CLAIMS

1. A method of identifying a flavivirus infection selected from Zika virus (ZIKV), dengue virus (DENV) and combination thereof in a subject, the method comprising:

determining whether a sample of the subject reacts with a peptide *P* that is capable of giving a relative binding capacity $BC_{relative} \leq 0.05$ or ≥ 0.1, wherein

$$BC_{relative} = \frac{R_{P1z} - R_{P2z}}{R_{P2z}} - \frac{R_{P1d} - R_{P2d}}{R_{P2d}}$$

(i) wherein where the peptide *P* comprises a ZIKV-derived peptide,

R_{P1z} = response of a ZIKV-induced antigen binding protein with peptide *P,*

R_{P2z} = response of the ZIKV-induced antigen binding protein with a corresponding peptide *C* comprising a DENV-derived peptide having a sequence homologous to the peptide *P*,

R_{P1d} = response of a DENV-induced antigen binding protein with the peptide *P,*

R_{P2d} = response of the DENV-induced antigen binding protein with the corresponding peptide *C* comprising a DENV-derived peptide having a sequence homologous to the peptide *P*,

$\frac{R_{P1z}-R_{P2z}}{R_{P2z}}$ = binding capacity of the ZIKV-induced antigen binding protein,

$\frac{R_{P1d}-R_{P2d}}{R_{P2d}}$ = binding capacity of the DENV-induced antigen binding protein,

or

(ii) wherein where the peptide *P* comprises a DENV-derived peptide,

R_{P1z} = response of a ZIKV-induced antigen binding protein with a corresponding peptide *C* comprising a ZIKV-derived peptide having a sequence homologous to the peptide *P*,

R_{P2z} = response of the ZIKV-induced antigen binding protein with the peptide *P*,

R_{P1d} = response of a DENV-induced antigen binding protein with the corresponding peptide *C* comprising a ZIKV-derived peptide having a sequence homologous to the peptide *P*,

R_{P2d} = response of the DENV-induced antigen binding protein with the peptide *P,*

$\frac{R_{P1z}-R_{P2z}}{R_{P2z}}$ = binding capacity of the ZIKV-induced antigen binding protein,

$\frac{R_{P1d}-R_{P2d}}{R_{P2d}}$ = binding capacity of the DENV-induced antigen binding protein,

wherein the response is a measure of a binding activity between the antigen-binding protein and the peptide as measured by an immunoassay,

wherein the sample is a fluid biological sample comprising antigen binding proteins, and

wherein the method distinguishes a flavivirus infection from other infections in the subject when the method determines the sample of the subject reacts with the peptide that is capable of giving a relative binding capacity $BC_{relative}$ ≤ 0.05, and/or

wherein the method distinguishes ZIKV and/or DENV infection from other flavivirus infection in the subject when the method determines the sample of the subject reacts with the peptide that is capable of giving a relative binding capacity $BC_{relative}$ ≤ 0.05, and/or

wherein the method distinguishes ZIKV infection from DENV infection, and/or DENV infection from ZIKV infection in the subject when the method determines the sample of the subject reacts with the peptide that is capable of giving a relative binding capacity $BC_{relative}$ ≥ 0.1.

2. The method of claim 1, wherein the peptide *P* comprises an epitope on a prM protein, an E glycoprotein or a NS1 protein of ZIKV or DENV.

3. The method of claim 2, wherein the epitope is located in a solvent-exposed region of the prM protein, the E glycoprotein or the NS1 protein.

4. The method of any one of the preceding claims, wherein the peptide *P* is from 10 to 25 amino acids long.

5. The method of any one of the preceding claims, wherein the peptide *P* shares no more than 75% sequence similarity with the corresponding peptide *C*.

6. The method of any one of the preceding claims, wherein the peptide *P* comprises

one or more ZIKV-derived peptide selected from the group consisting of:
SEQ ID NO: 7 (LDEGVEPDDVDCWCNTT);
SEQ ID NO: 36 (SVEGELNAILEENGVQ);
SEQ ID NO: 38 (GKSYFVRAAKTNNSFVVD);
SEQ ID NO: 39 (GDTLKECPLKHRAWNSFL);
SEQ ID NO: 46 (KVHVEETCGTRGPSLRST);
SEQ ID NO: 49 (ECTMPPLSFRAK);
SEQ ID NO: 3 (SFPTTLGMNKCYIQIMDL);
SEQ ID NO: 26 (GALEAEMDGAKGRLSSGH);
SEQ ID NO: 32 (FKSLFGGMSWFSQILIGT);
SEQ ID NO: 9 (YGTCHHKKGEARRSR);
SEQ ID NO: 17 (PENLEYRIMLSVHGSQHS);
SEQ ID NO: 45 (IRFEECPGTKVHVEETCG);
a peptide sharing at least 85% sequence identity thereto; or
a peptide differing by one or two amino acids thereto; and/or
one or more DENV-derived peptide selected from the group consisting of:
SEQ ID NO: 58 (HITEVEPEDIDCWCNLT);
SEQ ID NO: 87 (QIANELNYILWENNIK);
SEQ ID NO: 89 (GKAKIVTAETQNSSFIID);
SEQ ID NO: 90 (GPNTPECPSASRAWNVWE);
SEQ ID NO: 97 (TVVITENCGTRGPSLRTT);

SEQ ID NO: 100 (SCTLPPLRYMGE);
SEQ ID NO: 54 (LFKTASGINMCTLIAMDL);
SEQ ID NO: 77 (GATEIQNSGGTSIFAGH);
SEQ ID NO: 83 (YTALFSGVSWVMKIGIGV);
SEQ ID NO: 60 (TSTWVTYGTCNQAG);
SEQ ID NO: 68 (YENLKYTVIITVHTGDQH);
SEQ ID NO: 94 (RPGYHTQTAGPWHLGKLE);
SEQ ID NO: 96 (LDFNYCEGTTVVITENCG); or
a peptide sharing at least 85% sequence identity thereto; or
a peptide differing by one or two amino acids thereto.

