

**MHC CLASS I ASSOCIATED PEPTIDES FOR PREVENTION AND
TREATMENT OF ZIKA VIRUS**

Field of the invention

5 The invention relates to vaccine compositions comprising flavivirus peptides, and the use of such compositions for the treatment and prevention of flavivirus infection.

Background to the invention

10 Flaviviruses are a family of positive sense, single stranded, enveloped RNA viruses that may infect humans and pose a significant threat to public health. In particular, flaviviruses are the causative agent of Zika fever, Dengue fever, yellow fever and West Nile fever. These diseases are commonly characterised by symptoms that include fever, vomiting, headache, joint pain and muscle pain, though each disease may also be associated with more serious symptoms. For instance, mother-to-child transmission of
15 Zika virus during pregnancy can cause brain malformations, and Zika virus infection has also been linked to Guillain-Barré syndrome. Dengue fever may progress into life-threatening Dengue haemorrhagic syndrome or Dengue shock syndrome. Yellow fever may induce liver damage, which may result in bleeding and kidney problems. West Nile fever may spread to the nervous system, causing encephalitis or meningitis.

20 Flaviviruses are arboviruses, meaning that they are transmitted by infected arthropod vectors such as mosquitos and ticks. The geographical distribution of flaviviruses is primarily determined by that of their arthropod vector. For the most part, the vectors are confined to tropical and sub-tropical regions, such as Southeast Asia and South America. However, climate change appears to be broadening the distribution of
25 some vectors, thereby increasing the population at risk of contracting flavivirus infections. Furthermore, the mosquito responsible for spreading Zika virus and yellow fever virus has been shown to be able to adapt to survive in high-density urban areas. It is therefore important to find effective methods for containing flavivirus infection.

 While some flaviviruses (such as West Nile virus) only incidentally infect humans,
30 other flaviviruses (such as yellow fever virus, Dengue virus and Zika virus) exist predominantly in an arthropod-human life cycle. Such flaviviruses grow well in the human host, and high viral titres allow infection to cycle back to arthropod vectors and onto new human hosts. In either case, vector-born transmission and the ability to infect

other species such as monkeys and birds means that flavivirus infection tend to spread quickly and easily. Controlling the spread of flavivirus infections is therefore challenging.

The structure of the flavivirus genome also contributes to the challenge of controlling spread. Few proof-reading and correction mechanisms exist for the replication of single-stranded RNA. Therefore, mutations arising in the course of replication frequently remain in the genome and are passed to the next generation. Flaviviruses therefore evolve quickly.

While a safe and effective vaccine exists for yellow fever infection, this is not the case for Zika virus, Dengue virus or West Nile virus infection. A vaccine for Dengue virus exists, but is recommended only for use in individuals who have previously had a Dengue virus infection, as outcomes may be worsened in those who have not previously been infected. Being exposed to one serotype of Dengue virus (such as DENV-1, DENV-2, DENV-3 or DENV-4) potentially worsens subsequent infections with another Dengue serotype, and so Dengue vaccine currently in trial include included Dengue serotypes in their formulations. As Zika virus is closely related to Dengue virus, any Zika virus vaccine also needs to minimize the possibility of antibody-dependent enhancement of Dengue virus infection. There is therefore a need for effective vaccines against Zika virus, Dengue virus and West Nile virus infection.

Summary of the invention

The present invention relates to a flavivirus vaccine composition that stimulates an immune response while avoiding the adverse clinical effects often associated with vaccines containing viruses. The vaccine composition may provide protection against multiple species of flavivirus (e.g. Zika virus, Dengue virus and/or West Nile virus) and/or multiple lineages or serotypes of a particular species (e.g. African Zika virus, Asian Zika virus, DENV-1, DENV-2, DENV-3 and/or DENV-4).

The present inventors have surprisingly identified that a nanoparticle, for example a gold nanoparticle, may be used to induce an efficient response to a vaccine composition designed to stimulate a T cell response against a flavivirus. Use of a nanoparticle abrogates the need to use a virus in the vaccine composition. The use of a traditional adjuvant, which may be associated with adverse reactions in the clinic, is also avoided. Therefore, the likelihood of an individual experiencing an adverse reaction following administration of the vaccine composition is reduced.

The present inventors have also identified number of peptides that are conserved between different flaviviruses and are presented by MHC molecules on cells infected with those viruses. Inclusion of such conserved peptides in the vaccine composition may confer protective capability against multiple species of flavivirus and/or multiple lineages or serotypes of a particular species. Including multiple conserved peptides that bind to different HLA supertypes in the vaccine composition results in a vaccine that is effective in individuals having different HLA types.

Accordingly, the present invention provides a vaccine composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. In some aspects, the flavivirus peptide may be attached to a nanoparticle.

The present invention further provides:

- a vaccine composition comprising (a) a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, or (b) the full complement of a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof
- a method of preventing or treating a flavivirus infection, comprising administering the vaccine composition of the invention to an individual infected with, or at risk of being infected with, a flavivirus;
- a vaccine composition of the invention for use in a method of preventing or treating a flavivirus infection in an individual;
- a method of preventing or treating a flavivirus infection in a subject, comprising (i) stimulating cytotoxic T lymphocytes (CTLs) obtained from a Zika virus- or Dengue virus- infected individual with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and (ii) providing the stimulated CTLs as passive immunotherapy to the subject;
- a composition for use in a method of preventing or treating a flavivirus infection in a subject, the composition comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and the method comprising (i) stimulating CTLs obtained from a Zika virus- or Dengue virus- infected individual with the composition and (ii) providing the stimulated CTLs as passive immunotherapy to the subject; and

- method of diagnosing a flavivirus infection in a subject, the method comprising (i) contacting CTLs obtained from the subject with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and (ii) detecting the presence or absence of a CTL response to the one or more CD8+ T cell epitopes.

Brief Description of the Figures

Figure 1: Epitope sequence confirmation of SEQ ID NO: 11.

Detailed Description of the Invention

Vaccine compositions

The present invention provides a vaccine composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11, or a variant thereof. This vaccine composition has a number of benefits which will become apparent from the discussion below. The key benefits are though summarised here.

Firstly, the vaccine composition of the invention advantageously comprises a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 and newly identified by the inventors, or a variant thereof. The vaccine composition is therefore capable of stimulating a cellular immune response (e.g. a CD8+ T cell response) against a flavivirus. CD8+ cytotoxic T lymphocytes (CTLs) mediate viral clearance via their cytotoxic activity against infected cells. Stimulating cellular immunity may therefore provide a beneficial defence against flavivirus infection.

Secondly, a number of the CD8+ T cell epitopes identified by the present inventors may be conserved between many different flaviviruses, and may be presented by MHC molecules on cells infected with those viruses. For instance, the present inventors have identified that certain CD8+ T cell epitopes expressed in cells infected with Zika virus may also expressed by other flaviviruses, such as Dengue virus and/or West Nile virus (see Tables 1 and 4). Inclusion of such conserved peptides in the vaccine composition may confer protective capability against multiple species of flavivirus and/or multiple lineages or serotypes of a particular species, i.e. confer cross-protection. 100% homology between flaviviruses is not required for cross-protection to be conferred. Rather, cross-protection

may arise following immunisation with a sequence that is, for example, about 50% or more (such as 60%, 70%, 75%, 80%, 90%, 95%, 98% or 99%) homologous to a CD8+ T cell epitope expressed in a cell infected with Zika virus, if certain residues are retained in the correct position. A vaccine composition comprising one or more CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 (or a variant thereof) may therefore be capable of providing cross-protection against a wide variety of existing flaviviruses over and above those recited in Table 1 and 4. Inclusion of one or more conserved peptides in the vaccine composition may also confer protective capability against emerging flavivirus strains associated with rapid evolution of the flavivirus genome. In this way, a single flavivirus vaccine composition can be used to confer protection against a variety of different flaviviruses. This provides a cost-effective means of controlling the spread of flavivirus infection.

Thirdly, different CD8+ T cell epitopes identified by the present inventors are capable of binding to different HLA supertypes. Inclusion of multiple peptides each comprising a CD8+ T cell epitope capable of binding to a different HLA supertype results in a vaccine composition that is effective in individuals having different HLA types. In this way, a single flavivirus vaccine composition can be used to confer protection in a large proportion of the human population. This again provides a cost-effective means of controlling the spread of flavivirus infection.

Fourthly, the flavivirus peptide comprised in the vaccine composition of the invention may be attached to a nanoparticle, for example a gold nanoparticle. As described in more detail below, attachment to a nanoparticle reduces or eliminates the need to include an adjuvant in the vaccine composition. Thus, the vaccine composition of the invention is less likely to cause adverse clinical effects upon administration to an individual.

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Peptides

The vaccine composition of the invention comprises a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11. The vaccine composition may comprise from about one to about 50 such peptides, such as about 2 to 40, 3 to 30, 4 to 25, 5 to 20, 6 to 15, 7, 8, 9 or 10 such peptides. SEQ ID NOs: 1 to 11 are set out in Table 1.

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Seq ID	Peptide sequence	HLA motif	Protein ID	Virus
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				Specificity
Seq ID 1	IHAVVSSAIL	A2	NS4B	ZIKV
Seq ID 2	PMAAVGLLIVS	A2/A24	NS2B	ZIKV
Seq ID 3	IMLLGLLGTV	A2	NS4	ZIKV
Seq ID 4	ALGLTAVRLVDPI	A2/A24	E protein, transmembrane	ZIKV
Seq ID 5	DESRKVEVTPNSPR	B44	Envelope glycoprotein	ZIKV
Seq ID 6	DPAVIGTAVK	B7	NS1	ZIKV
Seq ID 7	WPPSEVLTAVG	B7	NS2	ZIKV
Seq ID 8	VILAGPMPVT	A2	Serine protease NS3	ZIKV, Dengue
Seq ID 9	AILEENG VQ	A2	NS4B	ZIKV, Dengue
Seq ID 10	SPRRLAAAV	B7	NS1	ZIKV, Dengue
Seq ID 11	WVTDHSGKTV	A2	HELICc	ZIKV, Dengue, West Nile

Table 1

- The flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 may comprise only one of the CD8+ T cell epitopes set out in
- 5 SEQ ID NOs: 1 to 11. Alternatively, the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 may comprise two or more, such as three or more, four or more, five or more, six or more, seven or more, eight or more, or nine or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11, in any

combination. The flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 may comprise all of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11.

Likewise, if the flavivirus peptide comprises one or more variants of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11, the flavivirus peptide may comprise a variant of only one of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11. Alternatively, the flavivirus peptide may comprise a variant of two or more, such as three or more, four or more, five or more, six or more, seven or more, eight or more, or nine or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11, in any combination. The flavivirus peptide may comprise a variant of each of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11.

As well as one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, the flavivirus peptide may comprise one or more other CD8+ T cell epitopes, one or more CD4+ T cell epitopes and/or one or more B cell epitopes. For example, the flavivirus peptide may comprise two or more, such as three or more, four or more, five or more, ten or more, fifteen or more, or twenty or more CD8+ T cell epitopes other than those set out in SEQ ID NOs: 1 to 11. The flavivirus peptide may comprise two or more, such as three or more, four or more, five or more, ten or more, fifteen or more, or twenty or more CD4+ T cell epitopes. The flavivirus peptide may comprise two or more, such as three or more, four or more, five or more, ten or more, fifteen or more, or twenty or more B cell epitopes.

