WHAT IS CLAIMED:

1. A protein comprising a mutant of a mature glycoprotein E (gE) of varicella-zoster virus (VZV), wherein the mutant comprises:
(a) (i) a truncation of 37 amino acid residues from the C-terminus of the mature gE, and (ii) amino acid residue substitutions Y569A and Y582G, wherein amino acid residue positions 569 and 582 are the amino acid residue position numbers of full length VZV gE;
(b) amino acid residue substitutions Y569A and Y582G, wherein amino acid residue positions 569 and 582 are the amino acid residue position numbers of full length VZV gE;
(c) amino acid residue substitutions Y569A, Y582G, S593A, S595A, T596A, and T598A, wherein amino acid residue positions 569, 582, 593, 595, 596, and 598 are the amino acid residue position numbers of full length VZV gE;
(d) amino acid residue substitutions Y582G, S593A, S595A, T596A, and T598A, wherein amino acid residue positions 582, 593, 595, 596, and 598 are the amino acid residue position numbers of full length VZV gE; or
(e) (i) a truncation of 50 amino acid residues from the C-terminus of the mature gE protein, and (ii) amino acid residue substitution Y569A, wherein amino acid residue position 569 is the amino acid residue position number of full length VZV gE.
2. The protein of claim 1, wherein the mutant comprises or consists of the amino acid sequence of SEQ ID NO: 6, 8, 10, 12, or 3; or wherein the mutant comprises an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NO: 6, 8, 10, or 12.
3. The protein of claim 1 or 2, which further comprises a VZV gE signal peptide; optionally wherein the signal peptide of the VZV gE comprises an amino acid sequence that is at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 18.
4. The protein of claim 1 or 2, which further comprises a heterologous signal peptide, wherein the N-terminal of the mutant is fused to the C-terminal of the heterologous signal peptide;
optionally wherein the heterologous signal peptide is a human IgE signal peptide;
optionally wherein the human IgE signal peptide comprises or consists of: (i) the amino acid sequence set forth in SEQ ID NO: 23, or (ii) an amino acid sequence that is at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 23;
optionally wherein the mutant consists of the amino acid sequence set forth in SEQ ID NO: 6, and the human IgE signal peptide consists of the amino acid sequence set forth in SEQ ID NO: 23; or wherein the protein comprises or consists of the amino acid sequence set forth in SEQ ID NO: 59;
optionally wherein the heterologous signal peptide is a human tPA signal peptide;
optionally wherein the human tPA signal peptide comprises or consists of: (i) the amino acid sequence set forth in SEQ ID NO: 27, or (ii) an amino acid sequence that is at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 27.
5. The protein of any one of claims 1 to 4, wherein the mature gE comprises the amino acid sequence set forth in SEQ ID NO: 1 and/or the full length VZV gE comprises the amino acid sequence set forth in SEQ ID NO: 55.

