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(54) Titre : COMPOSITIONS PEPTIDIQUES DE LIAISON A UNE PROTEINE DE CHOC THERMIQUE (HSP) ET LEURS METHODES D'UTILISATION

(54) Title: HEAT SHOCK PROTEIN-BINDING PEPTIDE COMPOSITIONS AND METHODS OF USE THEREOF

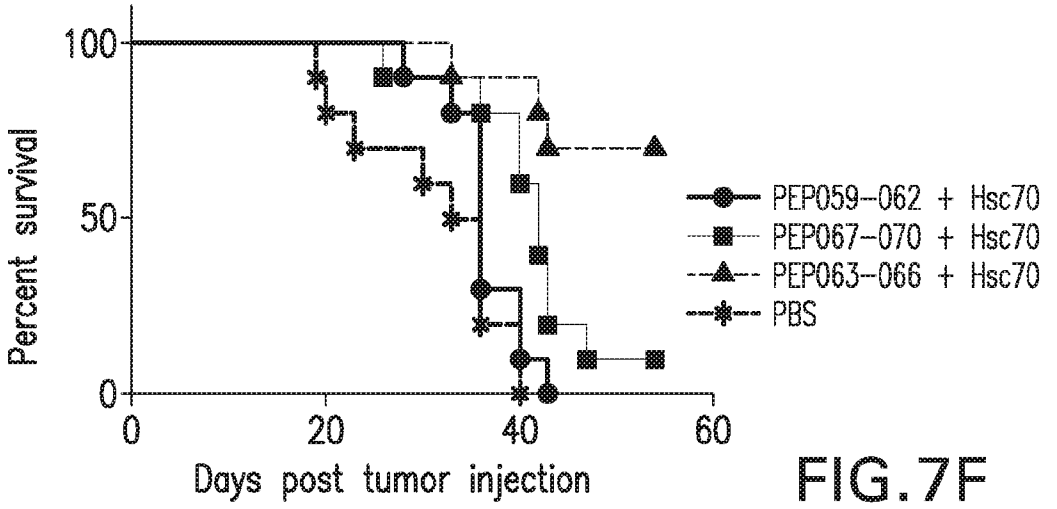

FIG.7F

(57) Abrégé/Abstract:
Provided are polypeptides and compositions comprising novel HSP-binding peptides. Such polypeptides and compositions are particularly useful as immunotherapeutics (e.g., cancer vaccines). Also provided are methods of inducing a cellular immune response using such polypeptides and compositions, methods of treating a disease using such polypeptides and compositions, kits comprising such polypeptides and compositions, and methods of making such compositions.

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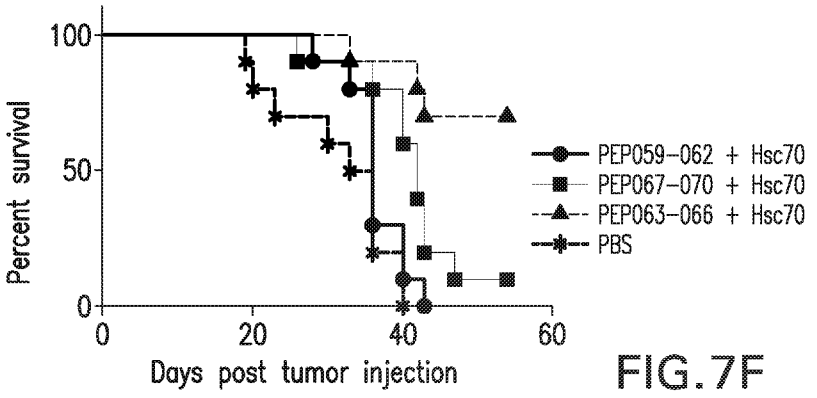

FIG.7F

(57) Abstract: Provided are polypeptides and compositions comprising novel HSP-binding peptides. Such polypeptides and compositions are particularly useful as immunotherapeutics (e.g., cancer vaccines). Also provided are methods of inducing a cellular immune response using such polypeptides and compositions, methods of treating a disease using such polypeptides and compositions, kits comprising such polypeptides and compositions, and methods of making such compositions.

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HEAT SHOCK PROTEIN-BINDING PEPTIDE COMPOSITIONS AND METHODS OF USE THEREOF

RELATED APPLICATIONS

This application claims priority to U.S. Provisional Patent Application Nos. 62/663,083, filed April 26, 2018, and 62/692,009, filed June 29, 2018, the entire disclosure of each of which is hereby incorporated herein by reference.

1. FIELD

[0001] The invention relates to heat shock protein (HSP)-binding peptide compositions, and uses of such compositions as immunotherapeutics (*e.g.*, cancer vaccines).

2. BACKGROUND

[0002] Immunotherapies are becoming important tools in the treatment of cancer. One immunotherapy approach involves the use of therapeutic cancer vaccines comprising cancer-specific antigenic peptides that actively educate a patient's immune system to target and destroy cancer cells. However, the generation of such therapeutic cancer vaccines is limited by the immunogenicity of cancer-specific antigenic peptides.

[0003] Accordingly, there is a need in the art for improved methods of generating highly immunogenic cancer-specific antigenic peptides and for creating effective anti-cancer vaccines comprising these peptides.

3. SUMMARY OF INVENTION

[0004] The instant disclosure provides polypeptides and compositions comprising novel HSP-binding peptides. Such polypeptides and compositions are particularly useful as immunotherapeutics (*e.g.*, cancer vaccines). Also provided are methods of inducing a cellular immune response using such polypeptides and compositions, methods of treating a disease using such polypeptides and compositions, kits comprising such polypeptides and compositions, and methods of making such compositions.

[0005] Accordingly, in one aspect, the disclosure provides an isolated polypeptide comprising a heat shock protein (HSP)-binding peptide comprising the amino acid sequence of $X_1LX_2LTX_3$ (SEQ ID NO: 1), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G. In another aspect, the disclosure provides an isolated polypeptide comprising an HSP-binding peptide comprising the amino acid sequence of $NWX_1X_2X_3X_4X_5$ (SEQ ID NO: 232), wherein X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K.

[0006] In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of: $NX_1LX_2LTX_3$ (SEQ ID NO: 2), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G; WLX_1LTX_2 (SEQ ID NO: 3), wherein X_1 is R or K; and X_2 is W or G; or $NWLX_1LTX_2$ (SEQ ID NO: 4), wherein X_1 is R or K; and X_2 is W or G.

[0007] In certain embodiments, the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12,98-113, 204, 205, and 207-215. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12,98-113, 204, 205, and 207-215. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 6. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 6. In certain embodiments, the HSP-binding peptide is no more than 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, 49, or 50 amino acid residues in length.

[0008] In certain embodiments, the polypeptide further comprises an antigenic peptide comprising one or more major histocompatibility complex (MHC)-binding epitopes. In certain embodiments, the MHC-binding epitope binds to an MHC I molecule with an IC_{50} of 500 nM or less. In certain embodiments, the MHC-binding epitope binds to an MHC II molecule with an IC_{50} of 1000 nM or less.

[0009] In certain embodiments, the MHC-binding epitope is from a cancer cell. In certain embodiments, the MHC-binding epitope comprises an amino acid mutation or a gene fusion mutation of the cancer cell. In certain embodiments, the amino acid mutation is a substitution, deletion, or insertion mutation. In certain embodiments, the amino acid mutation or gene fusion mutation is at or about the middle of the antigenic peptide. In certain embodiments, the amino acid mutation or gene fusion mutation is at position 1, 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, 49, or 50 of the amino acid sequence of the antigenic peptide.

[0010] In certain embodiments, the MHC-binding epitope is from a pathogenic microbe. In certain embodiments, the pathogenic microbe is a virus. In certain embodiments, the virus is a human papillomavirus (HPV). In certain embodiments, the antigenic peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

[0011] In another aspect, the instant disclosure provides an isolated polypeptide comprising an HSP-binding peptide and an antigenic peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

[0012] In certain embodiments, the amino acid sequence of the antigenic peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53. In certain embodiments, the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-12, 98-113, 204, 205, 207-215, and 232. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-12, 98-113, 204, 205, 207-215, and 232.

[0013] In certain embodiments, the MHC-binding epitope comprises a modified amino acid residue. In certain embodiments, the modified amino acid residue is a Tyr, Ser, Thr, Arg, Lys, or His that has been phosphorylated on a side chain hydroxyl or amine. In certain embodiments, the modified amino acid residue is a mimetic of a Tyr, Ser, Thr, Arg, Lys, or His amino acid that has been phosphorylated on a side chain hydroxyl or amine. In some embodiments, the mimetic is a non-hydrolyzable analogue of a phosphorylated residue. In certain embodiments, the modified amino acid residue is an Asn that has been glycosylated on a side chain amide, a Ser or Thr that has been glycosylated on a side chain hydroxyl, a Lys or Arg that has been methylated on a side chain amino, a Lys that has been acetylated on a side chain amino, an N-terminal residue that has been acetylated on the α-amino, or a C-terminal residue that has been amidated on the α-carboxyl. In certain embodiments, the modified amino acid residue is at or about the middle of the antigenic peptide. In certain embodiments, the modified amino acid residue is at position 1, 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, 49, or 50 of the amino acid sequence of the antigenic peptide.

[0014] In certain embodiments, the HSP-binding peptide is linked to the antigenic peptide via a chemical linker. In certain embodiments, the HSP-binding peptide is linked to the antigenic peptide via a peptide linker. In certain embodiments, the peptide linker comprises the amino acid sequence of FFRK (SEQ ID NO: 13) or FR.

[0015] In certain embodiments, the HSP-binding peptide is at the C-terminus of the polypeptide. In certain embodiments, the polypeptide comprises the amino acid sequence of: (a) $FFRKX_1LX_2LTX_3$ (SEQ ID NO: 14), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;

(b) FFRKNX$_1$LX$_2$LTX$_3$ (SEQ ID NO: 15), wherein X$_1$ is W or F; X$_2$ is R or K; and X$_3$ is W, F, or G;

(c) FFRKWLX$_1$LTX$_2$ (SEQ ID NO: 16), wherein X$_1$ is R or K; and X$_2$ is W or G; (d) FFRKNWLX$_1$LTX$_2$ (SEQ ID NO: 17), wherein X$_1$ is R or K; and X$_2$ is W or G; or

(e) FFRKNWX$_1$X$_2$X$_3$X$_4$X$_5$ (SEQ ID NO: 233), wherein, X$_1$ is L or I; X$_2$ is L, R, or K; X$_3$ is L or I; X$_4$ is T, L, F, K, R, or W; and X$_5$ is W or K, at the C-terminus of the polypeptide. In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-25, 71-75, 166, 167, 173, and 174, at the C-terminus of the polypeptide.