The vaccine composition may comprise two or more flavivirus peptides each comprising a CD8+ T cell epitope comprising a different sequence selected from SEQ ID NOs: 1 to 11, or a variant thereof. Each of the flavivirus peptides may have any of the properties set out in the preceding paragraphs. For instance, each flavivirus peptide may comprise multiple CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof and, optionally, one or more other CD8+ T cell epitopes, one or more CD4+ T cell epitopes and/or one or more B cell epitopes. In one aspect, the vaccine composition may comprise three or more, four or more, five or more, six or more, seven or more, eight or more, or nine or more flavivirus peptides each comprising a CD8+ T cell epitope comprising a different sequence selected from SEQ ID NOs: 1 to 11 or a variant thereof. The vaccine composition may, for example, comprise 11 flavivirus peptides each

comprising a CD8+ T cell epitope comprising a different sequence selected from SEQ ID NOs: 1 to 11 or a variant thereof.

The vaccine composition may further comprise one or more (such as about 1 to 50, 2 to 40, 3 to 30, 4 to 25, 5 to 20, 6 to 15, 7, 8, 10 or 10) additional peptides each
 5 comprising one or more epitopes. The epitope may be a CD8+ T cell epitope, a CD4+ T cell epitope and/or a B cell epitope. The CD8+ T cell epitope is preferably a CD8+ T cell epitope other than the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11. The CD8+ T cell epitope may, for example, be a flavivirus CD8+ epitope, i.e. a peptide that is expressed by one or more flaviviruses and that is capable of (i) presentation by a class I MHC
 10 molecule and (ii) recognition by a T cell receptor (TCR) present on a CD8+ T cell. Alternatively, the CD8+ T cell epitope may be an CD8+ T cell epitope that is not expressed by one or more flaviviruses. The CD4+ T cell epitope may, for example, be a flavivirus CD4+ epitope, i.e. a peptide that is expressed by one or more flaviviruses and that is capable of (i) presentation by a class II MHC molecule and (ii) recognition by
 15 a T cell receptor (TCR) present on a CD4+ T cell. Alternatively, the CD4+ T cell epitope may be a CD4+ T cell epitope that is not expressed by one or more flaviviruses. CD8+ and CD4+ T cell epitopes are described in more detail below.

A flavivirus peptide is a peptide that is expressed by one or more flaviviruses. Numerous species of flavivirus exist, including Zika virus, Dengue virus, West Nile virus
 20 and yellow fever virus, as well as St. Louis encephalitis virus, Japanese encephalitis virus, Murray Valley encephalitis virus, Tick-borne encephalitis virus, Kunjin encephalitis virus, Rocio encephalitis virus, Russian Spring Summer encephalitis virus, Negeishi virus, Kyasanur Forest virus, Omsk Hemorrhagic Fever virus, Powassan virus, Louping Ill virus, Rio Bravo virus, Tyuleny virus, Ntaya virus and Modoc virus. There are four serotypes
 25 of Dengue virus (DENV-1, DENV-2, DENV-3 and DENV-4) and two strains of Zika virus (African Zika virus and Asian Zika virus).

Any flavivirus peptide comprised in the vaccine composition of the invention may comprise a peptide that is expressed by one or more of Zika virus, Dengue virus, West Nile virus, yellow fever virus, St. Louis encephalitis virus, Japanese encephalitis virus, Murray
 30 Valley encephalitis virus, Tick-borne encephalitis virus, Kunjin encephalitis virus, Rocio encephalitis virus, Russian Spring Summer encephalitis virus, Negeishi virus, Kyasanur Forest virus, Omsk Hemorrhagic Fever virus, Powassan virus, Louping Ill virus, Rio Bravo virus, Tyuleny virus, Ntaya virus and Modoc virus. For example, a flavivirus peptide

comprised in the vaccine composition of the invention may comprise a peptide that is expressed by Zika virus and Dengue virus, or Zika virus, Dengue virus and West Nile virus. For instance, the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof may be expressed by (i) one or
5 more of Zika virus, Dengue virus, West Nile virus, yellow fever virus, St. Louis encephalitis virus, Japanese encephalitis virus, Murray Valley encephalitis virus, Tick-borne encephalitis virus, Kunjin encephalitis virus, Rocio encephalitis virus, Russian Spring Summer encephalitis virus, Negeishi virus, Kyasanur Forest virus, Omsk Hemorrhagic Fever virus, Powassan virus, Louping Ill virus, Rio Bravo virus, Tyuleni
10 virus, Ntaya virus and Modoc virus; (ii) Zika virus and Dengue virus; or (iii) Zika virus, Dengue virus and West Nile virus. Likewise, when the composition comprises an additional peptide that is a flavivirus peptide, that additional flavivirus peptide may be expressed by (i) one or more of Zika virus, Dengue virus, West Nile virus, yellow fever virus, St. Louis encephalitis virus, Japanese encephalitis virus, Murray Valley encephalitis
15 virus, Tick-borne encephalitis virus, Kunjin encephalitis virus, Rocio encephalitis virus, Russian Spring Summer encephalitis virus, Negeishi virus, Kyasanur Forest, Omsk Hemorrhagic Fever virus, Powassan virus, Louping Ill virus, Rio Bravo virus, Tyuleni virus, Ntaya virus and Modoc virus; (ii) Zika virus and Dengue virus; or (iii) Zika virus, Dengue virus and West Nile virus. Accordingly, the vaccine composition may comprise
20 flavivirus peptides from one or more species of flavivirus, such as 1 to 20, 2 to 19, 3 to 18, 4 to 17, 5 to 16, 6 to 15, 7 to 14, 8 to 13, 9 to 12, 10 or 11 species of flavivirus.

When a flavivirus peptide comprised in the vaccine composition of the invention comprises a peptide that is expressed by Zika virus, the peptide may be expressed by African Zika virus, Asian Zika virus, or both African Zika virus and Asian Zika virus.
25 When a flavivirus peptide comprised in the vaccine composition of the invention comprises a peptide that is expressed by Dengue virus, the peptide may be expressed by one or more of DENV-1, DENV-2, DENV-3 and DENV-4 in any combination such as, for example: 1; 2; 3; 4; 1 and 2; 1 and 3; 1 and 4; 2 and 3; 2 and 4; 3 and 4; 1, 2 and 3; 1, 2 and 4; 1, 3 and 4; 2, 3 and 4; or 1, 2, 3 and 4.

30 The flavivirus peptide may be a peptide that is expressed on the surface of one or more flaviviruses, or intracellularly within one or more flaviviruses. The peptide may be a structural peptide or a functional peptide, such as a peptide involved in the metabolism or replication of the flavivirus. Preferably, the peptide is an internal peptide. Preferably, the

peptide is conserved between two or more different flaviviruses or flavivirus serotypes. A peptide is conserved between two or more different flaviviruses or flavivirus serotypes if each of the two or more different flaviviruses or flavivirus serotypes encodes a sequence that is 50% or more (such as 60%, 70%, 75%, 80%, 90%, 95%, 98% or 99%) homologous
5 to the peptide.

The flavivirus peptide may contain any number of amino acids, i.e. be of any length. Typically, the flavivirus peptide is about 8 to about 30, 35 or 40 amino acids in length, such as about 9 to about 29, about 10 to about 28, about 11 to about 27, about 12 to about 26, about 13 to about 25, about 13 to about 24, about 14 to about 23, about 15 to
10 about 22, about 16 to about 21, about 17 to about 20, or about 18 to about 29 amino acids in length.

The flavivirus peptide may be chemically derived from a polypeptide flavivirus antigen, for example by proteolytic cleavage. More typically, the flavivirus peptide may be synthesised using methods well known in the art.

15 The term "peptide" includes not only molecules in which amino acid residues are joined by peptide (-CO-NH-) linkages but also molecules in which the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere et al (1997) J. Immunol.159, 3230-3237. This approach involves making pseudopeptides containing changes involving the
20 backbone, and not the orientation of side chains. Meziere et al (1997) show that, at least for MHC class II and T helper cell responses, these pseudopeptides are useful. Retro-inverse peptides, which contain NH-CO bonds instead of CO-NH peptide bonds, are much more resistant to proteolysis.

Similarly, the peptide bond may be dispensed with altogether provided that an
25 appropriate linker moiety which retains the spacing between the carbon atoms of the amino acid residues is used; it is particularly preferred if the linker moiety has substantially the same charge distribution and substantially the same planarity as a peptide bond. It will also be appreciated that the peptide may conveniently be blocked at its N-or C-terminus so as to help reduce susceptibility to exoproteolytic digestion. For example, the N-terminal
30 amino group of the peptides may be protected by reacting with a carboxylic acid and the C-terminal carboxyl group of the peptide may be protected by reacting with an amine. Other examples of modifications include glycosylation and phosphorylation. Another potential

modification is that hydrogens on the side chain amines of R or K may be replaced with methylene groups (-NH₂ may be modified to -NH(Me) or -N(Me)₂).

The term “peptide” also includes peptide variants that increase or decrease the half-life of the peptide in vivo. Examples of analogues capable of increasing the half-life of peptides used according to the invention include peptoid analogues of the peptides, D-amino acid derivatives of the peptides, and peptide-peptoid hybrids. A further embodiment of the variant polypeptides used according to the invention comprises D-amino acid forms of the polypeptide. The preparation of polypeptides using D-amino acids rather than L-amino acids greatly decreases any unwanted breakdown of such an agent by normal metabolic processes, decreasing the amounts of agent which needs to be administered, along with the frequency of its administration.

CD8+ T cell epitopes

The vaccine composition of the invention comprises a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 (see Table 1) or a variant thereof. The flavivirus peptide may further comprise one or more (such as two or more, three or more, four or more, five or more, ten or more, fifteen or more, or twenty or more) other CD8+ T cell epitopes. The vaccine composition may further comprise one or more (such as 1 to 50, 2 to 40, 3 to 30, 4 to 25, 5 to 20, 6 to 15, 7, 8, 9 or 10) additional peptides each comprising one or more CD8+ T cell epitopes. Preferably, the additional peptide is a flavivirus peptide.

A CD8+ T cell epitope is a peptide that is capable of (i) presentation by a class I MHC molecule and (ii) recognition by a T cell receptor (TCR) present on a CD8+ T cell. Preferably, recognition by the TCR results in activation of the CD8+ T cell. CD8+ T cell activation may lead to increased proliferation, cytokine production and/or cytotoxic effects.

Typically, the CD8+ T cell epitope is around 9 amino acids in length. The CD8+ T cell epitope may though be shorter or longer. For example, the CD8+ T cell epitope may be about 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in length. The CD8+ T cell epitope may be about 8 to 15, 9 to 14 or 10 to 12 amino acids in length.

Flavivirus peptides comprising a CD8+ T cell epitope are known in the art. Methods for identifying CD8+ T cell epitopes are known in the art. Epitope mapping methods include X-ray co-crystallography, array-based oligo-peptide scanning (sometimes called overlapping peptide scan or pepscan analysis), site-directed mutagenesis, high

throughput mutagenesis mapping, hydrogen–deuterium exchange, crosslinking coupled mass spectrometry, phage display and limited proteolysis. MHC motif prediction methodologies may also be used.

CD8+ T cell epitopes presented by flavivirus-infected cells can be identified in order to directly identify CD8+ T cell epitopes for inclusion in the vaccine composition. This is an efficient and logical method which can be used alone or to confirm the utility of potential CD8+ T cell epitopes identified by MHC motif prediction methodologies. This method was used by the inventors to identify the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 (see Example 1).

To perform the method, cells are infected with a flavivirus and maintained in culture for a period of around 72 hours at a temperature of around 37°C. Following culture, the cells are then harvested and washed. Next, the cells are lysed, for instance by homogenisation and freezing/thawing in buffer containing 1% NP40. Lysates are cleared by centrifugation at 2000rpm for 30 minutes to remove cell debris.