7. The method of any one of the preceding claims, wherein the method comprises determining whether the sample reacts with one or more peptide selected from the group consisting of:

SEQ ID NO: 7 (LDEGVEPDDVDCWCNTT);
SEQ ID NO: 36 (SVEGELNAILEENGVQ);
SEQ ID NO: 38 (GKSYFVRAAKTNNSFVVD);
SEQ ID NO: 39 (GDTLKECPLKHRAWNSFL);
SEQ ID NO: 46 (KVHVEETCGTRGPSLRST);
SEQ ID NO: 49 (ECTMPPLSFRAK);
SEQ ID NO: 58 (HITEVEPEDIDCWCNLT);
SEQ ID NO: 87 (QIANELNYILWENNIK);
SEQ ID NO: 89 (GKAKIVTAETQNSSFIID);
SEQ ID NO: 90 (GPNTPECPSASRAWNVWE);
SEQ ID NO: 97 (TVVITENCGTRGPSLRTT);
SEQ ID NO: 100 (SCTLPPLRYMGE);
a peptide sharing at least 85% sequence identity thereto; or
a peptide differing by one or two amino acids thereto;; and/or

wherein where the sample reacts with the one or more peptide, the subject is indicated for flavivirus infection.

8. The method of any one of the preceding claims, wherein the method is a method of identifying a flavivirus infection in an acute phase, and the method comprises determining whether the sample reacts with one or more peptide selected from the group consisting of:

SEQ ID NO: 7 (LDEGVEPDDVDCWCNTT);

SEQ ID NO: 36 (SVEGELNAILEENGVQ);

SEQ ID NO: 38 (GKSYFVRAAKTNNSFVVD);

SEQ ID NO: 58 (HITEVEPEDIDCWCNLT);

SEQ ID NO: 87 (QIANELNYILWENNIK);

SEQ ID NO: 89 (GKAKIVTAETQNSSFIID);

wherein where the sample reacts with the one or more peptide, the subject is indicated for flavivirus infection in an acute phase.

9. The method of any one of the preceding claims, wherein the method comprises determining whether the sample reacts with one or more peptide selected from the group consisting of:

SEQ ID NO: 3 (SFPTTLGMNKCYIQIMDL);

SEQ ID NO: 26 (GALEAEMDGAKGRLSSGH);

SEQ ID NO: 32 (FKSLFGGMSWFSQILIGT);

a peptide sharing at least 85% sequence identity thereto; or

a peptide differing by one or two amino acids thereto;

wherein where the sample reacts with the one or more peptide, the subject is indicated for ZIKV infection.

10. The method of any one of the preceding claims, wherein the method is a method of identifying a ZIKV infection in an acute phase, and the method comprises determining whether the sample reacts with:

SEQ ID NO: 32 (FKSLFGGMSWFSQILIGT);

a peptide sharing at least 85% sequence identity thereto; or

a peptide differing by one or two amino acids thereto;

wherein where the sample reacts with the peptide, the subject is indicated for ZIKV infection in an acute phase.

11. The method of any one of the preceding claims, wherein the method comprises determining whether the sample reacts with one or more peptide selected from the group consisting of:

SEQ ID NO: 60 (TSTWVTYGTCNQAG);

SEQ ID NO: 68 (YENLKYTVIITVHTGDQH);

SEQ ID NO: 94 (RPGYHTQTAGPWHLGKLE);

SEQ ID NO: 96 (LDFNYCEGTTVVITENCG); and/or

a peptide sharing at least 85% sequence identity thereto; or

a peptide differing by one or two amino acids thereto;

wherein where the sample reacts with the one or more peptide, the subject is indicated for DENV infection.

12. The method of any one of the preceding claims, wherein determining whether the sample reacts with the peptide *P* comprises performing an immunoassay to assess whether antigen-binding proteins that are capable of binding to the peptide are present in the sample.

13. The method of any one of the preceding claims, wherein the sample is a blood, a serum and/or a plasma sample.

14. The method of any one of the preceding claims, wherein the subject comprises an Asian subject.

15. The method of claim 1, wherein said method further distinguishes ZIKV infection from DENV infection in the subject, the method comprising:

determining whether a sample of the subject reacts with a peptide of SEQ ID NO: 32 (FKSLFGGMSWFSQILIGT); a peptide sharing at least 85% sequence identity thereto; or a peptide differing by one or two amino acids thereto; wherein where the sample reacts with the peptide, the subject is indicated for ZIKV infection; and/or

determining whether a sample of the subject reacts with a peptide of SEQ ID NO: 9 (YGTCHHKKGEARRSR); a peptide sharing at least 85% sequence identity thereto; or a peptide differing by one or two amino acids thereto; wherein where the sample reacts with the peptide, the subject is indicated for DENV infection.