[0016] In certain embodiments, the HSP-binding peptide is at the N-terminus of the polypeptide. In certain embodiments, the polypeptide comprises the amino acid sequence of:

(a) X$_1$LX$_2$LTX$_3$FFRK (SEQ ID NO: 26), wherein X$_1$ is W or F; X$_2$ is R or K; and X$_3$ is W, F, or G;

(b) NX$_1$LX$_2$LTX$_3$FFRK (SEQ ID NO: 27), wherein X$_1$ is W or F; X$_2$ is R or K; and X$_3$ is W, F, or G;

(c) WLX$_1$LTX$_2$FFRK (SEQ ID NO: 28), wherein X$_1$ is R or K; and X$_2$ is W or G;

(d) NWLX$_1$LTX$_2$FFRK (SEQ ID NO: 29), wherein X$_1$ is R or K; and X$_2$ is W or G; or

[0017] (e) FFRKNWX$_1$X$_2$X$_3$X$_4$X$_5$ (SEQ ID NO: 35), wherein X$_1$ is L or I; X$_2$ is L, R, or K; X$_3$ is L or I; X$_4$ is T, L, F, K, R, or W; and X$_5$ is W or K, at the N-terminus of the polypeptide. In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 30-37, and 216-229, at the N-terminus of the polypeptide.

[0018] In certain embodiments, the polypeptide is 12 to 50 amino acids in length (*e.g.*, 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, 49, or 50 amino acids in length). In certain embodiments, the polypeptide is 20 to 40 amino acids in length.

[0019] In certain embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69. In certain embodiments, the amino acid sequence of the polypeptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69.

[0020] In certain embodiments, the polypeptide is chemically synthesized.

[0021] In another aspect, the instant disclosure provides a composition comprising a complex of the polypeptide disclosed herein and a purified stress protein. In certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70,

Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant or fusion protein thereof. In certain embodiments, the stress protein is Hsc70. In certain embodiments, the stress protein is human Hsc70. In certain embodiments, the stress protein is a recombinant protein.

[0022] In another aspect, the instant disclosure provides a composition comprising a plurality of the polypeptides as disclosed herein, optionally further comprising a purified stress protein as disclosed herein. In certain embodiments, the composition comprises 2-20 different polypeptides as disclosed herein. In certain embodiments, each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide.

[0023] In certain embodiments, the antigenic peptide of each one of the polypeptides comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53. In certain embodiments, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different antigenic peptides. In certain embodiments, each one of the polypeptides comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69. In certain embodiments, the amino acid sequence of each one of the polypeptides consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69. In certain embodiments, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different polypeptides. In certain embodiments, the total amount of the polypeptide(s) in the composition is about 0.1 to 20 nmol. In certain embodiments, the total amount of the polypeptide(s) in the composition is about 3, 4, 5, or 6 nmol. In certain embodiments, the amount of the stress protein in the composition is about 10 μg to 600 μg. In certain embodiments, the amount of the stress protein in the composition is about 250 μg to 290 μg.

[0024] In certain embodiments, the molar ratio of the polypeptide(s) to the stress protein is about 0.5:1 to 5:1. In certain embodiments, the molar ratio of the polypeptide(s) to the stress protein is about 1:1 to 2:1. In certain embodiments, the molar ratio of the polypeptide(s) to the stress protein is about 1:1, 1.25:1, or 1.5:1.

[0025] In certain embodiments, the total amount of the polypeptide(s) and stress protein in the composition is about 10 μg to 600 μg. In certain embodiments, the total amount of the polypeptide(s) and stress protein in the composition is about 300 μg.

[0026] In certain embodiments, the composition further comprises an adjuvant. In certain embodiments, the adjuvant comprises a saponin or an immunostimulatory nucleic acid. In certain embodiments, the adjuvant comprises QS-21. In certain embodiments, the amount of the QS-21 in the composition is about 10 μg, 25 μg, or 50 μg. In certain embodiments, the adjuvant comprises a Toll-like receptor (TLR) agonist. In certain embodiments, the TRL

agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[0027] In certain embodiments, the composition is a pharmaceutical composition comprising a pharmaceutically acceptable carrier or excipient. In certain embodiments, the composition is in a unit dosage form.

[0028] In another aspect, the instant disclosure provides a method of inducing a cellular immune response to an antigenic peptide in a subject, the method comprising administering to the subject an effective amount of a composition or a unit dosage form as disclosed herein. In certain embodiments, the subject has cancer. In certain embodiments, the subject has an infection of a pathogenic microbe.

[0029] In another aspect, the instant disclosure provides a method of treating a disease in a subject, the method comprising administering to the subject an effective amount of a composition or a unit dosage form as disclosed herein. In certain embodiments, the disease is cancer. In certain embodiments, the disease is an infection of a pathogenic microbe.

[0030] In certain embodiments, the MHC-binding epitope is present in the subject's cancer cells. In certain embodiments, the MHC-binding epitope is present in the pathogenic microbe.

[0031] In certain embodiments, the composition or unit dosage form is administered to the subject weekly for four weeks. In certain embodiments, at least two further doses of the composition or unit dosage form are administered biweekly to the subject after the four weekly doses. In certain embodiments, at least one booster dose of the composition or unit dosage form is administered three months after the final weekly or biweekly dose. In certain embodiments, the composition or unit dosage form is further administered every three months for at least 1 year.

[0032] In certain embodiments, the method further comprises administering to the subject lenalidomide, dexamethasone, interleukin-2, recombinant interferon alfa-2b, or PEG-interferon alfa-2b. In certain embodiments, the method further comprises administering to the subject an indoleamine dioxygenase-1 (IDO-1) inhibitor. In certain embodiments, the IDO-1 inhibitor is 4-amino-N-(3-chloro-4-fluorophenyl)-N'-hydroxy-1,2,5-oxadiazole-3-carboximidamide. In certain embodiments, the method further comprises administering to the subject an immune checkpoint antibody. In certain embodiments, the immune checkpoint antibody is selected from the group consisting of an agonistic anti-GITR antibody, an agonistic anti-OX40 antibody, an antagonistic anti-PD-1 antibody, an antagonistic anti-

CTLA-4 antibody, an antagonistic anti-TIM-3 antibody, an antagonistic anti-LAG-3 antibody, an antagonistic anti-TIGIT antibody, an agonistic anti-CD96 antibody, an antagonistic anti-VISTA antibody, an antagonistic anti-CD73 antibody, an agonistic anti-CD137 antibody, an antagonist anti-CEACAM1 antibody, an agonist anti-ICOS antibody, and or an antigen-binding fragment thereof.

[0033] In another aspect, the instant disclosure provides a kit comprising a first container containing the polypeptide as disclosed herein, and a second container containing a purified stress protein capable of binding to the polypeptide.

[0034] In certain embodiments, the first container contains 2-20 different polypeptides as disclosed herein. In certain embodiments, each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide. In certain embodiments, the total amount of the polypeptide(s) in the first container is about 0.1 to 20 nmol. In certain embodiments, the total amount of the polypeptide(s) in the first container is about 3, 4, 5, or 6 nmol.

[0035] In certain embodiments, the first container contains a single polypeptide as disclosed here in. In certain embodiments, the first container contains at least 20 different polypeptides as disclosed herein. In certain embodiments, each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide. In certain embodiments, the total amount of the polypeptide(s) in the first container is about 0.1 to 20 nmol. In certain embodiments, the total amount of the polypeptide(s) in the first container is about 3, 4, 5, or 6 nmol.

[0036] In certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant thereof. In certain embodiments, the stress protein is Hsc70. In certain embodiments, the stress protein is human Hsc70. In certain embodiments, the stress protein is a recombinant protein. In certain embodiments, the amount of the stress protein in the second container is about 10 μg to 600 μg. In certain embodiments, the amount of the stress protein in the second container is about 250 μg to 290 μg.

[0037] In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 0.5:1 to 5:1. In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 1:1 to 2:1. In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 1:1, 1.25:1, or 1.5:1. In certain embodiments, the total amount of the polypeptide(s) in the first container and the stress protein in the second container is about 10

μg to 600 μg. In certain embodiments, the total amount of the polypeptide(s) in the first container and the stress protein in the second container is 300 μg.

[0038] In certain embodiments, the kit further comprises a third container containing an adjuvant. In certain embodiments, the adjuvant comprises a saponin or an immunostimulatory nucleic acid. In certain embodiments, the adjuvant comprises QS-21. In certain embodiments, the amount of the QS-21 in the third container is about 10 μg, 25 μg, or 50 μg. In certain embodiments, the adjuvant comprises a TLR agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[0039] In another aspect, the instant disclosure provides a method of making a vaccine, the method comprising mixing one or more polypeptides as disclosed herein with a purified stress protein under suitable conditions such that the purified stress protein binds to at least one of the polypeptides. In certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant thereof. In certain embodiments, the stress protein is Hsc70. In certain embodiments, the stress protein is human Hsc70. In certain embodiments, the stress protein is a recombinant protein. In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 0.5:1 to 5:1. In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 1:1 to 2:1. In certain embodiments, the molar ratio of the polypeptide to the stress protein is about 1:1, 1.25:1, or 1.5:1. In certain embodiments, the suitable conditions comprise a temperature of about 37 °C.

4. BRIEF DESCRIPTION OF THE DRAWINGS

[0040] **Figure 1** is an exemplary size exclusion chromatography (SEC) chromatogram showing the UV absorbance of uncomplexed Hsc70 (top) and peptide complexed Hsc70 (bottom). "C", "D", "T", and "HMW" indicate the segments of the chromatogram corresponding to peptide-Hsc70 complexes, Hsc70 dimers, Hsc70 trimers, and high molecular weight oligomeric Hsc70 species, respectively. "M_{sh}" refers to a monomer shoulder.

[0041] **Figure 2** is a chromatogram showing the UV absorbance of PEP006 mixed with Hsc70 at a range of molar ratios from 0.25:1 to 3:1, wherein the compositions in the mixture were separated by size exclusion chromatography.

[0042] **Figure 3A** is a chromatogram showing the UV absorbance of a polypeptide comprising PEP006 mixed with Hsc70 at a range of molar ratios from 0.125:1 to 4:1, wherein

the compositions in the mixture were separated by size exclusion chromatography. **Figure 3B** is a graph showing percent complexation with Hsc70 for a PEP006-containing polypeptide, over a range of polypeptide:Hsc70 molar ratios from 0.125:1 to 4:1, as calculated from size exclusion chromatography traces similar to those in Figure 3A. Three independent experiments are shown.

[0043] **Figure 4A** is a graph showing percent complexation with Hsc70 for five different peptides, where each of the five different peptides was synthesized in three forms: one with a C-terminal PEP001 sequence, one with a C-terminal PEP006 sequence, and one without a C-terminal HSP-binding peptide ("Naked Peptide"). **Figure 4B** is a graph showing percent complexation with Hsc70 for six different peptides, where each of the six different peptides was synthesized in two forms: one with a C-terminal PEP001 sequence and one with a C-terminal PEP006 sequence.