MHC/peptide complexes are then isolated from the lysates by immunoaffinity chromatography using protein A/G beads (UltraLink Immobilized Protein A/G, pierce, Rockford, IL) coated with W6/32 (a monoclonal antibody recognising pan MHC class I molecule). To coat the beads with the antibody, the beads are washed with low pH buffer followed by PBS rinses, incubated with 0.5mg of the antibody at room temperature for 2 hours, and washed three times to remove unbound antibody. For immunoaffinity chromatography, the coated beads are incubate with lysate for 2 hours at room temperature with continuous rocking. The beads are then separated from the lysate by centrifuging at 1000 rpm for 5 minutes. Bound MHC complexes are eluted from the beads by the addition of 0.1% trifluoroacetic acid (TFA), pH 1.5.

The eluate is next heated at 85°C for 15 minutes to dissociate the bound peptides from the MHC molecules. After cooling to room temperature, peptides are separated from the antibody by centrifugation using, for example, 3 kDa molecular mass cutoff membrane filters (Millipore). The filtrate is concentrated using vacuum centrifugation and reconstituted to a final volume of 100µl. The purified peptide mixture is fractionated, for example using a C-18 reversed phase (RP) column (e.g. 4.6 mm diameter x 150 mm length) using an offline HPLC. For this step, mobile phase A may be 2% acetonitrile (CAN) and 0.1% formic acid (FA) in water, while mobile phase B may be 0.1% FA and 90% CAN in water.

The peptide-containing fractions are then eluted from the column, dried under a vacuum, and analysed by mass spectrometry to identify the sequences of the fractions. The acquired spectral data can then be searched against all databased flavivirus proteins to identify peptide sequences associated with flavivirus. Synthetic peptides may then be made according to the identified sequences and subjected to mass spectrometry to confirm their identity to the peptides in the peptide-containing fractions.

In this method, any type of cells may be infected with flavivirus. The cells may be antigen presenting cells. The cells may be hepatoma cells such as HepG2 cells, EBV-transformed lymphoblastoid B cells such as JY cells, or lymphoblasts such as T2 cells.

Likewise, any flavivirus of interest may be used to infect the cells. For instance, the flavivirus may be Zika virus, Dengue virus, West Nile virus, yellow fever virus, St. Louis encephalitis virus, Japanese encephalitis virus, Murray Valley encephalitis virus, Tick-borne encephalitis virus, Kunjin encephalitis virus, Rocio encephalitis virus, Russian Spring Summer encephalitis virus, Negeishi virus, Kyasanur Forest , Omsk Hemorrhagic Fever virus, Powassan virus, Louping Ill virus, Rio Bravo virus , Tyuleniy virus, Ntaya virus and Modoc virus. The Zika virus may, for example, be African Zika Virus or Asian Zika Virus. The Dengue virus may, for example, be DENV-1, DENV-2, DENV-3 or DENV-4.

The direct identification of CD8+ T cell epitopes presented by flavivirus-infected cells is advantageous compared to MHC motif prediction methodologies. The immune epitope database (IEDB; <http://www.iedb.org>) is generated by motif prediction methods, and not functional methods, and contains numerous predicted HLA-specific flavivirus T cell epitopes, including some shared epitopes with high MHC binding scores and limited CTL characterization. As both dominant and subdominant epitopes may be presented by flavivirus-infected cells, it is difficult to sort out the dominance hierarchies of naturally presented epitopes using the database. Thus, it is not clear from the immune epitope database alone which of the listed epitopes may be expected to efficiently induce a CD8+ T cell response when included in a vaccine composition. The direct identification method set out above provides a mechanism for confirming the utility of the epitopes.

Vaccine compositions based on epitopes presented by flavivirus-infected cells, such as the vaccine composition of the invention, are superior to vaccines based on a viral protein subunit or a motif predicted epitope. Protein processing by the immune system is likely to alter native viral epitopes. Basing a vaccine composition on peptides

demonstrated to be presented by infected cells removes this source of uncertainty, because the peptides have already undergone protein processing.

Furthermore, the direct identification method may be used to identify conserved CD8⁺ T cell epitopes presented by cells infected by different flaviviruses. In this way, CD8⁺ T cell epitopes suitable for inclusion in a cross-protective vaccine may be identified. As set out in the Examples, the present inventors confirmed that the peptides VILAGPMPVT (SEQ ID NO: 8), AILEENGVQ (SEQ ID NO: 9) and SPRRLAAAV (SEQ ID NO: 10), are Zika virus CD8⁺ T cell epitopes having 100% homology with sequences encoded by Dengue virus, and that WVTDHSGKTV (SEQ ID NO: 11) is a Dengue virus CD8⁺ T cell epitope having 100% homology with sequences encoded by Zika virus and West Nile virus.

Variants of SEQ ID Nos: 1 to 11

The vaccine composition of the invention may comprise a flavivirus peptide comprising a variant of one or more of the CD8⁺ T cell epitopes set out in SEQ ID NOs: 1 to 11. The variant may itself be a CD8⁺ T cell epitope. CD8⁺ T cell epitopes are defined above.

The variant may have the same MHC class I binding ability as the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. For instance, the variant may be able to bind to the same MHC class I supertypes as the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. Alternatively, the variant may have a different MHC class I binding ability compared to the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. For instance, the variant may be able to bind to different MHC class I supertypes compared to the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. The variant may be able to bind to a greater number of MHC class I supertypes than the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based.

The variant may have the same or a similar ability to stimulate a CD8⁺ T cell response as the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. The variant may have a improved ability to stimulate a CD8⁺ T cell response compared to the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based. Methods for assessing CD8⁺ T cell responses are well-known in the art and include, for example, the measurement of CD8⁺ T cell proliferation and/or the production of cytokines (e.g. IFN- γ) and/or cytotoxins (e.g. perforin, granzymes and granulysin). T cell proliferation may be

measured by, for example, the incorporation of tritiated thymidine into a T cell culture. T cell proliferation may be measured by, for example, measuring the metabolic activity of a T cell population using, for example, tetrazolium salts or Alamar Blue. T cell proliferation may be measured by, for example, assessing cell division by flow cytometry based on
5 dilution of a dye such as carboxyfluorescein succinimidyl ester (CFSE). The production of cytokines and/or cytotoxins may be analysed by, for example, flow cytometry, an enzyme-linked immunosorbent assay (ELISA) or an enzyme linked immunospot (ELISPOT) assay.

Typically, the variant is around 9 amino acids in length. The variant may though be shorter or longer. For example, the variant may be about 8, 9, 10, 11, 12, 13, 14 or 15
10 amino acids in length. The variant may be about 8 to 15, 9 to 14 or 10 to 12 amino acids in length.

The variant may differ from one of SEQ ID NOs: 1 to 11 by insertion, deletion and/or substitution. For example, the variant may differ from one of SEQ ID NOs: 1 to 11 by insertion of one or more, such as two or more, three or more, four or more, or five or
15 more, amino acids. The variant may differ from one of SEQ ID NOs: 1 to 11 by deletion of one or more, such as two or more, three or more, four or more, or five or more, amino acids. The variant may differ from one of SEQ ID NOs: 1 to 11 by substitution of one or more, such as two or more, three or more, four or more, or five or more, amino acids. The variant may comprise one or more amino acid insertions and one or more amino acid
20 substitutions relative to one of SEQ ID NOs: 1 to 11. The variant may comprise one or more amino acid insertions and one or more amino acid deletions relative to one of SEQ ID NOs: 1 to 11. The variant may comprise one or more amino acid deletions and one or more amino acid substitutions relative to one of SEQ ID NOs: 1 to 11. The variant may comprise one or more amino acid insertions, one or more amino acid deletions and one or
25 more amino acid substitutions relative to one of SEQ ID NOs: 1 to 11. In each case, an amino acid substitution may be a conservative amino acid substitution.

Preferably, the variant differs from one of SEQ ID NOs: 1 to 11 by insertion, deletion or substitution of no more than one amino acid. In other words, the variant may differ from one or more of SEQ ID NOs: 1 to 11 by a single amino acid insertion, a single
30 amino acid deletion, or a single amino acid substitution. Preferably, the single amino acid substitution is a conservative amino acid substitution.

Conservative substitutions replace amino acids with other amino acids of similar chemical structure, similar chemical properties or similar side-chain volume. The amino

acids introduced may have similar polarity, hydrophilicity, hydrophobicity, basicity, acidity, neutrality or charge to the amino acids they replace. Alternatively, the conservative substitution may introduce another amino acid that is aromatic or aliphatic in the place of a pre-existing aromatic or aliphatic amino acid. Conservative amino acid changes are well-known in the art and may be selected in accordance with the properties of the 20 main amino acids as defined in Table 2 below. Where amino acids have similar polarity, this can also be determined by reference to the hydropathy scale for amino acid side chains in Table 3.

Table 2 – Chemical properties of amino acids

Ala	aliphatic, hydrophobic, neutral	Met	hydrophobic, neutral
Cys	polar, hydrophobic, neutral	Asn	polar, hydrophilic, neutral
Asp	polar, hydrophilic, charged (-)	Pro	hydrophobic, neutral
Glu	polar, hydrophilic, charged (-)	Gln	polar, hydrophilic, neutral
Phe	aromatic, hydrophobic, neutral	Arg	polar, hydrophilic, charged (+)
Gly	aliphatic, neutral	Ser	polar, hydrophilic, neutral
His	aromatic, polar, hydrophilic, charged (+)	Thr	polar, hydrophilic, neutral
Ile	aliphatic, hydrophobic, neutral	Val	aliphatic, hydrophobic, neutral
Lys	polar, hydrophilic, charged(+)	Trp	aromatic, hydrophobic, neutral
Leu	aliphatic, hydrophobic, neutral	Tyr	aromatic, polar, hydrophobic

Table 3- Hydropathy scale

	Side Chain	Hydropathy
15	Ile	4.5
	Val	4.2
	Leu	3.8
20	Phe	2.8
	Cys	2.5
	Met	1.9
	Ala	1.8
	Gly	-0.4
25	Thr	-0.7
	Ser	-0.8
	Trp	-0.9
	Tyr	-1.3
	Pro	-1.6

	His	-3.2
	Glu	-3.5
	Gln	-3.5
	Asp	-3.5
5	Asn	-3.5
	Lys	-3.9
	Arg	-4.5

The variant is preferably at least 50% identical to the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based, over the entire length of that sequence. More preferably, the variant is at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% and more preferably at least 95%, 97% or 99% identical to the sequence selected from SEQ ID NOs: 1 to 11 upon which it is based, over the entire length of that sequence. Standard methods in the art may be used to determine identity. For example the UWGCG Package provides the BESTFIT program which can be used to calculate homology, for example used on its default settings (Devereux *et al* (1984) *Nucleic Acids Research* **12**, p387-395). The PILEUP and BLAST algorithms can be used to calculate homology or line up sequences (such as identifying equivalent residues or corresponding sequences (typically on their default settings)), for example as described in Altschul S. F. (1993) *J Mol Evol* 36:290-300; Altschul, S.F *et al* (1990) *J Mol Biol* 215:403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>).