6. A fragment of a mature glycoprotein E (gE) of varicella-zoster virus (VZV), wherein the fragment comprises a truncation of at least one and at most 50, 49, 48, 47, 46, 45, 44, 43, or 42 amino acid residues from the C-terminal of the mature gE, optionally the truncation is a truncation of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or 49 amino acid residues from the C-terminal of the mature gE, or optionally the truncation is a truncation of 11, 12, 13, 14, 15, 16, 17, 18, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 amino acid residues from the C-terminal of the mature gE, or optionally the truncation is a truncation of 14 or 37 amino acid residues from the C-terminal of the mature gE.
7. The fragment of claim 6, (i) wherein the fragment further comprises the amino acid residue substitution Y569A, and wherein amino acid residue position 569 is the amino acid residue position number according to the full length VZV gE;
(ii) wherein the fragment comprises a truncation of at most 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, or 31 amino acid residues from the C-terminal of the mature gE; optionally wherein the fragment further comprises the amino acid residue substitution Y582G, and wherein amino acid residue position 582 is the amino acid residue position number according to the full length VZV gE protein;
(iii) wherein the fragment comprises a truncation of at most 30 or 29 amino acid residues from the C-terminal of the mature gE; optionally wherein the fragment further comprises the amino acid residue substitution S593A, and wherein amino acid residue position 593 is the amino acid residue position number according to the full length VZV gE;
(iv) wherein the fragment comprises a truncation of at most 28 amino acid residues from the C-terminal of the mature gE; optionally wherein the fragment comprises the amino acid residue substitution S595A, and wherein amino acid residue position 595 is the amino acid residue position number according to the full length VZV gE;
(v) wherein the fragment comprises a truncation of at most 27 or 26 amino acid residues from the C-terminal of the mature gE; optionally wherein the fragment further comprises the amino acid residue substitution T596A, and wherein amino acid residue position 596 is the amino acid residue position number according to the full length VZV gE;
(vi) wherein the fragment comprises a truncation of at most 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 amino acid residues or at most one amino acid residue from the C-terminal of the mature gE; optionally wherein the fragment further comprises the amino acid residue substitution T598A, and wherein amino acid residue position 598 is the amino acid residue position number according to the full length VZV gE; or
(vii) wherein the fragment comprises a truncation of 37 amino acid residues from the C-terminal of the mature gE; optionally wherein the fragment further comprises the amino acid residue substitutions Y569A and Y582G, and wherein amino acid residue positions 569 and 582 are amino acid residue position numbers according to the full length VZV gE.
8. The fragment of claim 6 or 7, wherein the mature gE comprises the amino acid sequence set forth in SEQ ID NO: 1 and/or the full length VZV gE comprises the amino acid sequence set forth in SEQ ID NO: 55; and/or wherein the fragment comprises an amino acid sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity with the amino acid sequence set forth in SEQ ID NO: 6, 3, 8, 10, or 12.
9. A fusion protein comprising the fragment of any one of claims 6 to 8, and a heterologous signal peptide, wherein the N-terminal of the fragment is fused to the C-terminal of the heterologous signal peptide,

optionally, (i) wherein the heterologous signal peptide is a human tPA signal peptide; optionally wherein the human tPA signal peptide comprises the amino acid sequence set forth in SEQ ID NO: 27; or
optionally, (ii) wherein the heterologous signal peptide is a human IgE signal peptide; optionally wherein the human IgE signal peptide comprises the amino acid sequence set forth in SEQ ID NO: 23.

10. A nucleic acid encoding the protein of any of claims 1 to 5, fragment of any one of claims 6 to 8, or the fusion protein of claim 9.
11. The nucleic acid of claim 10, which comprises or consists of (1) a nucleotide sequence set forth in SEQ ID NO: 63, 7, 51, 60, 62, 62, 64, 9, 11, 13, 52, 53, 54, 58, 49, 50, 4, or 5; or (2) a nucleotide sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity with the nucleotide sequence set forth in SEQ ID NO: 63, 7, 51, 60, 62, 62, 64, 9, 11, 13, 52, 53, 54, 58, 49, 50, 4, or 5.
12. A vector comprising the nucleic acid of claim 10 or 11; preferably, wherein the vector is an IVT (*In Vitro* Transcription) plasmid.
13. A host cell comprising the nucleic acid of claim 10 or 11 or the vector of claim 12.
14. A pharmaceutical composition comprising the protein of any of claims 1 to 5, fragment of any one of claims 6 to 8, the fusion protein of claim 9, the nucleic acid of claim 10 or 11 or the vector of claim 12.
15. A protein of any of claims 1 to 5, a fragment of any one of claims 6 to 8, a fusion protein of claim 9, a nucleic acid of claim 10 or 11, a vector of claim 12, or a pharmaceutical composition of claim 14, for use in a method for managing, preventing or treating a disease or disorder caused by VZV or by infection with VZV in a subject, optionally wherein the subject is human, optionally a human adult or elderly human.