CLAIMS:

1. A modified haemagglutinin (HA) protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof is modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype.

2. The modified HA protein of Claim 1, wherein an influenza virus expressing the modified HA protein is capable of growth in cells.

3. The modified HA protein of Claim 1 or Claim 2, which is capable of forming a HA trimer when expressed by an influenza virus grown in cells.

4. The modified HA protein of any one of the preceding claims, wherein the modifications to the one or more amino acid residues of the trimer interface region increases the stability of a HA trimer formed from the modified HA protein relative to a HA trimer formed from a corresponding unmodified HA protein.

5. The modified HA protein of any one of the preceding claims, wherein the modified HA protein is of a H2, H1, H5, H3, H7 or H9 subtype.

6. The modified HA protein of any one of Claims 1 to 4, wherein the modified HA protein is of a H2, H1, or H5 subtype.

7. The modified HA protein of any one of Claims 1 to 4, wherein the modified HA protein is of a H2 subtype.

8. The modified HA protein of Claim 7, wherein the one or more amino acid residues that are modified are selected from the group consisting of V39, L219, V233, V320, K383, I388, N390, K391, V392, S394, A405, R416, D430, F450, and any combination thereof, of a full length H2 amino acid sequence.

9. The modified HA protein of Claim 8, wherein the modifications to the one or more amino acid residues are selected from the group consisting of V39I, L219P, V233A, V320A, V320I, K383E, I388T, N390I, K391R, K391N, V392A, S394Y, A405T, R416G, D430N, F450S and any combination thereof, of a full length H2 amino acid sequence.

10. The modified HA protein of any one of the preceding claims, wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 383 to 394, 439 to 452, 31 to 40 and optionally 325 to 335 of a full length HA protein of a H2 subtype.

11. The modified HA protein of any one of the preceding claims, wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues N26 to D46, L325 to P335, D377 to E397 and L439 to D452 of a full length HA protein of a H2 subtype.

12. The modified HA protein of Claim 11, wherein the lower region of the stalk domain comprises amino acid residues N26 to D46, D377 to E397 and L439 to D452 of a full length HA protein of a H2 subtype.

13. The modified HA protein of any one of the preceding claims, comprising, consisting of or consisting essentially of the amino acid sequence as set forth in any one of SEQ ID NOs: 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66 or 68, or a fragment, variant or derivative thereof.

14. An isolated nucleic acid comprising a nucleotide sequence encoding a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof is modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype.

15. The isolated nucleic acid of Claim 14, wherein an influenza virus expressing the modified HA protein is capable of growth in cells, or a nucleotide sequence complementary thereto.

16. The isolated nucleic acid of Claim 14 or Claim 15, comprising, consisting of or consisting essentially of: a nucleotide sequence selected from the group consisting of SEQ ID NQs: 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65 or 67, or a fragment, variant or derivative thereof; or a nucleotide sequence complementary thereto.

17. An isolated influenza virus, comprising a HA viral segment encoding a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof are modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype.

18. The isolated influenza virus of Claim 17, wherein the modified HA protein is of a H2, H1, H5, H3, H7 or H9 subtype.

19. The isolated influenza virus of Claim 17 or Claim 18, wherein the HA viral segment comprises, consists of or consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NQs: 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65 or 67, or a fragment, variant or derivative thereof.

20. A vaccine composition, wherein the vaccine composition comprises:

(a) an isolated influenza virus comprising a HA viral segment encoding a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof are modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype, and a pharmaceutically acceptable carrier, diluent or excipient;

(b) a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof are modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype, and a pharmaceutically acceptable carrier, diluent or excipient; or

(c) an isolated nucleic acid comprising a nucleotide sequence encoding a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof is modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype and a pharmaceutically acceptable carrier, diluent or excipient.

21. Use of: (a) an isolated influenza virus comprising a HA viral segment encoding a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof are modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype; (b) the modified HA protein; (c) an isolated nucleic acid encoding the modified HA protein; or (d) a vaccine composition comprising the isolated influenza virus, the modified HA protein or the isolated nucleic acid encoding the modified HA protein; in the manufacture of a medicament for eliciting an immune response and/or preventing and/or treating an influenza-associated disease, disorder or condition in a subject.

22. A method of improving the growth, stability and/or manufacture of an influenza virus in cells, said method including the step of modifying the influenza virus to express a modified HA protein comprising an amino acid sequence wherein one or more amino acid residues of a trimer interface region thereof is modified, wherein one or more of the modified amino acid residues are present in a lower region of a stalk domain and wherein the lower region of the stalk domain comprises, consists of or consists essentially of amino acid residues at positions 377 to 397, 439 to 452, 26 to 46 and optionally 325 to 335 of a full length HA protein of a H2 subtype.