[0044] **Figures 5A** and **5B** are graphs showing the relative number of IFNγ-producing splenocytes from mice immunized with vaccines comprising PEP001- or PEP006-containing HPV pooled peptides, or HPV pooled peptides not linked to an HSP-binding peptide (naked HPV peptides), as free peptides or mixed with Hsc70 protein at 2:1 or 1:1 ratio (n=3 mice per treatment group).

[0045] **Figure 6** is a graph showing the relative number of IFNγ-producing splenocytes from mice immunized with the indicated pools of MC38 peptides, either as free peptides, or mixed with Hsc70 protein at 2:1 or 1:1 ratios (n=3 mice per treatment group).

[0046] **Figure 7A** is a graph showing the mean volumes of tumors in a syngeneic mouse tumor model, wherein the mice were immunized with vaccines comprising PEP001-containing HPV peptides ("PEP067-070"), PEP006-containing HPV peptides ("PEP063-066"), or naked HPV peptides ("PEP059-062"), in each case mixed with Hsc70 protein as described in Section 6.2.2 herein, or PBS as negative control (n=10 mice per treatment group). **Figures 7B-7E** show the tumor volume of each mouse in these four treatment groups. **Figure 7F** shows a set of survival curves of the mice.

[0047] **Figure 8A** is a graph showing the mean volumes of tumors in a syngeneic mouse tumor model, wherein the mice were immunized with vaccines comprising a new pool of PEP006-containing HPV peptides ("PEP071-086") or a previously tested pool of PEP006-containing HPV peptides ("PEP063-066"), in each case mixed with Hsc70 protein as described in Section 6.2.3 herein, or PBS as negative control (n=13 mice per treatment group; error bars: standard deviations). **Figure 8B** shows a set of survival curves of the mice.

[0048] **Figure 9A** is a series of graphs showing tumor growth kinetics in individual mice treated with two different formulations of HSC70-based vaccine loaded with 16 different HPV peptides comprising PEP006 as compared to PBS. **Figure 9B** is a graph showing group mean tumor growth kinetics of mice in the same mice. **Figure 9C** is a graph showing overall survival in the same experiment.

[0049] **Figure 10A** is a series of chromatograms showing the reverse phase chromatography signals of the chemical synthesis products of an Ova peptide, naked (SEQ ID NO:97) or linked with PEP001 (SEQ ID NO:230) or PEP006 (SEQ ID NO:231). The arrows indicate the retention time of the pure peptides.

[0050] **Figure 10B** is a graph showing quantification of the signals in Figure 10A.

[0051] **Figure 11** is a graph showing crude purity of naked peptides (A-Y) versus the same peptides (A-Y) with a C-terminal PEP006 sequence.

5. DETAILED DESCRIPTION

[0052] The instant disclosure provides polypeptides and compositions comprising novel HSP-binding peptides. Such polypeptides and compositions are particularly useful as immunotherapeutics (*e.g.*, cancer vaccines). Also provided are methods of inducing a cellular immune response using such polypeptides and compositions, methods of treating a disease using such polypeptides and compositions, kits comprising such polypeptides and compositions, and methods of making such compositions.

5.1 Definitions

[0053] Unless otherwise defined herein, scientific and technical terms used herein have the meanings that are commonly understood by those of ordinary skill in the art. In the event of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. The use of "or" means "and/or" unless stated otherwise. The use of the term "including", as well as other forms, such as "includes" and "included", is not limiting.

[0054] As used herein, the terms "about" and "approximately," when used to modify a numeric value or numeric range, indicate that deviations of 5% to 10% above (*e.g.*, up to 5% to 10% above) and 5% to 10% below (*e.g.*, up to 5% to 10% below) the recited value or range remain within the intended meaning of the recited value or range.

[0055] As used herein, the term "polypeptide" refers to a non-naturally occurring polymer comprising a peptide of six or more amino acid residues. A polypeptide can further

comprise one or more non-amino-acid-residue structures. In certain embodiments, a polypeptide comprises a chemical linker. In certain embodiments, a polypeptide comprises a chemical linker linking two portions of the polypeptide. In certain embodiments, a polypeptide does not comprise the entire amino acid sequence of a protein (*e.g.*, a naturally occurring protein) comprising the amino acid sequence of SEQ ID NO: 1. In certain embodiments, a polypeptide does not comprise an amino acid sequence comprising more than 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 contiguous amino acids of a protein (*e.g.*, a naturally occurring protein) that comprises the amino acid sequence of SEQ ID NO: 1.

[0056] As used herein, the term "isolated polypeptide" refers to a polypeptide that is separated from one or more molecules present after the expression (*e.g.*, recombinant expression) or synthesis (*e.g.*, chemical synthesis) of the polypeptide.

[0057] As used herein, the terms "major histocompatibility complex" and "MHC" are used interchangeably and refer to an MHC class I molecule and/or an MHC class II molecule.

[0058] As used herein, the terms "human leukocyte antigen" and "HLA" are used interchangeably and refer to major histocompatibility complex (MHC) in humans. An HLA molecule may be a class I MHC molecule (*e.g.*, HLA-A, HLA-B, HLA-C) or a class II MHC molecule (*e.g.*, HLA-DP, HLA-DQ, HLA-DR).

[0059] As used herein, the term "major histocompatibility complex (MHC)-binding epitope" refers to a peptide that binds to or is predicted to bind to an MHC molecule.

[0060] As used herein, the terms "heat shock protein-binding peptide" and "HSP-binding peptide" are used interchangeably and refer to a peptide that non-covalently binds to an HSP. In certain embodiments, an HSP-binding peptide does not comprise an amino acid sequence containing more than 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, or 50 contiguous amino acids of a protein (*e.g.*, a naturally occurring protein) that comprises the amino acid sequence of SEQ ID NO: 1.

[0061] As used herein, the term "peptide linker" refers to a peptide bond or a peptide sequence that links a C-terminal amino acid residue of a first peptide to an N-terminal amino acid residue of a second peptide.

[0062] As used herein, the term "chemical linker" refers to any chemical bond or moiety that is capable of linking two molecules, wherein the bond or moiety is not a peptide linker.

[0063] As used herein, the terms "treat," "treating," and "treatment" refer to therapeutic or preventative measures described herein. The methods of "treatment" employ administration of an antibody to a subject having a disease or disorder, or predisposed to

having such a disease or disorder, in order to prevent, cure, delay, reduce the severity of, or ameliorate one or more symptoms of the disease or disorder or recurring disease or disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

[0064] As used herein, the term "effective amount" in the context of the administration of a therapy to a subject refers to the amount of a therapy that achieves a desired prophylactic or therapeutic effect.

[0065] As used herein, the term "subject" includes any human or non-human animal.

5.2 Heat Shock Protein (HSP)-Binding Peptides

[0066] In one aspect, the instant disclosure provides a polypeptide comprising an HSP-binding peptide comprising any one of the amino acid sequences provided in Table 1.

Table 1. Amino acid sequences of HSP-binding peptides

Description	Amino Acid Sequence	SEQ ID NO
Consensus sequence 1	$X_1LX_2LTX_3$, wherein: X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G	1
Consensus sequence 2	$NX_1LX_2LTX_3$, wherein: X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G	2
Consensus sequence 3	WLX_1LTX_2, wherein: X_1 is R or K; and X_2 is W or G	3
Consensus sequence 4	$NWLX_1LTX_2$, wherein: X_1 is R or K; and X_2 is W or G	4
Consensus sequence 5	$NWX_1X_2X_3X_4X_5$, wherein: X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K	232

Description	Amino Acid Sequence	SEQ ID NO
PEP016	WLRLTW	5
PEP017	NWLRLTW	6
PEP018	WLKLTW	7
PEP019	NWLKLTW	8
PEP020	WLRLTG	9
PEP021	NWLRLTG	10
PEP022	FLRLTF	11
PEP023	NFLRLTF	12
PEP024	WLRLTF	98
PEP025	NWLRLTF	99
PEP040	WLKLTF	100
PEP041	NWLKLTF	101
PEP042	WLKLTG	102
PEP043	NWLKLTG	103
PEP044	FLRLTW	104
PEP045	NFLRLTW	105
PEP046	FLRLTG	106
PEP047	NFLRLTG	107
PEP048	FLKLTW	108
PEP049	NFLKLTW	109
PEP050	FLKLTF	110
PEP051	NFLKLTF	111
PEP103	FLKLTG	112
PEP104	NFLKLTG	113
PEP185	NWLLLTW	204
PEP186	NLLRWTG	205
PEP188	FWLRLTW	207
PEP189	NWLRLLW	208
PEP190	NWLRLFW	209
PEP191	NWLRLKW	210
PEP192	NWIRITW	211
PEP193	QWLRLTW	212

Description	Amino Acid Sequence	SEQ ID NO
PEP194	NWLKLKW	213
PEP195	NWLKLRW	214
PEP196	NWLKLWK	215

[0067] In one aspect, the instant disclosure provides a polypeptide comprising an HSP-binding peptide comprising the amino acid sequence of $X_1LX_2LTX_3$ (SEQ ID NO: 1), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G. In another aspect, the instant disclosure provides a polypeptide comprising an HSP-binding peptide comprising the amino acid sequence of $NWX_1X_2X_3X_4X_5$ (SEQ ID NO: 232), wherein X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K. In certain embodiments, the HSP-binding peptide binds to an HSP (*e.g.*, Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin) with a K_d lower than 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M. In certain embodiments, the HSP-binding peptide binds to Hsc70 (*e.g.*, human Hsc70) with a K_d of 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, or lower.

[0068] In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of $NX_1LX_2LTX_3$ (SEQ ID NO: 2), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of WLX_1LTX_2 (SEQ ID NO: 3), wherein X_1 is R or K; and X_2 is W or G. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of $NWLX_1LTX_2$ (SEQ ID NO: 4), wherein X_1 is R or K; and X_2 is W or G.

[0069] In certain embodiments, the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12, 98-113, 204-205, and 207-215. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 5. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 6. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 7. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 8. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 9. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 10. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 11. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 12. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 98. In certain embodiments, the

HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 99. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 100. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 101. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 102. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 103. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 104. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 105. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 106. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 107. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 108. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 109. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 110. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 111. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 112. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 113. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 204. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 205. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 207. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 208. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 209. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 210. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 211. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 212. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 213. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 214. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 215.

[0070] In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 1. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID

NO: 2. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 3. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 4. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 232.

[0071] In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12, 98-113, 204, 205, and 207-215. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 5. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 6. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 7. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 8. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 9. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 10. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 11. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 12. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 98. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 99. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 100. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 101. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 102. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 103. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 104. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 105. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 106. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid

sequence of SEQ ID NO: 107. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 108. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 109. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 110. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 111. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 112. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 113. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 204. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 205. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 207. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 208. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 209. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 210. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 211. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 212. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 213. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 214. In certain embodiments, the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 215.