25

Cross-protective vaccine compositions

Each of SEQ ID NOs: 1 to 11 identified by the present inventors is either (i) derived from Zika virus infected cells, or (ii) derived from Dengue virus infected cells but 100% homologous with a sequence encoded by Zika virus. The vaccine composition of the invention is therefore designed to elicit a protective immune response against Zika virus infection. However, the vaccine composition may also induce cross-protection against a wide range of other flaviviruses, as the SEQ ID NOs: 1 to 11 are highly conserved between flaviviruses. A variant of SEQ ID NOs: 1 to 11 may also be highly conserved between flaviviruses

As shown in Table 1, many of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 have 100% homology with a sequence encoded by a flavivirus other than that in which the epitope was initially identified. For instance, VILAGPMPVT (SEQ ID NO: 8), AILEENGVQ (SEQ ID NO: 9) and SPRRLAAAV (SEQ ID NO: 10) were identified in
 5 Zika virus infected cells, but are each 100% homologous to a sequence encoded by Dengue virus. WVTDHSGKTV (SEQ ID NO: 11) was identified in Dengue virus infected cells but has 100% homology with a sequence encoded by Zika virus and a sequence encoded by West Nile virus. An immune response generated by vaccination with a composition that comprises an epitope that is 100% homologous with a sequence from another
 10 flavivirus may protect against subsequent infection with that flavivirus.

An immune response generated by vaccination with a composition that comprises an epitope that is about 50% or more (such as 60%, 70%, 75%, 80%, 90%, 95%, 98% or 99%) homologous with a sequence encoded by another flavivirus may protect against subsequent infection with that flavivirus. In some cases, the protective effect is associated
 15 with the conservation of certain residues between the epitope and the sequence encoded by the other flavivirus. Immunisation with a vaccine composition of the invention may therefore induce a protective immune response against a wide variety of flaviviruses not mentioned in Table 1.

Accordingly, the vaccine composition of the invention may have built-in cross-
 20 species and/or cross-genus efficacy, i.e. be a cross-protective flavivirus vaccine composition. In this way, a single flavivirus vaccine composition can be used to confer protection against a variety of different flaviviruses. This provides a cost-effective means of controlling the spread of flavivirus infection.

Inclusion of conserved peptides in the vaccine composition may confer protective
 25 capability against emerging flavivirus strains associated with rapid evolution of the flavivirus genome. This may assist in the long-term control of the flavivirus infection.

Inclusion of a flavivirus peptide comprising a conserved CD8+ T cell epitope in the vaccine composition of the invention may beneficially prevent or minimise the development of antibody-dependent enhancement of Dengue virus infection following
 30 administration of the vaccine composition.

Interaction with HLA supertypes

The vaccine composition may comprise at least two flavivirus peptides comprising a CD8+ T cell epitope which each interacts with a different HLA supertype. Including a plurality of such peptides in the vaccine composition allows the vaccine composition to elicit a CD8+ T cell response in a greater proportion of individuals to which the vaccine composition is administered. This is because the vaccine composition should be capable of eliciting a CD8+ T cell response in all individuals of an HLA supertype that interacts with one of the CD8+ T cell epitopes comprised in the plurality of flavivirus peptides. Each CD8+ T cell epitope may interact with HLA-A1, HLA-A2, HLA-A3, HLA-A24, HLA-B7, HLA-B8, HLA-B27, HLA-B44, HLA-B58 or HLA-B62, or any other HLA supertype known in the art. Any combination of flavivirus peptides comprising such a CD8+ T cell epitope is possible.

The vaccine composition may comprise at least one flavivirus peptide comprising a CD8+ T cell epitope which interacts at least two different HLA supertypes. Again, this allows the vaccine composition to elicit a CD8+ T cell response in a greater proportion of individuals to which the vaccine composition is administered. The vaccine composition may comprise at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, at least twenty, at least twenty-one, at least twenty-two, at least twenty-three, at least twenty-four, at least twenty-five, at least twenty-six, at least twenty-seven, at least twenty-eight, at least twenty-nine, at least thirty, at least thirty-one, at least thirty-two, at least thirty-three, at least thirty-four, at least thirty-five, at least thirty-six, at least thirty-seven, at least thirty-eight, at least thirty-nine, at least forty, at least forty-one, at least forty-two, at least forty-three, at least forty-four, at least forty-five, at least forty-six, at least forty-seven, at least forty-eight, at least forty-nine, at least fifty, at least fifty-one, at least fifty-two, at least fifty-three, at least fifty-four, at least fifty-five, at least fifty-six, at least fifty-seven, at least fifty-eight, at least fifty-nine, at least sixty, at least sixty-one, at least sixty-two, at least sixty-three, at least sixty-four, at least sixty-five, at least sixty-six, at least sixty-seven, at least sixty-eight, at least sixty-nine, at least seventy, at least seventy-one, at least seventy-two, at least seventy-three, at least seventy-four, at least seventy-five, at least seventy-six, at least seventy-seven, at least seventy-eight, at least seventy-nine, at least eighty, at least eighty-one, at least eighty-two, at least eighty-three, at least eighty-four, at least eighty-five, at least eighty-six, at least eighty-seven, at least eighty-eight, at least eighty-nine, at least ninety, at least ninety-one, at least ninety-two, at least ninety-three, at least ninety-four, at least ninety-five, at least ninety-six, at least ninety-seven, at least ninety-eight, at least ninety-nine, at least one hundred, or more than one hundred flavivirus peptides comprising a CD8+ T cell epitope that each interact with at least two different HLA subtypes. Each flavivirus peptide may interact with at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, at least twenty, at least twenty-one, at least twenty-two, at least twenty-three, at least twenty-four, at least twenty-five, at least twenty-six, at least twenty-seven, at least twenty-eight, at least twenty-nine, at least thirty, at least thirty-one, at least thirty-two, at least thirty-three, at least thirty-four, at least thirty-five, at least thirty-six, at least thirty-seven, at least thirty-eight, at least thirty-nine, at least forty, at least forty-one, at least forty-two, at least forty-three, at least forty-four, at least forty-five, at least forty-six, at least forty-seven, at least forty-eight, at least forty-nine, at least fifty, at least fifty-one, at least fifty-two, at least fifty-three, at least fifty-four, at least fifty-five, at least fifty-six, at least fifty-seven, at least fifty-eight, at least fifty-nine, at least sixty, at least sixty-one, at least sixty-two, at least sixty-three, at least sixty-four, at least sixty-five, at least sixty-six, at least sixty-seven, at least sixty-eight, at least sixty-nine, at least seventy, at least seventy-one, at least seventy-two, at least seventy-three, at least seventy-four, at least seventy-five, at least seventy-six, at least seventy-seven, at least seventy-eight, at least seventy-nine, at least eighty, at least eighty-one, at least eighty-two, at least eighty-three, at least eighty-four, at least eighty-five, at least eighty-six, at least eighty-seven, at least eighty-eight, at least eighty-nine, at least ninety, at least ninety-one, at least ninety-two, at least ninety-three, at least ninety-four, at least ninety-five, at least ninety-six, at least ninety-seven, at least ninety-eight, at least ninety-nine, at least one hundred, or more than one hundred different HLA supertypes. Each flavivirus peptide may interact with two or more of HLA-A1, HLA-A2, HLA-A3, HLA-A24, HLA-B7, HLA-B8, HLA-B27, HLA-B44, HLA-B58 or HLA-B62, or any other HLA supertype known in the art, in any combination. Preferably, the vaccine composition comprises a flavivirus peptide comprising a CD8+ T cell epitope that interacts with HLA-A2 and HLA-A24. In this case, the vaccine composition may, for example, comprise a flavivirus peptide comprising a CD8+ T cell set out in SEQ ID NO: 2 or SEQ ID NO: 4.

CD4+ T cell epitopes

The vaccine composition of the invention may comprise a peptide comprising a CD4+ T cell epitope. The vaccine composition may comprise two or more, such as three or more, four or more, five or more, ten or more, fifteen or more or twenty or more peptides comprising a CD4+ T cell epitope. A CD4+ T cell epitope is a peptide that is capable of (i) presentation by a class II MHC molecule and (ii) recognition by a T cell

receptor (TCR) present on a CD4+ T cell. Preferably, recognition by the TCR results in activation of the CD4+ T cell. CD4+ T cell activation may lead to increased proliferation and/or cytokine production.

The CD4+ T cell epitope may be a flavivirus CD4+ T cell epitope. That is, the CD4+ T cell epitope may be a peptide that is expressed by one or more flaviviruses and that is that is capable of (i) presentation by a class II MHC molecule and (ii) recognition by a T cell receptor (TCR) present on a CD4+ T cell. Such peptides are known in the art.

The CD4+ T cell epitope may be a CD4+ T cell epitope other than a flavivirus CD4+ T cell epitope. For example, the CD4+ T cell may be expressed by an organism other than a flavivirus. The CD4+ T cell epitope may, for example, be expressed by *Clostridium tetani*. For instance, the CD4+ T cell epitope may be derived from tetanus toxin.

The CD4+ T cell epitope may be a CD4+ T cell epitope that reacts with all class II HLA types, i.e. a so-called “promiscuous” epitope. Inclusion of a promiscuous epitope in the vaccine composition may improve the ability of the vaccine composition to induce an immune response to the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. The CD4+ T cell epitope may, for example, comprise the sequence FKLQTMVKLFNRIKNNVA (SEQ ID NO: 12) and/or the sequence LQTMVKLFNRIKNNVAGGC (SEQ ID NO: 13). SEQ ID NOs 12 and 13 are promiscuous epitopes derived from tetanus toxin.

The peptide comprising a CD4+ T cell epitope may be a different peptide from the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. The CD4+ T cell epitope may, for instance, be comprised in an additional peptide in the vaccine composition, i.e. in a peptide that does not comprise one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. As mentioned above, the additional peptide may comprise one or more CD8+ T cell epitopes and/or one or more B cell epitopes as well as the CD4+ T cell epitope. For instance, the additional peptide may comprise one or more flavivirus CD8+ T cell epitopes.

The peptide comprising a CD4+ T cell epitope may be the same peptide as the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. That is, the flavivirus peptide comprising one or more of

the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof may further comprise a CD4+ T cell epitope.

When the peptide comprising a CD4+ T cell epitope also comprises a CD8+ T cell epitope (such as one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof), the CD8+ epitope may be nested within the CD4+ T cell epitope. CD4+ T cell epitopes are typically longer than CD8+ T cell epitopes. Therefore, extending one or both termini of the CD8+ T cell epitope may yield a longer, CD4+ T cell epitope whose sequence still comprises the CD8+ T cell epitope. Therefore, the CD4+ T cell epitope may comprise a CD8+ T cell epitope, such as a CD8+ T cell epitope set out in SEQ ID NOs: 1 to 11 or a variant thereof, extended at its N-terminus or C-terminus. The CD8+ T cell epitope may be extended by 1, 2, 3, 4 or 5 amino acids at its N terminus. The CD8+ T cell epitope may be extended by 1, 2, 3, 4 or 5 amino acids at its C terminus. Preferably, the CD8+ T cell epitope is extended by 3 amino acids at the N terminus, and 3 amino acids at the C terminus. However, the CD8+ T cell epitope need not be extended by the same number of amino acids at each terminus.

The CD8+ T cell epitope nested within a CD4+ T cell epitope may be capable of generating a robust CTL response. The extended peptide (CD4+ T cell epitope) may be capable of inducing T helper mediated cytokine responses. Thus, inclusion of a flavivirus peptide comprising a CD8+ T cell epitope and a CD4+ T cell epitope in the vaccine composition may allow the vaccine composition to induce both cytotoxic and helper T cell responses.

The flavivirus peptide comprising a CD4+ T cell epitope may be attached to a nanoparticle. When the peptide comprising a CD4+ T cell epitope is a different peptide from the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, each peptide may be attached to the same nanoparticle or to a different nanoparticle. The nanoparticle may be a gold nanoparticle. Nanoparticles and attachment thereto are described below.

