CLAIMS

1. A modified Secreted Aspartyl Proteinase 2 (Sap2) protein comprising amino acid residues 19-398 of SEQ ID NO: 1 or an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to amino acid residues 19-398 of SEQ ID NO: 1, modified in that the amino acid sequence comprises one or more consensus sequences comprising an amino acid sequence of D/E-X-N-Z-S/T, wherein X and Z are independently any amino acid except proline.

2. The modified Sap2 protein of claim 1, wherein the protein further comprises a substitution at amino acid residue 274 of amino acid residues 19-398 of SEQ ID NO: 1 or at an equivalent position within an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to amino acid residues 19-398 of SEQ ID NO: 1, optionally wherein the protein comprises an Aspartic Acid (D) to Asparagine (N) substitution at amino acid residue 274 of amino acid residues 19-398 of SEQ ID NO: 1 or at an equivalent position within an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to amino acid residues 19-398 of SEQ ID NO: 1.

3. The modified Sap2 protein of any of claim 1 and 2, wherein the modified Sap2 protein is from *Candida albicans*, and wherein the modified Sap2 protein further comprises at least one Fructose biphosphate aldolase-1 (Fba) peptide comprising an amino acid sequence of YGKDVKDLFDYAQE (SEQ ID NO: 3) or an amino acid sequence at least 70%, 80%, 85%, 90%, or 92% identical to SEQ ID NO: 3.

4. The modified Sap2 protein of any of claims 1 to 3, wherein the one or more consensus sequences are selected from the group consisting of DQNAT (SEQ ID NO: 4) and DQNVT (SEQ ID NO: 5), and wherein the modified Sap2 protein comprises at least one additional consensus sequence comprising an amino acid sequence of J-U-B-D/E-X-N-Z-S/T-J-U-B, wherein X and Z are independently any amino acid except proline and J, U and B independently comprise 1 to 5 naturally occurring amino acid residues, wherein the at least one consensus sequence has been added next to C-terminal amino acid residue of SEQ ID NO: 3 or at an equivalent position within an amino acid sequence at least 80%, 85%, 90%, 92%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 3.

5. The modified Sap2 protein of claim 1 comprising an amino acid sequence of SEQ ID NO: 9 or SEQ ID NO: 10.

6. A conjugate comprising the modified Sap2 protein of any of claims 1 to 5 linked to at least one saccharide antigen, optionally wherein the conjugate is a bioconjugate.

7. The conjugate of claim 6, wherein said saccharide antigen is from a Candida species.

8. The conjugate of any of claims 6 or 7, wherein the at least one saccharide antigen comprises a β-1,2 mannan polymer, optionally comprising at least five consecutive β-1,2 linked mannose molecules.

9. A polynucleotide sequence encoding the modified Sap2 protein of any of claims 1 to 5.

10. A vector comprising the polynucleotide sequence of claim 9.

11. An immunogenic composition comprising the modified Sap2 protein of any of claims 1 to 5, the conjugate or the bioconjugate of any of claims 6 to 8.

12. A vaccine comprising the immunogenic composition of claim 11 and, optionally, a pharmaceutically acceptable excipient or carrier.

13. The modified Sap2 protein of any of claims 1 to 5, the conjugate or the bioconjugate of any of claims 6 to 8, the immunogenic composition of claim 11, or the vaccine of claim 12 for use in treatment or prevention of a disease caused by *Candida albicans* infection.

14. A method of producing a bioconjugate as defined in claims 6 to 8 in a prokaryotic host cell, the method comprising the steps of:

    a. obtaining a prokaryotic host cell that produces a β-1,2 mannan polymer; and

    b. further introducing and expressing in the host cell:

i. a nucleotide sequence encoding a modified carrier protein comprising a glycosylation site comprising a consensus sequence D/E-X-N-Z-S/T, wherein X and Z are any amino acid except proline, and wherein the modified carrier protein further comprises an N-terminal bacterial signal sequence capable of transporting the modified carrier protein to the periplasmic side of the inner membrane of the prokaryotic host cell; and

ii. a nucleotide sequence encoding an oligosaccharyl transferase capable of producing a bioconjugate by transferring the β-1,2 mannan polymer from a lipid carrier to the modified carrier protein, wherein the oligosaccharyl transferase is PglB from *Campylobacter*, optionally from *Campylobacter jejuni* or *Campylobacter coli*.

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