[0072] In certain embodiments, the HSP-binding peptide is no more than 100 (*e.g.*, no more than 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, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95) amino acid residues in length. In certain embodiments, the HSP-binding peptide is from 6 to 50 (*e.g.*, 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, 49, or 50) amino acid residues in length.

[0073] In certain embodiments, the amino acid sequence of the polypeptide consists of the amino acid sequence of the HSP-binding peptide.

[0074] In certain embodiments, the HSP-binding peptide further comprises a linker. The linker can be any chemical linker or peptide linker known in the art.

[0075] In certain embodiments, the linker comprises a moiety for chemical crosslinking or ultraviolet (UV) crosslinking. Any chemical crosslinking or UV crosslinking moieties known in the art (see, *e.g.*, Wong, 1991, Chemistry of Protein Conjugation and Cross-Linking, CRC Press, incorporated herein by reference in its entirety) can be employed. In certain embodiments, the linker comprises a click chemistry handle. As used herein, the term "click chemistry handle" refers to a reactant or a reactive group that can partake in a click chemistry reaction. Exemplary click chemistry handles are demonstrated in U.S. Patent Publication 20130266512, which is incorporated by reference herein in its entirety.

[0076] In certain embodiments, the linker comprises a peptide linker. In certain embodiments, the peptide linker comprises an amino acid sequence that can be recognized and/or cleaved by a protease. In certain embodiments, the protease is expressed in a mammalian cell (*e.g.*, a human cell). In certain embodiments, the protease is expressed in an antigen-presenting cell (*e.g.*, B cell, macrophage, dendritic cell). In certain embodiments, the protease is a serine protease. In certain embodiments, the protease is trypsin, chymotrypsin, papain, V8 protease, or elastase. In certain embodiments, the peptide linker comprises or consists of the amino acid sequence of FFRK (SEQ ID NO: 13). In certain embodiments, the peptide linker comprises or consists of the amino acid sequence of FR.

Table 2. Amino acid sequences of linkers and HSP-binding peptides with linkers

Description	Amino Acid Sequence	SEQ ID NO
Linker	FFRK	13
Linker	FR	N/A
Consensus sequence 1 with N-terminal linker	FFRKX_1LX_2LTX_3, wherein: X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G	14
Consensus sequence 2 with N-terminal linker	FFRKNX_1LX_2LTX_3, wherein: X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G	15
Consensus sequence 3 with N-terminal linker	FFRKWLX_1LTX_2, wherein: X_1 is R or K; and X_2 is W or G	16

Description	Amino Acid Sequence	SEQ ID NO
Consensus sequence 4 with N-terminal linker	FFRKNWLX$_1$LTX$_2$, wherein: X$_1$ is R or K; and X$_2$ is W or G	17
Consensus sequence 5 with N-terminal linker	FFRKNWX$_1$X$_2$X$_3$X$_4$X$_5$, wherein: X$_1$ is L or I; X$_2$ is L, R, or K; X$_3$ is L or I; X$_4$ is T, L, F, K, R, or W; and X$_5$ is W or K	233
PEP001	FFRKNLLRLTG	71
PEP003	FFRKNWLLLTW	166
PEP004	FFRKNLLRWTG	167
PEP006	FFRKNWLRLTW	18
PEP012	FFRKNWLKLTW	19
PEP013	FFRKNWIRITW	173
PEP014	FFRKQWLRLTW	174
PEP026	FFRKNWLRLTG	20
PEP027	FFRKNFLRLTF	21
PEP028	FRNWLRLTW	22
PEP029	FRNWLKLTW	23
PEP030	FRNWLRLTG	24
PEP031	FRNFLRLTF	25
PEP055	FFRKNWLKLKW	72
PEP057	FFRKNWLKLRW	74
PEP058	FFRKNWLKLWK	75
Consensus sequence 1 with C-terminal linker	X$_1$LX$_2$LTX$_3$FFRK, wherein: X$_1$ is W or F; X$_2$ is R or K; and X$_3$ is W, F, or G	26
Consensus sequence 2 with C-terminal linker	NX$_1$LX$_2$LTX$_3$FFRK, wherein: X$_1$ is W or F; X$_2$ is R or K; and X$_3$ is W, F, or G	27
Consensus sequence 3 with C-terminal linker	WLX$_1$LTX$_2$FFRK, wherein: X$_1$ is R or K; and X$_2$ is W or G	28
Consensus sequence 4 with C-terminal linker	NWLX$_1$LTX$_2$FFRK, wherein: X$_1$ is R or K; and X$_2$ is W or G	29

Consensus sequence 5 with C-terminal linker	$NWX_1X_2X_3X_4X_5FFRK$, wherein: X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K	234
PEP032	NWLRLTWFFRK	30
PEP033	NWLKLTWFFRK	31
PEP034	NWLRLTGFFRK	32
PEP035	NFLRLTFFFRK	33
PEP036	NWLRLTWFR	34
PEP037	NWLKLTWFR	35
PEP038	NWLRLTGFR	36
PEP039	NFLRLTFFR	37
PEP197	NLLRLTWFFRK	216
PEP198	NRLLLTGFFRK	217
PEP199	NWLLLTWFFRK	218
PEP200	NLLRWTGFFRK	219
PEP201	NRLWLTGFFRK	220
PEP202	FWLRLTWFFRK	221
PEP203	NWLRLLWFFRK	222
PEP204	NWLRLFWFFRK	223
PEP205	NWLRLKWFFRK	224
PEP206	NWIRITWFFRK	225
PEP207	QWLRLTWFFRK	226
PEP208	NWLKLKWFFRK	227
PEP209	NWLKLRWFFRK	228
PEP210	NWLKLWKFFRK	229

[0077] In certain embodiments, the polypeptide comprises any one of the amino acid sequences provided in Table 2.

[0078] In certain embodiments, the linker is N-terminal to the HSP-binding peptide. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 14, 15, 16, 17, or 233. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 71, 72, 74, 75, 166, 167, 173, or 174. In certain embodiments, the amino acid sequence of the polypeptide consists of the amino acid sequence of SEQ ID NO: 14, 15, 16, 17, or 233. In certain embodiments, the amino acid sequence of the polypeptide consists of the amino acid sequence of SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 71, 72, 74, 75, 166, 167, 173, or 174.

[0079] In certain embodiments, the linker is C-terminal to the HSP-binding peptide. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 26, 27, 28, 29, or 234. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 30, 31, 32, 33, 34, 35, 36, 37, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, or 229. In certain embodiments, the amino acid sequence of the polypeptide consists of the amino acid sequence of SEQ ID NO: 26, 27, 28, 29, or 234. In certain embodiments, the amino acid sequence of the polypeptide consists of the amino acid sequence of SEQ ID NO: 30, 31, 32, 33, 34, 35, 36, 37, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, or 229.

5.3 Polypeptides Comprising HSP-Binding Peptides

[0080] In one aspect, the instant disclosure provides a polypeptide comprising an HSP-binding peptide as disclosed herein and an antigenic peptide comprising one or more MHC-binding epitopes.

[0081] MHC-binding epitopes can be identified by methods known in the art, *e.g.*, by an assay that measures the binding of a peptide to an MHC molecule (*e.g.*, an HLA molecule). Non-limiting examples of such assays include inhibition of antigen presentation (Sette, et al., J. Immunol. 141:3893, 1991), in vitro assembly assays (Townsend, et al., Cell 62:285, 1990), and FACS based assays using mutated cells, such as RMA.S (Melief, et al., Eur. J. Immunol. 21:2963, 1991). In some instances, an MHC-binding epitope can be predicted to bind an MHC molecule (*e.g.*, an HLA molecule) by a software program (*e.g.* SYFPEITHI, Rammensee, et al., Immunogenetics 50, 213-219, 1999, incorporated herein by reference in its entirety). Other methods that can be used to identify an MHC-binding epitope include, without limitation, those disclosed in Guan, P. et al., (2003) Applied Bioinformatics, 2: 63-66; Blythe, M. J. et al., (2002) Bioinformatics, 18: 434-439; Flower, D. R. and Doytchinova, I. A. (2002). Applied Bioinformatics, 1: 167-176; Yu, K. et al., (2002) Molecular Medicine, 8: 137-48; Brusic, V. et al., (2002) Immunology and Cell Biology, 80: 280-285; Jung, G. et al., (2001) Biologicals, 29: 179-181 (which describes T cell epitope prediction programme EPIPREDICT); Kwok, W. W. et al., (2001) Trends in Immunology, 22: 583-588; Mallios, R. R. (2001) Bioinformatics, 17: 942-948; Romisch, K. (2001). Trends in Biochemical Sciences, 26: 531; Schirle, M. et al., (2001) Journal of Immunological Methods, 257: 1-16; Singh, H. and Raghava, G. P. S. (2001) Bioinformatics, 17: 1236-1237; Andersen, M. H. et al., (2000) Tissue Antigens, 55: 519-531; Buus, S. (1999). Current Opinion in Immunology, 11: 209-213; Mallios, R. R. (1999) Bioinformatics, 15: 432-439; Maffei, A. and Harris, P. E. (1998). Peptides, 19: 179-198; and Vita R. et al., (2015) Nucleic Acids Res., 43: D405-D412 (which

describes the immune epitope database (IEDB) 3.0., available at www.iedb.org) (each of which is incorporated herein by reference in its entirety).

[0082] MHC molecules are classified as either Class I or Class II molecules. Class II MHC molecules are expressed primarily on cells involved in initiating and sustaining immune responses, such as dendritic cells, B lymphocytes, macrophages, etc. Class II MHC molecules are recognized by helper T lymphocytes and induce proliferation of helper T lymphocytes and amplification of the immune response to the particular immunogenic peptide that is displayed. Class I MHC molecules are expressed on almost all nucleated cells and are recognized by cytotoxic T lymphocytes (CTLs), which then destroy the antigen-bearing cells. Cytotoxic T lymphocytes are particularly important in tumor rejection and in fighting viral infections. The CTL recognizes the antigen in the form of a peptide fragment bound to the MHC class I molecules rather than the intact foreign antigen itself. The capacity of peptides to bind MHC molecules can be measured in a variety of different ways, such as by inhibition of antigen presentation (Sette, et al., J. Immunol. 141:3893, 1991, incorporated herein by reference in its entirety), *in vitro* assembly assays (Townsend, et al., Cell 62:285, 1990), and FACS based assays using mutated cells, such as RMA.S (Melief, et al., Eur. J. Immunol. 21:2963, 1991, incorporated herein by reference in its entirety). MHC-binding epitopes predicted to bind MHC class I molecules are typically between 8 to 11 residues, while MHC-binding epitopes predicted to bind MHC class II molecules are typically in the range of 10 to 20 residues.

[0083] In certain embodiments, the MHC-binding epitope is an HLA-binding epitope. In certain embodiments, the MHC-binding epitope binds to an MHC I molecule with an IC50 smaller than or equal to 500 nM (*e.g.*, smaller than or equal to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, or 450 nM). In certain embodiments, the MHC-binding epitope binds to an MHC II molecule with an IC50 smaller than or equal to 1000 nM (*e.g.*, smaller than or equal to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, or 900 nM).