B cell epitopes

The vaccine composition of the invention may comprise a peptide comprising a B cell epitope. The vaccine composition may comprise two or more, such as three or more, four or more, five or more, ten or more, fifteen or more or twenty or more peptides comprising a B cell epitope. A B cell epitope is a peptide that is capable of recognition by

a B cell receptor (BCR) present on a B cell. Preferably, recognition by the BCR results in activation and/or maturation of the B cell. B cell activation may lead to increased proliferation, and/or antibody production.

5 The B cell epitope may be a flavivirus B cell epitope. That is, the B cell epitope may be a peptide that is expressed by one or more flaviviruses and that is capable of recognition by a B cell receptor (BCR) present on a B cell. Such peptides are known in the art.

10 The B cell epitope may be a linear epitope, i.e. an epitope that is defined by the primary amino acid sequence of a particular region of a flavivirus protein. Alternatively, the epitope may be a conformational epitope, i.e. an epitope that is defined by the conformational structure of a native flavivirus protein. In this case, the epitope may be continuous (i.e. the components that interact with the antibody are situated next to each other sequentially on the protein) or discontinuous (i.e. the components that interact with the antibody are situated on disparate parts of the protein, which are brought close to each other in the folded native protein structure).

15 Typically, the B cell epitope is around 5 to 20 amino acids in length, such as 6 to 19, 7 to 18, 8 to 17, 9 to 16, 10 to 15, 11 to 14 or 12 to 13 amino acids in length.

20 Methods for identifying B cell epitopes are also known in the art. For instance, epitope mapping methods may be used to identify B cell epitopes. These methods include structural approaches, wherein the known or modelled structure of a protein is used in an algorithm based approach to predict surface epitopes, and functional approaches, wherein the binding of whole proteins, protein fragments or peptides to an antibody can be quantitated e.g. using an Enzyme-Linked Immunosorbent Assay (ELISA). Competition mapping, antigen modification or protein fragmentation methods may also be used.

25

Nanoparticles

30 In the vaccine composition of the invention, the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof may be attached to a nanoparticle. Any other peptides further comprised in the vaccine composition may also be attached to a nanoparticle. Attachment to a nanoparticle, for example a gold nanoparticle, is beneficial.

As set out above, attachment of the peptide to a nanoparticle (such as a gold nanoparticle) reduces or eliminates the need to include a virus or an adjuvant in the vaccine

composition. The nanoparticles may contain immune “danger signals” that help to effectively induce an immune response to the peptides. The nanoparticles may induce dendritic cell (DC) activation and maturation, required for a robust immune response. The nanoparticles may contain non-self components that improve uptake of the nanoparticles and thus the peptides by cells, such as antigen presenting cells. Attachment of a peptide to a nanoparticle may therefore enhance the ability of antigen presenting cells to stimulate virus-specific T and/or B cells. Attachment to a nanoparticle also facilitates delivery of the vaccine compositions via the subcutaneous, intradermal, transdermal and oral/buccal routes, providing flexibility in administration.

10 Nanoparticles are particles between 1 and 100 nanometers (nm) in size which can be used as a substrate for immobilising ligands. In the vaccine compositions of the invention, the nanoparticle may have a mean diameter of 1 to 100, 20 to 90, 30 to 80, 40 to 70 or 50 to 60 nm. Preferably, the nanoparticle has a mean diameter of 20 to 40nm. A mean diameter of 20 to 40nm facilitates uptake of the nanoparticle to the cytosol. The mean diameter can be measured using techniques well known in the art such as transmission electron microscopy.

Nanoparticles suitable for the delivery of antigen, such as a flavivirus peptide, are known in the art. Methods for the production of such nanoparticles are also known.

20 The nanoparticle may, for example, be a polymeric nanoparticle, an inorganic nanoparticle, a liposome, an immune stimulating complex (ISCOM), a virus-like particle (VLP), or a self-assembling protein. The nanoparticle is preferably a calcium phosphate nanoparticle, a silicon nanoparticle or a gold nanoparticle.

25 The nanoparticle may be a polymeric nanoparticle. The polymeric nanoparticle may comprise one or more synthetic polymers, such as poly(d,l-lactide-co-glycolide) (PLG), poly(d,l-lactic-coglycolic acid) (PLGA), poly(g-glutamic acid) (g-PGA)m poly(ethylene glycol) (PEG), or polystyrene. The polymeric nanoparticle may comprise one or more natural polymers such as a polysaccharide, for example pullulan, alginate, inulin, and chitosan. The use of a polymeric nanoparticle may be advantageous due to the properties of the polymers that may be include in the nanoparticle. For instance, the natural and synthetic polymers recited above may have good biocompatibility and biodegradability, a non-toxic nature and/or the ability to be manipulated into desired shapes and sizes. The polymeric nanoparticle may form a hydrogel nanoparticle. Hydrogel nanoparticles are a type of nano-sized hydrophilic three-dimensional polymer

network. Hydrogel nanoparticles have favourable properties including flexible mesh size, large surface area for multivalent conjugation, high water content, and high loading capacity for antigens. Polymers such as Poly(L-lactic acid) (PLA), PLGA, PEG, and polysaccharides are particularly suitable for forming hydrogel nanoparticles.

5 The nanoparticle may be an inorganic nanoparticle. Typically, inorganic nanoparticles have a rigid structure and are non-biodegradable. However, the inorganic nanoparticle may be biodegradable. The inorganic nanoparticle may comprise a shell in which an antigen may be encapsulated. The inorganic nanoparticle may comprise a core to which an antigen may be covalently attached. The core may comprise a metal. For
10 example, the core may comprise gold (Au), silver (Ag) or copper (Cu) atoms. The core may be formed of more than one type of atom. For instance, the core may comprise an alloy, such as an alloy of Au/Ag, Au/Cu, Au/Ag/Cu, Au/Pt, Au/Pd or Au/Ag/Cu/Pd. The core may comprise calcium phosphate (CaP). The core may comprise a semiconductor material, for example cadmium selenide.

15 Other exemplary inorganic nanoparticles include carbon nanoparticles and silica-based nanoparticles. Carbon nanoparticles have good biocompatibility and can be synthesized into nanotubes and mesoporous spheres. Silica-based nanoparticles (SiNPs) are biocompatible and can be prepared with tunable structural parameters to suit their therapeutic application.

20 The nanoparticle may be a silicon nanoparticle, such as an elemental silicon nanoparticle. The nanoparticle may be mesoporous or have a honeycomb pore structure. Preferably, the nanoparticle is an elemental silicon particle having a honeycomb pore structure. Such nanoparticles are known in the art and offer tunable and controlled drug
25 loading, targeting and release that can be tailored to almost any load, route of administration, target or release profile. For example, such nanoparticles may increase the bioavailability of their load, and/or improve the intestinal permeability and absorption of orally administered actives. The nanoparticles may have an exceptionally high loading capacity due to their porous structure and large surface area. The nanoparticles may release their load over days, weeks or months, depending on their physical properties.
30 Since silicon is a naturally occurring element of the human body, the nanoparticles may elicit no response from the immune system. This is advantageous to the *in vivo* safety of the nanoparticles.

Any of the SiNPs described above may be biodegradable or non-biodegradable. A biodegradable SiNP may dissolve to orthosilic acid, the bioavailable form of silicon. Orthosilic acid has been shown to be beneficial for the health of bones, connective tissue, hair, and skin.

5 The nanoparticle may be a liposome. Liposomes are typically formed from biodegradable, non-toxic phospholipids and comprise a self-assembling phospholipid bilayer shell with an aqueous core. A liposome may be an unilamellar vesicle comprising a single phospholipid bilayer, or a multilamellar vesicle that comprises several concentric phospholipid shells separated by layers of water. As a consequence, liposomes can be
10 tailored to incorporate either hydrophilic molecules into the aqueous core or hydrophobic molecules within the phospholipid bilayers. Liposomes may encapsulate antigen within the core for delivery. Liposomes may incorporate viral envelope glycoproteins to the shell to form virosomes. A number of liposome-based products are established in the art and are approved for human use.

15 The nanoparticle may be an immune-stimulating complex (ISCOM). ISCOMs are cage-like particles which are typically formed from colloidal saponin-containing micelles. ISCOMs may comprise cholesterol, phospholipid (such as phosphatidylethanolamine or phosphatidylcholine) and saponin (such as Quil A from the tree *Quillaia saponaria*). ISCOMs have traditionally been used to entrap viral envelope proteins, such as envelope
20 proteins from herpes simplex virus type 1, hepatitis B, or influenza virus.

 The nanoparticle may be a virus-like particle (VLP). VLPs are self-assembling nanoparticles that lack infectious nucleic acid, which are formed by self-assembly of biocompatible capsid protein. VLPs are typically about 20 to about 150nm, such as about
25 20 to about 40nm, about 30 to about 140nm, about 40 to about 130nm, about 50 to about 120nm, about 60 to about 110nm, about 70 to about 100nm, or about 80 to about 90nm in diameter. VLPs advantageously harness the power of evolved viral structure, which is naturally optimized for interaction with the immune system. The naturally-optimized nanoparticle size and repetitive structural order means that VLPs induce potent immune responses, even in the absence of adjuvant.

30 The nanoparticle may be a self-assembling protein. For instance, the nanoparticle may comprise ferritin. Ferritin is a protein that can self-assemble into nearly-spherical 10 nm structures. The nanoparticle may comprise major vault protein (MVP). Ninety-six

units of MVP can self-assemble into a barrel-shaped vault nanoparticle, with a size of approximately 40 nm wide and 70 nm long.

The nanoparticle may be a calcium phosphate (CaP) nanoparticle. CaP nanoparticles may comprise a core comprising one or more (such as two or more, 10 or more, 20 or more, 50 or more, 100 or more, 200 or more, or 500 or more) molecules of CaP. CaP nanoparticles and methods for their production are known in the art. For instance, a stable nano-suspension of CAP nanoparticles may be generated by mixing inorganic salt solutions of calcium and phosphates in pre-determined ratios under constant mixing.

The CaP nanoparticle may have an average particle size of about 80 to about 100nm, such as about 82 to about 98nm, about 84 to about 96nm, about 86 to about 94nm, or about 88 to about 92nm. This particle size may produce a better performance in terms of immune cell uptake and immune response than other, larger particle sizes. The particle size may be stable (i.e. show no significant change), for instance when measured over a period of 1 month, 2 months, 3 months, 6 months, 12 months, 18 months, 24 months, 36 months or 48 months.

CaP nanoparticles can be co-formulated with one or multiple antigens either adsorbed on the surface of the nanoparticle or co-precipitated with CaP during particle synthesis. For example, a peptide, such as a flavivirus peptide, may be attached to the CaP nanoparticle by dissolving the peptide in DMSO (for example at a concentration of about 10 mg/ml), adding to a suspension of CaP nanoparticles together with N-acetyl-glucosamine (GlcNAc) (for example at 0.093mol/L and ultra-pure water, and mixing at room temperature for a period of about 4 hours (for example, 1 hour, 2 hours, 3 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours or 10 hours).

The vaccine composition may comprise about 0.15 to about 0.8%, such as 0.2 to about 0.75%, 0.25 to about 0.7%, 0.3 to about 0.6%, 0.35 to about 0.65%, 0.4 to about 0.6%, or 0.45 to about 0.55%, CaP nanoparticles. Preferably the vaccine composition comprises about 0.3% CaP nanoparticles.

CaP nanoparticles have a high degree of biocompatibility due to their chemical similarity to human hard tissues such as bone and teeth. Advantageously, therefore, CaP nanoparticles are non-toxic when used for therapeutic applications. CaP nanoparticles are safe for administration via intramuscular, subcutaneous, oral, or inhalation routes. CaP nanoparticles are also simple to synthesise commercially. Furthermore, CaP nanoparticles

may be associated with slow release of antigen, which may enhance the induction of an immune response to a peptide attached to the nanoparticle. CaP nanoparticles may be used both as an adjuvant, and as a drug delivery vehicle.

