545                 550                 555                 560
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Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu
                565   570   575

Lys Lys Ile Thr His His Trp His Arg Ser Gly
            580   585

<210> 170
<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Native nucleotide sequence of insert 5

<400> 170
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gtcttggaac atggaggttg tgtcaccgta atggcacagg acaaaccgac tgtcgacata   180

gagctggtta caacaacagt cagcaacatg gcggaggtaa gatcctactg ctatgaggca   240

tcaatatcgg acatggcttc ggacagccgc tgcccaacac aaggtgaagc ctaccttgac   300

aagcaatcag acactcaata tgtctgcaaa agaacgttag tggacagagg ctggggaaat   360

ggatgtggac tttttggcaa agggagcctg gtgacatgcg ctaagtttgc atgctccaag   420

aaaatgaccg ggaagagcat ccagccagag aatctggagt accggataat gctgtcagtt   480

catggctccc agcacagtgg gatgatcgtt aatgacacag gacatgaaac tgatgagaat   540

agagcgaagg ttgagataac gcccaattca ccaagagccg aagccaccct gggggggttt   600

ggaagcctag gacttgattg tgaaccgagg acaggccttg acttttcaga tttgtattac   660

ttgactatga ataacaagca ctggttggtt cacaaggagt ggttccacga cattccatta   720

ccttggcacg ctggggcaga caccggaact ccacactgga acaacaaaga agcactggta   780

gagttcaagg acgcacatgc caaaaggcaa actgtcgtgg ttctagggag tcaagaagga   840

gcagttcaca cggcccttgc tggagctctg gaggctgaga tggatggtgc aaagggaagg   900

ctgtcctctg gccacttgaa atgtcgcctg aaaatggata aacttagatt gaagggcgtg   960

tcatactcct tgtgtaccgc agcgttcaca ttcaccaaga tcccggctga aacactgcac   1020 gggacagtca cagtggaggt acagtacgca gggacagatg gaccttgcaa ggttccagct 1080

cagatggcgg tggacatgca aactctgacc ccagttggga ggttgataac cgctaacccc 1140

gtaatcactg aaagcactga gaactctaag atgatgctgg aacttgatcc accatttggg 1200

gactcttaca ttgtcatagg agtcggggag aagaagatca cccaccactg gcacaggagt 1260

ggcagcacca ttggaaaagc atttgaagcc actgtgagag gtgccaagag aatggcagtc 1320

ttgggagaca cagcctggga ctttggatca gttggaggcg ctctcaactc attgggcaag 1380

ggcatctaat aa 1392

<210> 171
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> Insert 5

<400> 171

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Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met
            20                  25                  30

Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val
        35                  40                  45

Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr
    50                  55                  60

Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala
65                  70                  75                  80

Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu
                85                  90                  95

Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr
            100                 105                 110
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Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
        115                 120                 125

Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly
    130                 135                 140

Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val
145                 150                 155                 160

His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu
                165                 170                 175

Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg
            180                 185                 190

Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu
        195                 200                 205

Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn
    210                 215                 220

Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu
225                 230                 235                 240

Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys
                245                 250                 255

Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val
            260                 265                 270

Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly
        275                 280                 285

Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly
    290                 295                 300

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val
305                 310                 315                 320
```

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Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala
                325                 330                 335

Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr
            340                 345                 350

Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr
        355                 360                 365

Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu
    370                 375                 380

Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly
385                 390                 395                 400

Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His
                405                 410                 415

Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val
            420                 425                 430

Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe
        435                 440                 445

Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile
    450                 455                 460
```