[0084] In certain embodiments, the sequence of the MHC-binding epitope is identified from one or more of a subject's cancer cells (*e.g.*, cells of cervical cancer, adenocarcinoma, glioblastoma, or multiple myeloma). In certain embodiments, the amino acid sequence of the MHC-binding epitope is 100% identical to the sequence identified from the cancer cell(s). In certain embodiments, the amino acid sequence of the MHC-binding epitope is at least 70%, 80%, 90%, or 95% identical to the sequence identified from the cancer cell, optionally wherein the difference comprises mostly or only conservative substitutions of amino acids.

The amino acid sequence identified from the cancer cell can be either wild-type or mutant relative to the most frequent sequence of the population of the species. Where the amino acid sequence identified from the cancer cell is mutant, it can comprise an amino acid mutation (*e.g.*, a substitution, deletion, or insertion mutation) or a gene fusion mutation (*e.g.*, as a result of genomic translocation or transposition).

[0085] In certain embodiments, the sequence of the MHC-binding epitope is identified from a pathogenic microbe. The pathogenic microbe can be a virus, a bacterium, a fungus, a protozoan, or a parasite. Exemplary viruses include hepatitis type A, hepatitis type B, hepatitis type C, influenza (*e.g.*, influenza A or influenza B), varicella, adenovirus, herpes simplex type I (HSV-I), herpes simplex type II (HSV-II), rinderpest, rhinovirus, echovirus, rotavirus, respiratory syncytial virus, papilloma virus (*e.g.*, human papillomavirus (HPV)), papova virus, cytomegalovirus, echinovirus, arbovirus, hantavirus, coxsackie virus, mumps virus, measles virus, rubella virus, polio virus, Epstein Barr virus (EBV), human immunodeficiency virus type I (HIV-I), human immunodeficiency virus type II (HIV-II), dengue virus, smallpox virus, and Zika virus. Exemplary bacteria include *Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Enterococcus faecalis, Proteus vulgaris, Staphylococcus viridans, and Pseudomonas aeruginosa*. Exemplary fungi include *Candida* (*e.g.*, *Candida glabrata*), *Pneumocystis carinii*, *Fusarium keratitis*, *coccidioidal*, *Aspergillus niger*, *Cryptococcus neoformans*, and *Curvularia geniculata*. Exemplary protozoa include leishmania, coccidiosis, trypanosoma schistosoma, and malaria. Exemplary parasites include chlamydia and rickettsia.

[0086] In certain embodiments, the MHC-binding epitope comprises a modified amino acid residue. In certain embodiments, the MHC-binding epitope comprises a phosphorylated residue (*e.g.*, a Tyr, Ser, Thr, Arg, Lys, or His that has been phosphorylated on a side chain hydroxyl or amine). In certain embodiments, the MHC-binding epitope comprises a phosphomimetic residue (*e.g.*, a mimetic of a Tyr, Ser, Thr, Arg, Lys, or His amino acid that has been phosphorylated on a side chain hydroxyl or amine). Non-limiting examples of phosphomimetic groups include O-boranophospho, borono, O-dithiophospho, phosphoramide, H-phosphonate, alkylphosphonate, phosphorothiolate, phosphodithiolate and phosphorofluoridate, any of which may be derivatized on Tyr, Thr, Ser, Arg, Lys, or His residues. In certain embodiments, an Asp or Glu residue is used as a phosphomimetic in place of a phospho-Tyr, phospho-Thr, phospho-Ser, phospho-Arg, phospho-Lys and/or phospho-His residue in a peptide. In certain embodiments, the phosphomimetic residue is a non-hydrolyzable analogue of a phosphorylated residue.

[0087] The antigenic peptide can comprise one or more MHC-binding epitopes. In certain embodiments, the antigenic peptide comprises one MHC-binding epitope. In certain embodiments, the antigenic peptide comprises two or more (*e.g.*, 3, 4, 5, 6, 7, 8, 9, 10, or more) MHC-binding epitopes. The two or more MHC-binding epitopes can be linked via a chemical linker or a peptide linker, wherein the peptide linker optionally comprises an amino acid sequence that can be recognized and/or cleaved by a protease.

[0088] In certain embodiments, the antigenic peptide is 8 to 50 amino acids (*e.g.*, 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, 49, or 50 amino acids) in length. In certain embodiments, the antigenic peptide is 12 to 50, 20 to 40, 20 to 35, 25 to 40, 20 to 30, 25 to 35, or 30 to 40 amino acids in length.

[0089] The HSP-binding peptide can be linked to the antigenic peptide via a chemical linker or a peptide linker. In certain embodiments, the HSP-binding peptide can be linked to the antigenic peptide via a chemical linker. Any chemical linkers can be employed to link the HSP-binding peptide and the antigenic peptide. Exemplary chemical linkers include moieties generated from chemical crosslinking (see, *e.g.*, Wong, 1991, Chemistry of Protein Conjugation and Cross-Linking, CRC Press, incorporated herein by reference in its entirety), UV crosslinking, and click chemistry reactions (see, *e.g.*, U.S. Patent Publication 20130266512, which is incorporated by reference herein in its entirety). In certain embodiments, the HSP-binding peptide can be linked to the antigenic peptide via a peptide linker (*e.g.*, a peptide linker as disclosed in Section 5.2).

[0090] The HSP-binding sequence can be linked to the antigenic peptide at any amino acid position. In certain embodiments, the C-terminus of the HSP-binding sequence is linked to the N-terminus of the antigenic peptide via a chemical linker. In certain embodiments, the N-terminus of the HSP-binding sequence is linked to the C-terminus of the antigenic peptide via a chemical linker. In certain embodiments, the C-terminus of the HSP-binding sequence is linked to the N-terminus of the antigenic peptide via a peptide linker. In certain embodiments, the N-terminus of the HSP-binding sequence is linked to the C-terminus of the antigenic peptide via a peptide linker. In certain embodiments, the HSP-binding peptide is at the C-terminus of the polypeptide. Polypeptides having an HSP-binding peptide at the C-terminus are generally advantageous in having an improved purity when produced by solid-phase synthesis. In certain embodiments, the HSP-binding peptide is at the N-terminus of the polypeptide. In certain embodiments, the heat shock protein-binding peptide is not at the N-

terminus or the C-terminus of the polypeptide. In certain embodiments, the heat shock protein-binding peptide is at the center of the polypeptide.

[0091] In certain embodiments, the polypeptide comprises, from N-terminus to C-terminus, an antigenic peptide comprising one or more MHC-binding epitopes, a peptide linker, and an HSP-binding peptide disclosed herein. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 14, 15, 16, 17, or 233. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 71, 72, 74, 75, 166, 167, 173, or 174. In certain embodiments, the amino acid sequence of the polypeptide consists of, from N-terminus to C-terminus, the amino acid sequence of an antigenic peptide disclosed herein, and the amino acid sequence of SEQ ID NO: 14, 15, 16, 17, or 233. In certain embodiments, the amino acid sequence of the polypeptide consists of, from N-terminus to C-terminus, the amino acid sequence of an antigenic peptide disclosed herein, and the amino acid sequence of SEQ ID NO: 18, 19, 20, 21, 22, 23, 24, 25, 71, 72, 74, 75, 166, 167, 173, or 174.

[0092] In certain embodiments, the polypeptide comprises, from N-terminus to C-terminus, an HSP-binding peptide disclosed herein, a peptide linker, and an antigenic peptide comprising one or more MHC-binding epitopes. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 26, 27, 28, 29, or 234. In certain embodiments, the polypeptide comprises the amino acid sequence of SEQ ID NO: 30, 31, 32, 33, 34, 35, 36, 37, or 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, or 229. In certain embodiments, the amino acid sequence of the polypeptide consists of, from N-terminus to C-terminus, the amino acid sequence of SEQ ID NO: 26, 27, 28, 29, or 234, and the amino acid sequence of an antigenic peptide disclosed herein. In certain embodiments, the amino acid sequence of the polypeptide consists of, from N-terminus to C-terminus, the amino acid sequence of SEQ ID NO: 30, 31, 32, 33, 34, 35, 36, 37, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, or 229, and the amino acid sequence of an antigenic peptide disclosed herein.

[0093] In certain embodiments, the polypeptide disclosed herein is no more than 500 amino acids (*e.g.*, no more than 400, 300, 200, 100, 90, 80, 70, 60, 50, or 40 amino acids) in length. In certain embodiments, the amino acid sequence of the polypeptide is not naturally occurring.

[0094] In certain embodiments, the polypeptide binds to an HSP (*e.g.*, Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin) with a K_d lower than 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M. In certain embodiments, the polypeptide binds to Hsc70

(*e.g.*, human Hsc70) with a K_d of 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, or lower.

5.3.1 Production of polypeptides by chemical synthesis

[0095] Polypeptides disclosed herein can be synthesized by standard chemical methods including the use of a peptide synthesizer. Conventional peptide synthesis or other synthetic protocols well known in the art can be used.

[0096] In certain embodiments, the polypeptide disclosed herein consists of amino acid residues linked by peptide bonds. Such polypeptides can be synthesized, for example, by solid-phase peptide synthesis using procedures similar to those described by Merrifield, 1963, J. Am. Chem. Soc., 85:2149, incorporated herein by reference in its entirety. During synthesis, N-α-protected amino acids having protected side chains are added stepwise to a growing polypeptide chain linked by its C-terminal and to an insoluble polymeric support *i.e.*, polystyrene beads. The polypeptides are synthesized by linking an amino group of an N-α-deprotected amino acid to an α-carboxyl group of an N-α-protected amino acid that has been activated by reacting it with a reagent such as dicyclohexylcarbodiimide or 2-(6-Chloro-1-H-benzotriazole-1-yl)-1,1,3,3-tetramethylaminium hexafluorophosphate. The attachment of a free amino group to the activated carboxyl leads to peptide bond formation. The most commonly used N-α-protecting groups include Boc which is acid labile and Fmoc which is base labile. Details of appropriate chemistries, resins, protecting groups, protected amino acids and reagents are well known in the art (See, Atherton, et al., 1989, Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, and Bodanszky, 1993, Peptide Chemistry, A Practical Textbook, 2nd Ed., Springer-Verlag, each of which is incorporated herein by reference in its entirety).

[0097] In addition, analogs and derivatives of polypeptides can be chemically synthesized as described supra. If desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the peptide sequence. Non-classical amino acids include, but are not limited to, the D-isomers of the common amino acids, α-amino isobutyric acid, 4-aminobutyric acid, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β-alanine, designer amino acids such as β-methyl amino acids, C-α-methyl amino acids, and N-α-methyl amino acids.