5 The nanoparticle may be a gold nanoparticle. Gold nanoparticles are known in the art and are described in particular in WO 2002/32404, WO 2006/037979, WO 2007/122388, WO 2007/015105 and WO 2013/034726. The gold nanoparticle attached to each peptide may be a gold nanoparticle described in any of WO 2002/32404, WO 2006/037979, WO 2007/122388, WO 2007/015105 and WO 2013/034726.

10 Gold nanoparticles comprise a core comprising a gold (Au) atom. The core may further comprise one or more Fe, Cu or Gd atoms. The core may be formed from a gold alloy, such as Au/Fe, Au/Cu, Au/Gd, Au/Fe/Cu, Au/Fe/Gd or Au/Fe/Cu/Gd. The total number of atoms in the core may be 100 to 500 atoms, such as 150 to 450, 200 to 400 or 250 to 350 atoms. The gold nanoparticle may have a mean diameter of 1 to 100, 20 to 90, 30 to 80, 40 to 70 or 50 to 60 nm. Preferably, the gold nanoparticle has a mean diameter of 15 20 to 40nm.

The nanoparticle may comprise a surface coated with alpha-galactose and/or beta-GlcNHAc. For instance, the nanoparticle may comprise a surface passivated with alpha-galactose and/or beta-GlcNHAc. In this case, the nanoparticle may, for example, be a nanoparticle which comprises a core including metal and/or semiconductor atoms. For 20 instance, the nanoparticle may be a gold nanoparticle. Beta-GlcNHAc is a bacterial pathogen-associated-molecular pattern (PAMP), which is capable of activating antigen-presenting cells. In this way, a nanoparticle comprising a surface coated or passivated with Beta-GlcNHAc may non-specifically stimulate an immune response. Attachment of the flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID 25 NOs: 1 to 11 to such a nanoparticle may therefore improve the immune response elicited by administration of the vaccine composition of the invention to an individual.

One or more ligands other than the peptide may be linked to the nanoparticle, which may be any of the types of nanoparticle described above. The ligands may form a “corona”, a layer or coating which may partially or completely cover the surface of the 30 core. The corona may be considered to be an organic layer that surrounds or partially surrounds the nanoparticle core. The corona may provide or participate in passivating the core of the nanoparticle. Thus, in certain cases the corona may be a sufficiently complete

coating layer to stabilise the core. The corona may facilitate solubility, such as water solubility, of the nanoparticles of the present invention.

The nanoparticle may comprise at least 10, at least 20, at least 30, at least 40 or at least 50 ligands. The ligands may include one or more peptides, protein domains, nucleic acid molecules, lipidic groups, carbohydrate groups, anionic groups, or cationic groups, glycolipids and/or glycoproteins. The carbohydrate group may be a polysaccharide, an oligosaccharide or a monosaccharide group (e.g. glucose). One or more of the ligands may be a non-self component, that renders the nanoparticle more likely to be taken up by antigen presenting cells due to its similarity to a pathogenic component. For instance, one or more ligands may comprise a carbohydrate moiety (such as a bacterial carbohydrate moiety), a surfactant moiety and/or a glutathione moiety. Exemplary ligands include glucose, N-acetylglucosamine (GlcNAc), glutathione, 2'-thioethyl- β -D-glucopyranoside and 2'-thioethyl- D-glucopyranoside. Preferred ligands include glycoconjugates, which form glyconanoparticles

Linkage of the ligands to the core may be facilitated by a linker. The linker may comprise a thiol group, an alkyl group, a glycol group or a peptide group. For instance, the linker may comprise C2-C15 alkyl and/or C2-C15 glycol. The linker may comprise a sulphur-containing group, amino-containing group, phosphate-containing group or oxygen-containing group that is capable of covalent attachment to the core. Alternatively, the ligands may be directly linked to the core, for example via a sulphur-containing group, amino-containing group, phosphate-containing group or oxygen-containing group comprised in the ligand.

Attachment to nanoparticles

The peptide may be attached at its N-terminus to the nanoparticle. Typically, the peptide is attached to the core of the nanoparticle, but attachment to the corona or a ligand may also be possible.

The peptide may be directly attached to the nanoparticle, for example by covalent bonding of an atom in a sulphur-containing group, amino-containing group, phosphate-containing group or oxygen-containing group in the peptide to an atom in the nanoparticle or its core.

A linker may be used to link the peptide to the nanoparticle. The linker may comprise a sulphur-containing group, amino-containing group, phosphate-containing group

or oxygen-containing group that is capable of covalent attachment to an atom in the core. For example, the linker may comprise a thiol group, an alkyl group, a glycol group or a peptide group.

The linker may comprise a peptide portion and a non-peptide portion. The peptide portion may comprise the sequence $X_1X_2Z_1$, wherein X_1 is an amino acid selected from A and G; X_2 is an amino acid selected from A and G; and Z_1 is an amino acid selected from Y and F. The peptide portion may comprise the sequence AAY or FLAAY. The peptide portion of the linker may be linked to the N-terminus of the peptide. The non-peptide portion of the linker may comprise a C2-C15 alkyl and/ a C2-C15 glycol, for example a thioethyl group or a thiopropyl group.

The linker may be (i) $HS-(CH_2)_2-CONH-AAY$; (ii) $HS-(CH_2)_2-CONH-LAAY$; (iii) $HS-(CH_2)_3-CONH-AAY$; (iv) $HS-(CH_2)_3-CONH-FLAAY$; (v) $HS-(CH_2)_{10}-(CH_2OCH_2)_7-CONH-AAY$; and (vi) $HS-(CH_2)_{10}-(CH_2OCH_2)_7-CONH-FLAAY$. In this case, the thiol group of the non-peptide portion of the linker links the linker to the core.

Other suitable linkers for attaching a peptide to a nanoparticle are known in the art, and may be readily identified and implemented by the skilled person.

As explained above, the vaccine composition may comprise multiple flavivirus peptides each comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. The vaccine composition may comprise one or more additional peptides each comprising an epitope, such as a CD4+ T cell epitope, a B cell epitope, or a CD8+ T cell epitope other than the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11. Thus, the vaccine composition may comprise more than one peptide.

When the vaccine composition comprises more than one peptide, two or more (such as three or more, four or more, five or more, ten or more, or twenty or more) of the peptides may be attached to the same nanoparticle. Two or more (such as three or more, four or more, five or more, ten or more, or twenty or more) of the peptides may each be attached to different nanoparticle. The nanoparticles to which the peptides are attached may though be the same type of nanoparticle. For instance, each peptide may be attached to a gold nanoparticle. Each peptide may be attached to a CaP nanoparticle. The nanoparticle to which the peptides are attached may be a different type of nanoparticle. For instance, one peptide may be attached to a gold nanoparticle, and another peptide may be attached to a CaP nanoparticle.

Further vaccine compositions

The invention further provides a vaccine composition comprising (a) a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, or (b) the full
5 complement of a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof.

Flavivirus peptides, CD8+ T cell epitopes and variants are described in detail above. Any of the aspects described above in connection with vaccine compositions comprising a flavivirus peptide may also apply to a vaccine composition comprising (a) a
10 polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, or (b) the full complement of a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof.

The polynucleotide may be DNA. The polynucleotide may be RNA. The
15 polynucleotide may contain one or more regions of DNA, and one or more regions of RNA.

The polynucleotide may be provided in the vaccine composition as a “*naked*” polynucleotide. Alternatively, the polynucleotide may be in a vector or plasmid.

20 Medicaments, methods and therapeutic use

The invention provides a method of preventing or treating a flavivirus infection, comprising administering the vaccine composition of the invention to a subject infected with, or at risk of being infected with, a flavivirus. The invention also provides a vaccine composition of the invention for use in a method of preventing or treating a
25 flavivirus infection in a subject;

The flavivirus infection may be, for example, a Zika virus infection, a Dengue virus infection, a West Nile virus infection, a yellow fever virus infection, a St. Louis encephalitis virus infection, a Japanese encephalitis virus infection, a Murray Valley encephalitis virus infection, a Tick-borne encephalitis virus infection, a Kunjin encephalitis
30 virus infection, a Rocio encephalitis virus infection, a Russian Spring Summer encephalitis virus infection, Negeishi virus infection, a Kyasanur Forest infection, a Omsk Hemorrhagic Fever virus infection, a Powassan virus infection, a Louping Ill virus infection, a Rio Bravo virus infection, a Tyuleny virus infection, a Ntaya virus infection or a Modoc virus

infection. The Zika virus infection may, for example, be African Zika Virus infection or Asian Zika Virus infection. The Dengue virus may, for example, be DENV-1 infection, DENV-2 infection, DENV-3 infection or DENV-4 infection.

The vaccine composition may be provided as a pharmaceutical composition. The pharmaceutical composition preferably comprises a pharmaceutically acceptable carrier or diluent. The pharmaceutical composition may be formulated using any suitable method. Formulation of cells with standard pharmaceutically acceptable carriers and/or excipients may be carried out using routine methods in the pharmaceutical art. The exact nature of a formulation will depend upon several factors including the cells to be administered and the desired route of administration. Suitable types of formulation are fully described in Remington's Pharmaceutical Sciences, 19th Edition, Mack Publishing Company, Eastern Pennsylvania, USA.

The vaccine composition or pharmaceutical composition may be administered by any route. Suitable routes include, but are not limited to, the intravenous, intramuscular, intraperitoneal, subcutaneous, intradermal, transdermal and oral/buccal routes.

Compositions may be prepared together with a physiologically acceptable carrier or diluent. Typically, such compositions are prepared as liquid suspensions of peptides and/or peptide-linked nanoparticles. The peptides and/or peptide-linked nanoparticles may be mixed with an excipient which is pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, of the like and combinations thereof.

In addition, if desired, the pharmaceutical compositions may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, and/or pH buffering agents.

The peptides or peptide-linked nanoparticles are administered in a manner compatible with the dosage formulation and in such amount will be therapeutically effective. The quantity to be administered depends on the subject to be treated, the disease to be treated, and the capacity of the subject's immune system. Precise amounts of nanoparticles required to be administered may depend on the judgement of the practitioner and may be peculiar to each subject.

Any suitable number of peptides or peptide-linked nanoparticles may be administered to a subject. For example, at least, or about, 0.2×10^6 , 0.25×10^6 , 0.5×10^6 , 1.5×10^6 , 4.0×10^6 or 5.0×10^6 peptides or peptide-linked nanoparticles per kg of patient

may administered. For example, at least, or about, 10^5 , 10^6 , 10^7 , 10^8 , 10^9 peptides or peptide-linked nanoparticles may be administered. As a guide, the number of peptides or peptide-linked nanoparticles to be administered may be from 10^5 to 10^9 , preferably from 10^6 to 10^8 .

5 The invention further provides:

- a method of preventing or treating a flavivirus infection in a subject, comprising (i) stimulating cytotoxic T lymphocytes (CTLs) obtained from a Zika virus- or Dengue virus- infected individual with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and (ii) providing the stimulated CTLs as passive immunotherapy to the subject; and
 - a composition for use in a method of preventing or treating a flavivirus infection in a subject, the composition comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and the method comprising (i) stimulating CTLs obtained from a Zika virus- or Dengue virus- infected individual with the composition and
- 10 (ii) providing the stimulated CTLs as passive immunotherapy to the subject.

