CLAIMS

1. A vaccine composition comprising an immunogenic peptide comprising a CD8+ T cell epitope from a polypeptide encoded by an open reading frame (ORF) encoded by at least part of the genome of a ssRNA virus in the opposite sense to positive sense RNA capable of translation.

2. The vaccine composition of claim 1, which comprises two or more immunogenic peptides.

3. The vaccine composition of claim 2, which comprises two or more immunogenic peptides each comprising a different CD8+ T cell epitope from a polypeptide encoded by an open reading frame (ORF) encoded by at least part of the genome of a ssRNA virus in the opposite sense to positive sense RNA capable of translation.

4. The vaccine composition of any one of the preceding claims, which comprises at least one immunogenic peptide that interacts with at least two different HLA supertypes.

5. The vaccine composition of any one of the preceding claims, wherein the polypeptide enhances the fitness of the ssRNA virus in humans.

6. The vaccine composition of any one of the preceding claims, wherein the ssRNA virus is a negative sense ssRNA virus and the ORF is negative sense.

7. The vaccine composition of claim 6, wherein the negative sense ssRNA virus is an Orthomyxovirus.

8. The vaccine composition of claim 7, wherein the Orthomyxovirus is an influenza virus.

9. The vaccine composition of claim 8, wherein the influenza virus is an influenza A virus.

10. The vaccine composition of claim 9, wherein the ORF is encoded by at least part of segment 8 of the genome of the influenza A virus.

11. The vaccine composition of claim 10, wherein the ORF is at least 85 codons in length.

12. The vaccine composition of claim 10 or 11, wherein the ORF is at least 167 codons in length.

13. The vaccine composition of any one of claim 10 to 12, wherein the ORF is at least 216 codons in length.

14. The vaccine composition of claim 12 or 13, wherein the influenza A virus is a Spanish flu virus or a reconstructed Spanish flu virus.

15. The vaccine composition of claim 14, wherein the ORF comprises the sequence of SEQ ID NO. 56 or a variant thereof, or the sequence of SEQ ID NO: 57 or a variant thereof.

16. The vaccine composition of any one of claims 9 to 15, wherein the CD8+ T cell epitope is conserved between human influenza A viruses.

17. The vaccine composition of any one of claims 9 to 16, wherein the CD8+ T cell epitope is conserved between human influenza A viruses and a swine, equine and/or avian influenza A virus.

18. The vaccine composition of any one of claims 9 to 17, wherein the CD8+ T cell epitope is present in a predicted ORF of at least 85, at least 167 or at least 216 codons in length in a swine, equine and/or avian influenza A virus.

19. The vaccine composition of claim 17 or 18, wherein the swine influenza A virus is of serotype H1N1.

20. The vaccine composition of any one of the preceding claims, comprising one or more of the peptides set out in SEQ ID NOs: 16 to 53.

21. The vaccine composition of any one of claims 1 to 6, wherein the ssRNA virus is a filovirus.

22. The vaccine composition of claim 21, wherein the filovirus virus is an ebolavirus or a marburgvirus.

23. The vaccine composition of any one of claims 1 to 5, wherein the ssRNA virus is a positive sense ssRNA virus and the ORF is negative sense.

24. The vaccine composition of claim 23, wherein the ssRNA virus is a flavivirus.

25. The vaccine composition of claim 24, wherein the flavivirus virus is a Dengue virus or a Zika virus.

26. A method preventing or treating a viral infection, comprising administering the vaccine composition of any one of the preceding claims to an individual infected with, or at risk of being infected with, an ssRNA virus.

27. The vaccine composition of any one of claims 1 to 25 for use in a method of preventing or treating a viral infection in an individual.

28. The method of claim 26 or vaccine composition for use according to claim 27, wherein the viral infection is caused by a zoonotic virus.

29. The method of claim 26 or 28 or vaccine composition for use according to claim 27 or 28, wherein the individual is human.

30. The method of claim 26 or vaccine composition for use according to claim 27, wherein the viral infection is a pandemic viral infection.

31. A method of identifying an immunogenic peptide comprising a CD8+ T cell epitope from an ORF encoded by at least part of the genome of a ssRNA virus in the opposite sense to positive sense RNA capable of translation by:

(a) identifying an ORF encoded by at least part of the genome of a ssRNA virus in the opposite sense to positive sense RNA capable of translation;

(b) predicting the sequence of the polypeptide encoded by the ORF; and

(c) assessing whether a peptide that binds a MHC Class I molecule comprises a sequence present in the predicted sequence,

thereby identifying an immunogenic peptide comprising a CD8+ T cell epitope.

32. The method of claim 31, wherein the ORF comprises a stop codon, the predicted sequence is predicted on the basis that the stop codon is mutated to a codon encoding an amino acid and the peptide comprises a sequence present in a part of the predicted sequence that is C-terminal to the mutated codon.

33. The method of claim 31 or 32, further comprising:

(d) contacting CD8+ T cells obtained from an individual infected with, or previously infected with, the ssRNA virus with the peptide; and

(e) measuring *in vitro* the immune response to the peptide.

34. The method of claim 33, wherein the immune response is measured *in vitro* by determining interferon gamma (IFNy) production.

35. An immunogenic peptide comprising a CD4+ T cell epitope or a B cell epitope from a polypeptide encoded by an ORF encoded by at least part of the genome of a ssRNA virus in the opposite sense to positive sense RNA capable of translation.

36. A method of determining the pandemic potential of an influenza A virus, the method comprising the steps of:

(i) identifying a first ORF encoded by at least part of segment 8 of the genome of the influenza A virus in the opposite sense to positive sense RNA capable of translation;

(ii) determining the number of codons comprised in the first ORF; and

(iii) comparing the number of codons comprised in the first ORF to the number of codons comprised in a second ORF encoded by at least part of segment 8 of the genome of a known pandemic influenza A virus in the opposite sense to positive sense RNA capable of translation,

wherein a difference in the number of codons in the first ORF compared to the second ORF is indicative of pandemic potential.