[0098] Polypeptides phosphorylated on the side chains of Tyr, Ser, Thr, Arg, Lys, and His can be synthesized in Fmoc solid phase synthesis using the appropriate side chain protected Fmoc-phospho amino acid. In this way, polypeptides with a combination of phosphorylated and non-phosphorylated Tyr, Ser, Thr, Arg, Lys, and His residues can be

synthesized. For example, the method of Staerkaer et al can be applied (1991, Tetrahedron Letters 32: 5389-5392). Other procedures (some for specific amino acids) are detailed in De Bont et al. (1987, Trav. Chim Pays Bas 106: 641, 642), Bannwarth and Trezeciak (1987, Helv. Chim. Acta 70: 175-186), Perich and Johns (1988, Tetrahedron Letters 29: 2369-2372), Kitas et al. (1990, J. Org. Chem. 55:4181-4187), Valerio et al. (1989, Int. J. Peptide Protein Res. 33:428-438), Perich et al. (1991, Tetrahedron Letters 32:4033-4034), Pennington (1994, Meth. Molec. Biol. 35:195-2), and Perich (1997, Methods Enzymol. 289:245-266, each of which is incorporated herein by reference in its entirety).

[0099] A phosphorylated polypeptide can also be produced by first culturing a cell transformed with a nucleic acid that encodes the amino acid sequence of the polypeptide. After producing such a polypeptide by cell culture, the hydroxyl groups of the appropriate amino acid are substituted by phosphate groups using organic synthesis or enzymatic methods with phosphorylation enzymes. For example, in the case of serine-specific phosphorylation, serine kinases can be used.

[00100] Phosphopeptide mimetics can also be synthesized, wherein a phosphorylated amino acid residue in a polypeptide is replaced with a phosphomimetic group. Non-limiting examples of phosphomimetic groups include O-boranophospho, borono, O-dithiophospho, phosphoramide, H-phosphonate, alkylphosphonate, phosphorothiolate, phosphodithiolate and phosphorofluoridate, any of which may be derivatized on Tyr, Thr, Ser, Arg, Lys, or His residues. In certain embodiments, an Asp or Glu residue is used as a phosphomimetic. Asp or Glu residues can also function as phosphomimetic groups, and be used in place of a phospho-Tyr, phospho-Thr, phospho-Ser, phospho-Arg, phospho-Lys and/or phospho-His residue in a peptide.

[00101] Purification of the resulting peptide is accomplished using conventional procedures, such as preparative HPLC using reverse-phase, gel permeation, partition and/or ion exchange chromatography. The choice of appropriate matrices and buffers are well known in the art and so are not described in detail herein.

5.3.2 Production of polypeptides using recombinant DNA technology

[00102] Polypeptides disclosed herein can also be prepared by recombinant DNA methods known in the art. A nucleic acid sequence encoding a polypeptide can be obtained by back translation of the amino acid sequence and synthesized by standard chemical methods, such as the use of an oligonucleotide synthesizer. Alternatively, coding information for polypeptides can be obtained from DNA templates using specifically designed oligonucleotide primers and PCR methodologies. Variations and fragments of the

polypeptides can be made by substitutions, insertions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, DNA sequences which encode the same or a variant of a polypeptide may be used in the practice of the present invention. These include, but are not limited to, nucleotide sequences which are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent or conservative change. The nucleic acid encoding a polypeptide can be inserted into an expression vector for propagation and expression in host cells.

[00103] As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc. 103:3185 (1981) (incorporated herein by reference in its entirety), modification can be made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired peptide or fusion protein. A number of such vectors and suitable host systems are now available. For expression of the peptide or fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host.

[00104] An expression construct refers to a nucleotide sequence encoding a polypeptide operably linked with one or more regulatory regions which enables expression of the peptide in an appropriate host cell. "Operably-linked" refers to an association in which the regulatory regions and the peptide sequence to be expressed are joined and positioned in such a way as to permit transcription, and ultimately, translation.

[00105] The regulatory regions necessary for transcription of the peptide can be provided by the expression vector. A translation initiation codon (ATG) may also be provided if the peptide gene sequence lacking its cognate initiation codon is to be expressed. In a compatible host-construct system, cellular transcriptional factors, such as RNA polymerase, will bind to the regulatory regions on the expression construct to effect transcription of the peptide sequence in the host organism. The precise nature of the regulatory regions needed for gene expression may vary from host cell to host cell. Generally, a promoter is required which is capable of binding RNA polymerase and promoting the transcription of an operably-associated nucleic acid sequence. Such regulatory regions may include those 5' non-coding sequences involved with initiation of transcription and translation, such as the TATA box,

capping sequence, CAAT sequence, and the like. The non-coding region 3' to the coding sequence may contain transcriptional termination regulatory sequences, such as terminators and polyadenylation sites.

[00106] In order to attach DNA sequences with regulatory functions, such as promoters, to the peptide gene sequence or to insert the peptide gene sequence into the cloning site of a vector, linkers or adapters providing the appropriate compatible restriction sites may be ligated to the ends of the cDNAs by techniques well known in the art (Wu et al., 1987, Methods in Enzymol 152:343-349, incorporated herein by reference in its entirety). Cleavage with a restriction enzyme can be followed by modification to create blunt ends by digesting back or filling in single-stranded DNA termini before ligation. Alternatively, a desired restriction enzyme site can be introduced into a fragment of DNA by amplification of the DNA by use of PCR with primers containing the desired restriction enzyme site.

[00107] An expression construct comprising a polypeptide coding sequence operably linked with regulatory regions can be directly introduced into appropriate host cells for expression and production of the peptide without further cloning. The expression constructs can also contain DNA sequences that facilitate integration of the DNA sequence into the genome of the host cell, *e.g.*, via homologous recombination. In this instance, it is not necessary to use an expression vector comprising a replication origin suitable for appropriate host cells in order to propagate and express the peptide in the host cells.

[00108] A variety of expression vectors may be used including plasmids, cosmids, phage, phagemids or modified viruses. Typically, such expression vectors comprise a functional origin of replication for propagation of the vector in an appropriate host cell, one or more restriction endonuclease sites for insertion of the peptide gene sequence, and one or more selection markers. Expression vectors may be constructed to carry nucleotide sequences for one or more of the polypeptides disclosed herein. The expression vector must be used with a compatible host cell which may be derived from a prokaryotic or eukaryotic organism including but not limited to bacteria, yeasts, insects, mammals and humans. Such host cells can be transformed to express one or more polypeptides disclosed herein, such as by transformation of the host cell with a single expression vector containing a plurality of nucleotide sequences encoding any of the polypeptides disclosed herein, or by transformation of the host cell with multiple expression vectors encoding different polypeptides disclosed herein.

[00109] In bacterial systems, a number of expression vectors may be advantageously selected to produce polypeptides. For example, when a large quantity of such a protein is to

be produced, such as for the generation of pharmaceutical compositions, vectors that direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2, 1791, incorporated herein by reference in its entirety), in which the peptide coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye and Inouye, 1985, Nucleic Acids Res. 13, 3101-3109; Van Heeke and Schuster, 1989, J. Biol. Chem 264, 5503-5509, each of which is incorporated herein by reference in its entirety); and the like. pGEX vectors may also be used to express these peptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the polypeptide can be released from the GST moiety.

[00110] Alternatively, for long term, high yield production of properly processed peptide complexes, stable expression in mammalian cells is preferred. Cell lines that stably express peptide complexes may be engineered by using a vector that contains a selectable marker. By way of example, following the introduction of the expression constructs, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the expression construct confers resistance to the selection and optimally allows cells to stably integrate the expression construct into their chromosomes and to grow in culture and to be expanded into cell lines. Such cells can be cultured for a long period of time while the peptide is expressed continuously.

[00111] The recombinant cells may be cultured under standard conditions of temperature, incubation time, optical density and media composition. However, conditions for growth of recombinant cells may be different from those for expression of the polypeptides. Modified culture conditions and media may also be used to enhance production of the peptides. For example, recombinant cells containing peptides with their cognate promoters may be exposed to heat or other environmental stress, or chemical stress. Any techniques known in the art may be applied to establish the optimal conditions for producing peptide complexes.

[00112] In one embodiment of the invention, a codon encoding methionine is added at the 5' end of the nucleotide sequence encoding a polypeptide to provide a signal for initiation of translation of the peptide. This methionine may remain attached to the polypeptide, or the methionine may be removed by the addition of an enzyme or enzymes that can catalyze the cleavage of methionine from the peptide. For example, in both prokaryotes and eukaryotes,

N-terminal methionine is removed by a methionine aminopeptidase (MAP) (Tsunasawa et al., 1985, J. Biol. Chem. 260, 5382-5391, incorporated herein by reference in its entirety). Methionine aminopeptidases have been isolated and cloned from several organisms, including *E. coli*, yeast, and rat.

[00113] The peptide may be recovered from the bacterial, mammalian, or other host cell types, or from the culture medium, by known methods (see, for example, Current Protocols in Immunology, vol. 2, chapter 8, Coligan et al. (ed.), John Wiley & Sons, Inc.; Pathogenic and Clinical Microbiology: A Laboratory Manual by Rowland et al., Little Brown & Co., June 1994, incorporated herein by reference in its entirety).

[00114] Both of the foregoing methods can be used for synthesizing a polypeptide disclosed herein. For example, a peptide comprising the amino acid sequence of the HSP-binding peptide can be synthesized chemically, and joined to an antigenic peptide, optionally produced by recombinant DNA technology, via a peptide bond.

[00115] Included within the scope of the invention are derivatives or analogs of the polypeptides disclosed herein that are modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation (*e.g.*, of the C-terminal carboxyl group), or derivatization by known protecting/blocking groups, or proteolytic cleavage. Any of numerous chemical modifications may be carried out by known techniques, including but not limited to, reagents useful for protection or modification of free NH_2- groups, free COOH- groups, OH- groups, side groups of Trp-, Tyr-, Phe-, His-, Arg-, or Lys-; specific chemical cleavage by cyanogen bromide, hydroxylamine, BNPS-Skatole, acid, or alkali hydrolysis; enzymatic cleavage by trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

5.4 Pharmaceutical Compositions

[00116] In another aspect, the instant disclosure provides a composition (*e.g.*, a pharmaceutical composition) comprising one or more polypeptide as disclosed herein. In certain embodiments, the instant disclosure provides a composition (*e.g.*, a pharmaceutical composition) comprising one or more (*e.g.*, two or more, three or more, four or more, five or more, ten or more, or 20 or more) different polypeptides as disclosed herein. In certain embodiments, the instant disclosure provides a composition (*e.g.*, a pharmaceutical composition) comprising no more than 30 different polypeptides as disclosed herein. In certain embodiments, the instant disclosure provides a composition (*e.g.*, a pharmaceutical composition) comprising 1 to 30 (*e.g.*, 2 to 20, 3 to 20, 4 to 20, 5 to 20, 5 to 15, or 5 to 10)

different polypeptides as disclosed herein. In certain embodiments, the different polypeptides each comprise the same HSP-binding peptide and a different antigenic peptide.