The flavivirus infection may be, for example, a Zika virus infection, a Dengue virus infection, a West Nile virus infection, a yellow fever virus infection, a St. Louis encephalitis virus infection, a Japanese encephalitis virus infection, a Murray Valley encephalitis virus infection, a Tick-borne encephalitis virus infection, a Kunjin encephalitis virus infection, a Rocio encephalitis virus infection, a Russian Spring Summer encephalitis virus infection, Negeishi virus infection, a Kyasanur Forest infection, a Omsk Hemorrhagic Fever virus infection, a Powassan virus infection, a Louping Ill virus infection, a Rio Bravo virus infection, a Tyuleniy virus infection, a Ntaya virus infection or a Modoc virus infection. The Zika virus infection may, for example, be African Zika Virus infection or Asian Zika Virus infection. The Dengue virus may, for example, be DENV-1 infection, DENV-2 infection, DENV-3 infection or DENV-4 infection.

20 The Zika virus- or Dengue virus- infected individual may also be the subject to which the stimulated CTLs are provided. In other words, the CTLs may be autologous to the subject. Alternatively, the Zika virus- or Dengue virus- infected individual may not be the subject to which the stimulated CTLs are provided. In other words, the CTLs may be allogeneic to the subject. If the CTLs are allogeneic to the subject, they are preferably HLA-matched with the subject.

25 The Zika virus- or Dengue virus- infected individual may also be the subject to which the stimulated CTLs are provided. In other words, the CTLs may be autologous to the subject. Alternatively, the Zika virus- or Dengue virus- infected individual may not be the subject to which the stimulated CTLs are provided. In other words, the CTLs may be allogeneic to the subject. If the CTLs are allogeneic to the subject, they are preferably HLA-matched with the subject.

The CTLs may be stimulated by contacting them with them with the composition comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof. The composition may further comprise additional components helpful to the stimulation of CTLs. For instance, the composition may comprise one or more

5 antigen-presenting cells. The composition may comprise one or more antibodies. The composition may comprise one or more cytokines, such as IL-2. Additional components helpful to the stimulation of CTLs may be provided separately from the composition. For instance, the CTLs may be contacted with one or antigen-presenting cells not forming part of the composition. The CTLs may be contacted with one or more antibodies not forming

10 part of the composition. The CTLs may be contacted with one or more cytokines, such as IL-2, not forming part of the composition. The invention also provides method of diagnosing a flavivirus infection in a subject, the method comprising (i) contacting CTLs obtained from the subject with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant

15 thereof, and (ii) detecting the presence or absence of a CTL response to the one or more CD8+ T cell epitopes.

The flavivirus infection may be, for example, a Zika virus infection, a Dengue virus infection, a West Nile virus infection, a yellow fever virus infection, a St. Louis encephalitis virus infection, a Japanese encephalitis virus infection, a Murray Valley

20 encephalitis virus infection, a Tick-borne encephalitis virus infection, a Kunjin encephalitis virus infection, a Rocio encephalitis virus infection, a Russian Spring Summer encephalitis virus infection, Negeishi virus infection, a Kyasanur Forest infection, a Omsk Hemorrhagic Fever virus infection, a Powassan virus infection, a Louping Ill virus infection, a Rio Bravo virus infection, a Tyuleniy virus infection, a Ntaya virus infection or a Modoc virus

25 infection. The Zika virus infection may, for example, be African Zika Virus infection or Asian Zika Virus infection. The Dengue virus may, for example, be DENV-1 infection, DENV-2 infection, DENV-3 infection or DENV-4 infection.

Methods for detecting a CTL response are well-known in the art and include, for example, the measurement of CD8+ T cell proliferation and/or the production of cytokines

30 (e.g. IFN- γ) and/or cytotoxins (e.g. perforin, granzymes and granulysin). T cell proliferation may be measured by, for example, the incorporation of tritiated thymidine into a T cell culture. T cell proliferation may be measured by, for example, measuring the metabolic activity of a T cell population using, for example, tetrazolium salts or Alamar

Blue. T cell proliferation may be measured by, for example, assessing cell division by flow cytometry based on dilution of a dye such as carboxyfluorescein succinimidyl ester (CFSE). The production of cytokines and/or cytotoxins may be analysed by, for example, flow cytometry, an enzyme-linked immunosorbent assay (ELISA) or an enzyme linked
5 immunospot (ELISpot) assay.

It is to be understood that different applications of the disclosed products and methods may be tailored to the specific needs in the art. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments of the
10 invention only, and is not intended to be limiting.

In addition, as used in this specification and the appended claims, the singular forms “a”, “an”, and “the” include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to “a peptide” includes “peptides”, reference to “a nanoparticle” includes two or more such nanoparticles, and the like.

15 All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

Further embodiments of the invention

1. An isolated oligopeptide or peptide in a pharmaceutical composition comprising at least one peptide having an amino acid sequence selected from the group consisting
5 of SEQ ID NO: 1 to 11, said oligopeptide or peptide consisting of 8 to about 30 amino acid residues, wherein said oligopeptide or peptide binds to class I MHC molecules or can be processed to bind to class I MHC molecules and activate T lymphocyte response and wherein the oligopeptide or peptide is in the form of a pharmaceutically acceptable salt.
10
2. The oligopeptide of item 1 wherein said oligopeptide comprises at least two epitopic peptides.
3. The oligopeptide of item 1 wherein said oligopeptide comprises at least three
15 epitopic peptides.
4. The oligopeptide of item 1 wherein said oligopeptide comprises at least four epitopic peptides.
- 20 5. The oligopeptide or peptide of item 1 wherein said oligopeptide or peptide differs from SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 wherein said difference is no more than one amino acid unit.
6. The oligopeptide or peptide of item 5 wherein said one amino acid difference is
25 the result of a conservative amino acid substitution.
7. The oligopeptide or peptide of item 5 wherein said one amino acid difference is the substitution of one hydrophobic amino acid with another hydrophobic amino acid.
30
8. The oligopeptide or peptide of item 5 wherein said amino acid difference is the addition or deletion of one amino acid to or from said epitopic peptide.

9. A polynucleotide in a pharmaceutical composition comprising a polynucleotide selected from the group consisting of: (a) a polynucleotide that encodes an oligopeptide or peptide of item 1, and (b) the full complement of (a) wherein the polynucleotide is in a form of a pharmaceutically acceptable salt.
- 5
10. The polynucleotide of item 9 wherein the polynucleotide of (a) is DNA.
11. The polynucleotide of item 9 wherein the polynucleotide of (a) is RNA.
- 10 12. A method for vaccinating and treating a subject for Zika virus or Dengue virus infection, said infected cells expressing any class I MHC molecule, comprising administering to said subject a composition that binds to class I MHC molecules or can be processed to bind to class I MHC molecules comprising: at least one polypeptide comprising an epitopic peptide comprising an amino acid sequence
- 15 selected from the group consisting of SEQ ID NO: 1 to 11 in an amount sufficient to induce a CTL response to said infected cells and in a form of a pharmaceutically acceptable salt; or at least one polypeptide comprising an epitopic peptide having at least one amino acid difference from an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 in an amount sufficient to induce a CTL
- 20 response to said infected cells and in a form of a pharmaceutically acceptable salt.
13. A method for vaccinating and treating a subject with Zika virus or Dengue virus infection, said infected cells expressing any class I MHC molecule, said method comprising administering to said subject a composition that binds to class I MHC
- 25 molecules or can be processed to bind to class I MHC molecules comprising: a polynucleotide comprising a nucleic acid sequence encoding at least one polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 in an amount sufficient to induce a CTL response to said infected cells and in a form of a pharmaceutically acceptable salt; or at least one
- 30 polypeptide comprising an epitopic peptide comprising one amino acid difference from an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 in an amount sufficient to induce a CTL response to said infected cells and in a form of a pharmaceutically acceptable salt.

14. A method for generating an immune response ex vivo using T cells from a subject infected with Zika virus or Dengue virus, said method comprising: stimulating the production of CTL response for use in passive immunotherapy, wherein said T cells
5 react with at least one polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 and in a form of a pharmaceutically acceptable salt; or at least one polypeptide comprising one amino acid difference from an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 and in a form of a pharmaceutically acceptable salt.
10
15. The method of item 14, wherein said T cell adoptive therapy generated from autologous or HLA matched subjects.
16. A method for assessing or diagnosing an immune response in a subject infected
15 with Zika virus or Dengue virus or vaccinated for Zika virus or Dengue virus and related viruses said method comprising: stimulating the production of CTL response, wherein said T cells react with at least one polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 and in a form of a pharmaceutically acceptable salt; or at least one polypeptide
20 comprising one amino acid difference from an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to 11 and in a form of a pharmaceutically acceptable salt.
17. A method for vaccinating humans against Zika virus or Dengue virus infection
25 using SEQ IDs 1 to 11 in a form of a pharmaceutically acceptable salt.

The following Examples illustrate the invention.

Example 1

5

ZIKV is a RNA virus transmitted to humans by Aedes mosquitoes. Until recently, it was thought to be relatively harmless with only 20% of infections resulting in mild, short-lived symptoms such as rash headache and conjunctivitis. Recent reports linking the current South American ZIKV outbreak to an increase in the number of microencephalic babies born in Brazil and Guillain-Barre syndrome cases in El Salvador has prompted a reassessment. The severity of these conditions increase drug industry interest in vaccine development. Efforts could focus on modification of vaccines for related diseases. The ZIKV virus is closely related to Dengue. ZIKV virus is a member of the Flaviviridae family, which includes dengue fever yellow fever, Japanese encephalitis, tick-borne encephalitis, and West Nile viruses. Presently there is no vaccine or specific treatment for ZIKV.

Human ZIKV-virus infection occurs when a blood-feeding female Aedes mosquito deposits the virus into human skin and the blood stream. Both human epidermal keratinocytes and dermal fibroblasts are permission to ZIKV virus infection The expression of pathogen recognition receptor (PRR)s, toll-like receptor (TLR), RIG-1 and MDA-5, which subsequently trigger the expression of type 1-IFNs, IFN stimulated genes, including OAS2, ISG-15 and MX-1, and inflammatory cytokines are upregulated by infection of dermal fibroblasts with ZIKV virus. Type 1- and 2-IFNs are known to be important for control of other flaviviruses infections. Both types of IFNs inhibit replication of ZIKV virus in human fibroblasts. The role of these cytokines in host- defense mechanisms is further confirmed in murine model, in which mice deficient in the type 1- IFN receptor (A129) or type 1- and type 2-IFN receptors (AG129) are highly susceptible to ZIKV virus infection, with viremia and age-dependent mortality. Serological analysis of patients with ZIKV virus disease demonstrated both anti-ZIKV-virus IgG and IgM and neutralizing antibodies, which were demonstrated to provide partial protection in infant and adult mice against lethal ZIKV virus infection. Neutralizing antibodies provide partial protection, whereas type 1- and type 2-IFNs are important in controlling ZIKV virus infection (1). Transmission of ZIKV virus in humans is demonstrated via blood

transfusion, sexual intercourse and perinatal transmission from mother to fetus at the time of delivery, in addition to the mosquito transmission. Thus, identifying immune factors that lead to viral clearance in periphery will provide significant visions into the development of immunotherapy and vaccines against the ZIKV virus infection (2).