[00117] In certain embodiments, the composition further comprises a purified stress protein. Such composition is useful as a vaccine formulation. Also provided is a method for making a vaccine, the method comprising mixing one or more compositions disclosed herein with a purified stress protein such that the purified stress protein binds to at least one of the HSP-binding antigenic conjugates or peptides.

5.4.1 Polypeptides in complex with stress proteins

[00118] In a particular aspect, the instant disclosure provides a composition (*e.g.*, a pharmaceutical composition) comprising one or more polypeptides as disclosed herein and a purified stress protein. In certain embodiments, at least a portion of the purified stress protein binds to the polypeptide in the composition. Such compositions are useful as vaccine formulations for the treatment of a cancer or an infection of a pathogenic microbe.

[00119] In certain embodiments, prior to complexation with purified stress proteins, the polypeptides may be reconstituted from powder in 100% DMSO. Equimolar amounts of the peptides may then be pooled in a solution of 75% DMSO diluted in sterile water.

[00120] In certain embodiments, prior to complexation with purified stress proteins, the polypeptides may be reconstituted in neutral water.

[00121] In certain embodiments, prior to complexation with purified stress proteins, the polypeptides may be reconstituted in acidic water containing HCl.

[00122] In certain embodiments, prior to complexation with purified stress proteins, the polypeptides may be reconstituted in basic water containing NaOH.

[00123] In certain embodiments, prior to complexation with purified stress proteins, the solubility of each polypeptide in water may be tested. If a polypeptide is soluble in neutral water, neutral water may be used as a solvent for the polypeptide. If the polypeptide is not soluble in neutral water, solubility in acidic water containing HCl, or another acid, *e.g.*, acetic acid, phosphoric acid, or sulfuric acid may be tested. If the polypeptide is soluble in acidic water containing HCl (or another acid), acidic water containing HCl (or another acid) may be used as the solvent for the polypeptide. If the polypeptide is not soluble in acidic water containing HCl (or another acid), solubility in basic water containing NaOH may be tested. If the polypeptide is soluble in basic water containing NaOH, basic water containing NaOH may be used as the solvent for the polypeptide. If the polypeptide is not soluble in basic water containing NaOH, the polypeptide may be dissolved in DMSO. If the polypeptide is not soluble in DMSO the polypeptide may be excluded from the vaccine. The dissolved

polypeptides may then be mixed to make a pool of polypeptides. The dissolved polypeptides may be mixed at equal volume. The dissolved polypeptides may be mixed in equimolar amounts.

[00124] Stress proteins, which are also referred to interchangeably herein as heat shock proteins (HSPs), useful in the practice of the instant invention can be selected from among any cellular protein that is capable of binding other proteins or peptides and capable of releasing the bound proteins or peptides in the presence of adenosine triphosphate (ATP) or under acidic conditions. The intracellular concentration of such protein may increase when a cell is exposed to a stressful stimulus. In addition to those heat shock proteins that are induced by stress, the HSP60, HSP70, HSP90, HSP100, sHSPs, and PDI families also include proteins that are related to stress-induced HSPs in sequence similarity, for example, having greater than 35% amino acid identity, but whose expression levels are not altered by stress. Therefore, stress protein or heat shock protein embraces other proteins, mutants, analogs, and variants thereof having at least 35% (*e.g.*, at least 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) amino acid identity with members of these families whose expression levels in a cell are enhanced in response to a stressful stimulus. Accordingly, in certain embodiments, the stress protein is a member of the hsp60, hsp70, or hsp90 family of stress proteins (*e.g.*, Hsc70, human Hsc70), or a mutant, analog, or variant thereof. In certain embodiments, the stress protein is selected from the group consisting of hsc70, hsp70, hsp90, hsp110, grp170, gp96, calreticulin, a mutant thereof, and combinations of two or more thereof. In certain embodiments, the stress protein is Hsc70 (*e.g.*, human Hsc70). In certain embodiments, the stress protein is Hsp70 (*e.g.*, human Hsp70). In certain embodiments, the stress protein (*e.g.*, human hsc70) is a recombinant protein.

[00125] Amino acid sequences and nucleotide sequences of naturally occurring HSPs are generally available in sequence databases, such as GenBank. For example, Homo sapiens heat shock protein HSP70 (Heat Shock 70kDa Protein 1A) has the following identifiers HGNC: 5232; Entrez Gene: 3303; Ensembl: ENSG00000204389; OMIM: 140550; UniProtKB: P08107 and NCBI Reference Sequence: NM_005345.5. Computer programs, such as Entrez, can be used to browse the database, and retrieve any amino acid sequence and genetic sequence data of interest by accession number. These databases can also be searched to identify sequences with various degrees of similarities to a query sequence using programs, such as FASTA and BLAST, which rank the similar sequences by alignment scores and statistics. Nucleotide sequences of non-limiting examples of HSPs that can be used for preparation of the HSP peptide-binding fragments of the invention are as follows: human

Hsp70, Genbank Accession No. NM_005345, Sargent et al., 1989, Proc. Natl. Acad. Sci. U.S.A., 86:1968-1972; human Hsc70: Genbank Accession Nos. P11142, Y00371; human Hsp90, Genbank Accession No. X15183, Yamazaki et al., Nucl. Acids Res. 17:7108; human gp96: Genbank Accession No. X15187, Maki et al., 1990, Proc. Natl. Acad Sci., 87: 5658-5562; human BiP: Genbank Accession No. M19645; Ting et al., 1988, DNA 7: 275-286; human Hsp27, Genbank Accession No. M24743; Hickey et al., 1986, Nucleic Acids Res. 14:4127-45; mouse Hsp70: Genbank Accession No. M35021, Hunt et al., 1990, Gene, 87:199-204; mouse gp96: Genbank Accession No. M16370, Srivastava et al., 1987, Proc. Natl. Acad. Sci., 85:3807-3811; and mouse BiP: Genbank Accession No. U16277, Haas et al., 1988, Proc. Natl. Acad. Sci. U.S.A., 85: 2250-2254 (each of these references is incorporated herein by reference in its entirety).

[00126] In addition to the major stress protein families described above, an endoplasmic reticulum resident protein, calreticulin, has also been identified as yet another heat shock protein useful for eliciting an immune response when complexed to antigenic molecules (Basu and Srivastava, 1999, J. Exp. Med. 189:797-202; incorporated herein by reference in its entirety). Other stress proteins that can be used in the invention include grp78 (or BiP), protein disulfide isomerase (PDI), hsp110, and grp170 (Lin et al., 1993, Mol. Biol. Cell, 4:1109-1119; Wang et al., 2001, J. Immunol., 165:490-497, each of which is incorporated herein by reference in its entirety). Many members of these families were found subsequently to be induced in response to other stressful stimuli including nutrient deprivation, metabolic disruption, oxygen radicals, hypoxia and infection with intracellular pathogens (*see* Welch, May 1993, Scientific American 56-64; Young, 1990, Annu. Rev. Immunol. 8:401-420; Craig, 1993, Science 260:1902-1903; Gething, et al., 1992, Nature 355:33-45; and Lindquist, et al., 1988, Annu. Rev. Genetics 22:631-677, each of which is incorporated herein by reference in its entirety). It is contemplated that HSPs/stress proteins belonging to all of these families can be used in the practice of the invention. In certain embodiments, a stress protein encompasses any chaperone protein that facilitates peptide-MHC presentation. Suitable chaperone proteins include, but are not limited to, ER chaperones and tapasin (*e.g.*, human tapasin).

[00127] The major stress proteins can accumulate to very high levels in stressed cells, but they occur at low to moderate levels in cells that have not been stressed. For example, the highly inducible mammalian hsp70 is hardly detectable at normal temperatures but becomes one of the most actively synthesized proteins in the cell upon heat shock (Welch, et al., 1985, J. Cell. Biol. 101:1198-1211, incorporated herein by reference in its entirety). In contrast,

hsp90 and hsp60 proteins are abundant at normal temperatures in most, but not all, mammalian cells and are further induced by heat (Lai, et al., 1984, Mol. Cell. Biol. 4:2802-10; van Bergen en Henegouwen, et al., 1987, Genes Dev. 1:525-31, each of which is incorporated herein by reference in its entirety).

[00128] In various embodiments, nucleotide sequences encoding heat shock protein within a family or variants of a heat shock protein can be identified and obtained by hybridization with a probe comprising nucleotide sequence encoding an HSP under conditions of low to medium stringency. By way of example, procedures using such conditions of low stringency are as follows (*see also* Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792). Filters containing DNA are pretreated for 6 h at 40ºC in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55° C in a solution containing 2 x SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for signal detection. If necessary, filters are washed for a third time at 65-68°C before signal detection. Other conditions of low stringency which may be used are well known in the art (*e.g.*, as used for cross-species hybridizations).

[00129] Where stress proteins are used, peptide-binding fragments of stress proteins and functionally active derivatives, analogs, and variants thereof can also be used. Accordingly, in certain embodiments, the stress protein is a full-length HSP. In certain embodiments, the stress protein is a polypeptide comprising a domain of an HSP (*e.g.*, a member of the Hsp60, Hsp70, or Hsp90 family, such as Hsc70, particularly human Hsc70), wherein the domain is capable of being noncovalently associated with a peptide (*e.g.*, an HSP-binding peptide as described herein) to form a complex and optionally eliciting an immune response, and wherein the stress protein is not a full-length HSP.

[00130] In certain embodiments, the stress protein is a polypeptide that is capable of being noncovalently associated with a peptide (*e.g.*, an HSP-binding peptide as described herein) to form a complex and optionally eliciting an immune response, wherein the stress protein shares a high degree of sequence similarity with a wild-type HSP (*e.g.*, a member of the Hsp60, Hsp70, or Hsp90 family, such as Hsc70, particularly human Hsc70). To determine a region of identity between two amino acid sequences or nucleic acid sequences, the

sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = number of identical overlapping positions/total number of positions x 100%). In one embodiment, the two sequences are the same length.

[00131] The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877 (each of which is incorporated herein by reference in its entirety). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al., 1990, J. Mol. Biol. 215:403-410 (incorporated herein by reference in its entirety). BLAST nucleotide searches can be performed with the NBLAST program, *e.g.*, score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, *e.g.*, score=50, wordlength=3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Altschul et al., 1997, supra). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

[00132] In certain embodiments, isolated peptide-binding domains of a stress protein (*e.g.*, Hsp70 and Hsc70) are employed. These peptide-binding domains can be identified by computer modeling of the three dimensional structure of the peptide-binding site of a stress protein (*e.g.*, Hsp70 and Hsc70). See for example, the peptide-binding fragments of HSPs disclosed in United States patent publication US 2001/0034042 (incorporated herein by reference in its entirety).