5 The advantage of ZIKV vaccine programs is that they can use similar mosquito-based diseases, part of a family called flaviviruses, like dengue, West Nile virus, and chikungunya as a “jumping off” point. While researchers are currently trying to learn more about the basics of the ZIKV virus and its effects on the human body given how new the disease is, they can already use past vaccine development platforms from other flaviviruses
10 as a foundation since they spread in similar ways. NIAID is actively pursuing multiple vaccine candidates to prevent ZIKV virus infection, including: a DNA-based vaccine, similar to a strategy used for West Nile virus, which has been found safe and effective in a phase one trial. It is also working on a more traditional live virus-vaccine, similar to those already developed to prevent dengue, an investigational ZIKV vaccine that uses a
15 genetically engineered version of vesicular stomatitis virus, an animal virus that primarily affects cattle, and a whole-particle inactivated ZIKV vaccine based on a similar vaccine approach used by the Walter Reed Army Institute of Research (WRAIR) to develop vaccines against the related Japanese Encephalitis and dengue viruses. It is possible that an investigational ZIKV vaccine will be ready to enter early-stage human trials in the fall of
20 2016. An early-stage trial would examine whether an experimental vaccine is safe and generates immune responses in vaccinated volunteers. A safe and effective, fully licensed ZIKV vaccine will likely not be available for several years.

 The ZIKV epidemic is primarily a fetal-maternal issue (3), given the lasting impact of congenital Zika syndrome on the health of a population. Evidence has confirmed a link
25 between ZIKV infections in viruspregnant mothers and birth defects (i.e. microcephaly, intracranial lesions, vision problems, hearing loss) (4, 5). It is also now proposed that in 20% of cases maternal ZIKV can lead to some form of neurologic damage to the fetus. In order to have an effective vaccination regime to combat the main fetal related pathological features of the ZIKV outbreak, a vaccine that is able to vaccinate both the mother and the
30 fetus simultaneously is required. Most current vaccine technologies are not suited to in utero vaccination (6-15). Antibody vaccines are not suited since antibodies cannot cross the placenta until late pregnancy so ZIKV related pathology that occurs in the fetus in 1st/2nd trimester will not be diminished by maternal antibodies. A vaccine that promotes

a T-cell response in the mother cannot protect the fetus, since maternal CD8⁺ CTL cells are destroyed by the placenta via the HLA-G system (11, 12). Any fetal or maternal microchimerism is also suppressed by fetal T regs (13). An attenuated live virus would be able to pass to the fetus and provoke an immune response (the fetus is immunologically competent - 10 weeks), but it may not be appropriate from a safety perspective to expose the fetus to live virus (6-15). Furthermore, there will always be a brief viremia phase (no vaccine is considered complete) even if the mother is pre-immunized against ZIKV, meaning the fetus will always be at risk of infection. A purely synthetic vaccine that is capable of generating a T cell immune response that eliminates the infected cells in the mother and reduces the prolonged viremia and more importantly, vaccinate the fetus, would have the potential to reduce the birth defects in the fetus. A vaccine of this nature has some important qualities that make it compatible with in utero vaccination.

Preliminary data supporting the technical approach

Our approach to T-cell epitope discovery is based on the premise that the immune system can mount an effective response to specific antigens expressed on diseased, but not healthy cells. The immunoproteomics methodology directly isolates MHC-associated peptides from infected cells and identifies epitopes (authentic T cell targets) as they are presented on the surface of the diseased cell. Using this technical approach, we have identified T-cell epitopes from, ZIKV, Dengue, HBV-, and influenza-virus-infected cells as well as various cancer indications.

ZIKV epitopes identified from ZIKV-infected cells by immunoproteomics analysis

For our initial discovery phase, we used HLA-A2 and A24 positive HepG2 cells for infection. ZIKV was acquired from ATCC (ATCC #1839) and propagated through infection of Vero cells for 72 hours. At 72 hours post infection (hpi) the viral titers from the supernatant was characterized by plaque assay. HepG2 cells were infected at a MOI of 0.1 for 72 hours. The infected HepG2 cells were harvested and assessed for infectivity by permeabilizing and staining with anti-flavivirus group antigen (anti-4G2 MAb; MAB10216, Millipore) antibody and analyzed by flow cytometry. The infected cells were processed further for immunoproteomics analysis as described elsewhere (16-18). Briefly, cell lysates were prepared from the infected cells and MHC/peptide complexes were isolated by immunoprecipitation using a pan MHC class I antibody, W632. Then, peptides

associated with the MHC molecules were isolated and purified using analytical methods. The purified peptide mixture was fractionated using an offline HPLC and the fractions were analyzed by data dependent nano LC-MS/MS experiments on an Velos LTQ-Orbitrap mass spectrometer (Thermo Fisher) interfaced with a nano ultimate HPLC (Dionex). MHC peptides and their sequences were identified by searching the LC-MS/MS raw data against ZIKV genome databases using proteome discoverer software (v 1.3) with Sequest search algorithm (Thermo). In addition, the data was searched against other flaviviruses, dengue and chikungunya genome databases. Immunoproteomics analysis of ZIKV infected cells resulted in identification of several T cell epitopes (Table 4). Most of the epitopes were HLA-A2 or A2/A24 dual HLA binding epitopes, as we have seen in our dengue vaccine studies (16). In addition, we identified B7 and B44 binding epitopes from various ZIKV proteins. Most importantly, we identified 4 epitopes that are conserved across ZIKV and dengue virus. These epitopes were derived from the conserved regions of the viral genome, which may be responsible for survival in the host mosquito. These epitopes were further confirmed by synthetic peptide co-elution experiments (Fig. 1- WVT peptide (Table 4) spectra obtained from experimental and synthetic peptide mass spec analysis).

Table 4: T cell epitopes identified from ZIKV infected cells

Seq ID	Peptide sequence	HLA motif	Protein ID	Virus Specificity
Seq ID 1	IHAVVSSAIL	A2	NS4B	ZIKV
Seq ID 2	PMAAVGLLIVS	A2/A24	NS2B	ZIKV
Seq ID 3	IMLLGLLGTV	A2	NS4	ZIKV
Seq ID 4	ALGLTAVRLVDPI	A2/A24	E protein, transmembrane	ZIKV
Seq ID 5	DESRKVEVTPNSPR	B44	Envelope glycoprotein	ZIKV
Seq ID 6	DPAVIGTAVK	B7	NS1	ZIKV

Seq ID 7	WPPSEVLTA VG	B7	NS2	ZIKV
Seq ID 8	VILAGPMPVT	A2	Serine protease NS3	ZIKV, Dengue
Seq ID 9	AILEENG VQ	A2	NS4B	ZIKV, Dengue
SeqID 10	SPRRLAAAV	B7	NS1	ZIKV, Dengue
Seq ID 11	WVTDHSGKTV	A2	HELICc	ZIKV, Dengue, West Nile

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CLAIMS

1. A vaccine composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof.
- 5 2. The vaccine composition of claim 1, wherein the flavivirus peptide is attached to a nanoparticle.
3. The vaccine composition of claim 2, wherein the nanoparticle is a gold
- 10 nanoparticle, a calcium phosphate nanoparticle, or a silicon nanoparticle.
4. The vaccine composition of claim 3, wherein the gold nanoparticle is coated with alpha-galactose and/or beta-GlcNHAc.
- 15 5. The vaccine composition of any one of claim 2s to 4, wherein the flavivirus peptide is attached to the nanoparticle via a linker.
6. The vaccine composition of any one of the preceding claims, which comprises two or more flavivirus peptides each comprising a different CD8+ T cell epitope.
- 20 7. The vaccine composition of claim 6, wherein each of the two or more flavivirus peptides comprises a CD8+ T cell epitope set out in SEQ ID NOs: 1 to 11 or a variant thereof.
- 25 8. The vaccine composition of claim 6 or 7, wherein each of the two or more flavivirus peptides is attached to a nanoparticle.
9. The vaccine composition of any one of the preceding claims, comprising at least two flavivirus peptides comprising a CD8+ T cell epitope, each of which interacts with a
- 30 different HLA supertype.
10. The vaccine composition of any one of the preceding claims, which comprises at

least one flavivirus peptide comprising a CD8+ T cell epitope that interacts with at least two different HLA supertypes.

11. The vaccine composition of claim 9 or 10, wherein the at least two different HLA
5 supertypes are selected from HLA-A1, HLA-A2, HLA-A3, HLA-A24, HLA-B7, HLA-B8, HLA-B27, HLA-B44, HLA-B58 and HLA-B62.

12. The vaccine composition of claim 11, wherein the at least two different HLA
10 supertypes are HLA-A2 and HLA-A24.

13. The vaccine composition of any one of the preceding claims, wherein the CD8+ T
cell epitope is conserved between flaviviruses.

14. The vaccine composition of any one of the preceding claims, wherein the CD8+ T
15 cell epitope is conserved between Zika viruses, West Nile viruses and/or Dengue viruses.

15. The vaccine composition of any one of the preceding claims, comprising a peptide
comprising a CD4+ T cell epitope.

20 16. The vaccine composition of claim 15, wherein the CD4+ T cell epitopes interacts with all HLA class II types.

17. The vaccine composition of claim 15 or 16, wherein the CD4+ T cell epitope
comprises the sequence set out in SEQ ID NO: 12 or 13.

25 18. A vaccine composition comprising (a) a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, or (b) the full complement of a polynucleotide that encodes a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID
30 NOs: 1 to 11 or a variant thereof.

19. The vaccine composition of any one of the preceding claims, wherein the variant differs from one of SEQ ID NOs: 1 to 11 by insertion, deletion or substitution of no more than one amino acid.
- 5 20. The vaccine composition of claim 19, wherein the variant differs from one of SEQ ID NOs: 1 to 11 by the conservative substitution of no more than one amino acid.
21. A method of preventing or treating a flavivirus infection, comprising administering the vaccine composition of any one of the preceding claims to a subject infected with, or at
10 risk of being infected with, a flavivirus.
22. The vaccine composition of any one of claims 1 to 17 for use in a method of preventing or treating a flavivirus infection in a subject.
- 15 23. A method of preventing or treating a flavivirus infection in a subject, comprising (i) stimulating cytotoxic T lymphocytes (CTLs) obtained from a Zika virus- or Dengue virus- infected individual with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and (ii) providing the stimulated CTLs as passive immunotherapy to the subject.
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24. A composition for use in a method of preventing or treating a flavivirus infection in a subject, the composition comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to 11 or a variant thereof, and the method comprising (i) stimulating CTLs obtained from a Zika virus- or Dengue virus- infected individual with the composition and
25 (ii) providing the stimulated CTLs as passive immunotherapy to the subject.
25. The method of claim 23 or composition for use of claim 24, wherein the CTLs are autologous to or HLA matched with the subject.
- 30 26. A method of diagnosing a flavivirus infection in a subject, the method comprising (i) contacting CTLs obtained from the subject with a composition comprising a flavivirus peptide comprising one or more of the CD8+ T cell epitopes set out in SEQ ID NOs: 1 to

11 or a variant thereof, and (ii) detecting the presence or absence of a CTL response to the one or more CD8⁺ T cell epitopes.

27. The method of claim 23, 25 or 26, or composition for use of claim 24 or 25,
5 wherein the variant differs from one of SEQ ID NOs: 1 to 11 by insertion, deletion or substitution of no more than one amino acid.

28. The method or composition for use of claim 27, wherein the variant differs from one of SEQ ID NOs: 1 to 11 by the conservative substitution of no more than one amino
10 acid.

29. The method of claim 21, 23 or 25 to 27, or the composition for use of claim 22 or 24 to 27, wherein the flavivirus infection is a Zika virus infection, West Nile virus
15 infection and/or Dengue virus infection.

30. The method or composition for use of claim 29, wherein:

(a) the Zika virus infection is an African Zika virus or an Asian Zika virus
20 infection; and/or

(b) the Dengue virus infection is a Dengue virus 1, Dengue virus 2, Dengue virus 3, or Dengue virus 4 infection.