[00133] In certain embodiments, the stress protein is a mutated stress protein which has an affinity for a target polypeptide that is greater than a native stress protein. Such mutated stress proteins can be useful when the target polypeptide is phosphorylated or is a phosphopeptide mimetic (such as non-hydrolyzable analogs) or has some other post-translational modification.

[00134] The stress proteins can be prepared by purification from tissues, or by recombinant DNA techniques. HSPs can be purified from tissues in the presence of ATP or under acidic conditions (pH 1 to pH 6.9), for subsequent *in vitro* complexing to one or more polypeptides. See Peng, et al., 1997, J. Immunol. Methods, 204:13-21; Li and Srivastava, 1993, EMBO J. 12:3143-3151 (each of these references is incorporated herein by reference in its entirety). "Purified" stress proteins are substantially free of materials that are associated with the proteins in a cell, in a cell extract, in a cell culture medium, or in an individual. In certain embodiments, the stress protein purified from a tissue is a mixture of different HSPs, for example, hsp70 and hsc70.

[00135] Using the defined amino acid or cDNA sequences of a given HSP or a peptide-binding domain thereof, one can make a genetic construct which is transfected into and expressed in a host cell. The recombinant host cells may contain one or more copies of a nucleic acid sequence comprising a sequence that encodes an HSP or a peptide-binding fragment, operably linked with regulatory region(s) that drives the expression of the HSP nucleic acid sequence in the host cell. Recombinant DNA techniques can be readily utilized to generate recombinant HSP genes or fragments of HSP genes, and standard techniques can be used to express such HSP gene fragments. Any nucleic acid sequence encoding an HSP peptide-binding domain, including cDNA and genomic DNA, can be used to prepare the HSPs or peptide-binding fragments of the invention. The nucleic acid sequence can be wild-type or a codon-optimized variant that encodes the same amino acid sequence. An HSP gene fragment containing the peptide-binding domain can be inserted into an appropriate cloning vector and introduced into host cells so that many copies of the gene sequence are generated. A large number of vector-host systems known in the art may be used such as, but not limited

to, bacteriophages such as lambda derivatives, or plasmids such as pBR322, pUC plasmid derivatives, the Bluescript vectors (Stratagene) or the pET series of vectors (Novagen). Any technique for mutagenesis known in the art can be used to modify individual nucleotides in a DNA sequence, for purpose of making amino acid substitution(s) in the expressed peptide sequence, or for creating/deleting restriction sites to facilitate further manipulations.

[00136] The stress proteins may be expressed as fusion proteins to facilitate recovery and purification from the cells in which they are expressed. For example, the stress proteins may contain a signal sequence leader peptide to direct its translocation across the endoplasmic reticulum membrane for secretion into culture medium. Further, the stress protein may contain an affinity label fused to any portion of the protein not involved in binding to a target polypeptide, for example, the carboxyl terminus. The affinity label can be used to facilitate purification of the protein, by binding to an affinity partner molecule. A variety of affinity labels known in the art may be used, non-limiting examples of which include the immunoglobulin constant regions, polyhistidine sequence (Petty, 1996, Metal-chelate affinity chromatography, in Current Protocols in Molecular Biology, Vol. 2, Ed. Ausubel et al., Greene Publish. Assoc. & Wiley Interscience, incorporated herein by reference in its entirety), glutathione S-transferase (GST; Smith, 1993, Methods Mol. Cell Bio. 4:220-229, incorporated herein by reference in its entirety), the *E. coli* maltose binding protein (Guan et al., 1987, Gene 67:21-30, incorporated herein by reference in its entirety), and various cellulose binding domains (U.S. Patent Nos. 5,496,934; 5,202,247; 5,137,819; Tomme et al., 1994, Protein Eng. 7:117-123, each of which is incorporated herein by reference in its entirety).

[00137] Such recombinant stress proteins can be assayed for peptide binding activity (*see, e.g.*, Klappa et al., 1998, EMBO J., 17:927-935, incorporated herein by reference in its entirety) for their ability to elicit an immune response. In certain embodiments, the recombinant stress protein produced in the host cell is of the same species as the intended recipient of the immunogenic composition (*e.g.*, human).

[00138] The stress protein may be bound to the polypeptide(s) non-covalently or covalently. In certain embodiments, the stress protein is non-covalently bound to the polypeptide. Methods of preparing such complexes are set forth *infra*.

[00139] The molar ratio of total polypeptide(s) to total stress protein(s) can be any ratio from about 0.01:1 to about 100:1, including but not limited to about 0.01:1, 0.02:1, 0.05:1. 0.1:1. 0.2:1, 0.5:1, 1:1, 1.5:1, 2:1, 2.5:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1. In certain

embodiments, the composition comprises a plurality of complexes each comprising a polypeptide disclosed herein and a stress protein, wherein the molar ratio of the polypeptide to the stress protein in each complex is at least about 1:1 (*e.g.*, about 1.5:1, 2:1, 2.5:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1).

[00140] In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 0.5:1 to 5:1. In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1 to 2:1. In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1, 1.25:1, or 1.5:1. Such ratios, particularly the ratios close to 1:1, are advantageous in that the composition does not comprise a great excess of free peptide(s) that is not bound to a stress protein. Since many antigenic peptides comprising MHC-binding epitopes tend to comprise hydrophobic regions, an excess amount of free peptide(s) may tend to aggregate during preparation and storage of the composition. Substantial complexation with a stress protein at a molar ratio of total polypeptide(s) to total stress protein(s) close to 1:1 (*e.g.*, 1:1, 1.25:1, 1.5:1, or 2:1) is enabled by a high binding affinity of the polypeptide to the stress protein. Accordingly, in certain embodiments, the polypeptide binds to an HSP (*e.g.*, Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin) with a K_d lower than 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M. In certain embodiments, the polypeptide binds to Hsc70 (*e.g.*, human Hsc70) with a K_d of 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, or lower.

[00141] In certain embodiments, at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% of the stress protein binds to the polypeptide in the composition. In certain embodiments, substantially all of the stress protein binds to the polypeptide in the composition.

[00142] Any number of different polypeptides can be included in a single composition as disclosed herein. In certain embodiments, the compositions comprise no more than 100 different polypeptides, *e.g.*, 2-50, 2-30, 2-20, 5-20, 5-15, 5-10, or 10-15 different polypeptides. In certain embodiments, each of the polypeptides comprises the same HSP-binding peptide and a different antigenic peptide. In certain embodiments, the composition comprises a single stress protein, wherein the stress protein is capable of binding to the HSP-binding peptide. Pharmaceutical compositions of the invention can be formulated to contain one or more pharmaceutically acceptable carriers or excipients including bulking agents, stabilizing agents, buffering agents, sodium chloride, calcium salts, surfactants, antioxidants, chelating agents, other excipients, and combinations thereof.

[00143] Bulking agents are preferred in the preparation of lyophilized formulations of the vaccine composition. Such bulking agents form the crystalline portion of the lyophilized product and may be selected from the group consisting of mannitol, glycine, alanine, and hydroxyethyl starch (HES).

[00144] Stabilizing agents may be selected from the group consisting of sucrose, trehalose, raffinose, and arginine. These agents are preferably present in amounts between 1-4%. Sodium chloride can be included in the present formulations preferably in an amount of 100-300 mM, or if used without the aforementioned bulking agents, can be included in the formulations in an amount of between 300-500 mM NaCl. Calcium salts include calcium chloride, calcium gluconate, calcium glubionate, or calcium gluceptate.

[00145] Buffering agents can be any physiologically acceptable chemical entity or combination of chemical entities which have a capacity to act as buffers, including but not limited to histidine, potassium phosphate, TRIS [tris-(hydroxymethyl)-aminomethane], BIS-Tris Propane (1,3-bis-[tris-(hydroxymethyl)methylamino]-propane), PIPES [piperazine-N,N'-bis-(2-ethanesulfonic acid)], MOPS [3-(N-morpholino)ethanesulfonic acid], HEPES (N-2-hydroxyethyl-piperazine-N'-2-ethanesulfonic acid), MES [2-(N-morpholino)ethanesulfonic acid], and ACES (N-2-acetamido-2-aminoethanesulfonic acid). Typically, the buffering agent is included in a concentration of 10-50 mM. Specific examples of base buffers include (i) PBS; (ii) 10mM KPO_4, 150 mM NaCl; (iii) 10 mM HEPES, 150 mM NaCl; (iv) 10 mM imidazole, 150 mM NaCl; and (v) 20 mM sodium citrate. Excipients that can be used include (i) glycerol (10%, 20%); (ii) Tween 50 (0.05%, 0.005%); (iii) 9% sucrose; (iv) 20% sorbitol; (v) 10 mM lysine; or (vi) 0.01 mM dextran sulfate.

[00146] Surfactants, if present, are preferably in a concentration of 0.1% or less, and may be chosen from the group including but not limited to polysorbate 20, polysorbate 80, pluronic polyols, and BRIJ 35 (polyoxyethylene 23 laurel ether). Antioxidants, if used, must be compatible for use with a pharmaceutical preparation, and are preferably water soluble. Suitable antioxidants include homocysteine, glutathione, lipoic acid, 6-hydroxy-2,5,7,8-tetramethylchroman-2-carboxylic acid (Trolox), methionine, sodium thiosulfate, platinum, glycine-glycine-histidine (tripeptide), and butylatedhydroxytoluene (BHT). Chelating agents should preferably bind metals such as copper and iron with greater affinity than calcium, if a calcium salt is being used in the composition. An exemplary chelator is deferoxamine.

[00147] Many formulations known in the art can be used. For example, U.S. Patent No. 5,763,401 describes a therapeutic formulation, comprising 15-60 mM sucrose, up to 50 mM NaCl, up to 5 mM calcium chloride, 65-400 mM glycine, and up to 50 mM histidine. In some

embodiments, the therapeutic formulation is a solution of 9% sucrose in potassium phosphate buffer.

[00148] U.S. Patent No. 5,733,873 (incorporated herein by reference in its entirety) discloses formulations which include between 0.01-1 mg/ml of a surfactant. This patent discloses formulations having the following ranges of excipients: polysorbate 20 or 80 in an amount of at least 0.01 mg/ml, preferably 0.02-1.0 mg/ml; at least 0.1 M NaCl; at least 0.5 mM calcium salt; and at least 1 mM histidine. More particularly, the following specific formulations are also disclosed: (1) 14.7-50-65 mM histidine, 0.31-0.6 M NaCl, 4 mM calcium chloride, 0.001-0.02-0.025% polysorbate 80, with or without 0.1% PEG 4000 or 19.9 mM sucrose; and (2) 20 mg/ml mannitol, 2.67 mg/ml histidine, 18 mg/ml NaCl, 3.7 mM calcium chloride, and 0.23 mg/ml polysorbate 80.

[00149] The use of low or high concentrations of sodium chloride has been described, for example U.S. Patent No. 4,877,608 (incorporated herein by reference in its entirety) teaches formulations with relatively low concentrations of sodium chloride, such as formulations comprising 0.5 mM-15 mM NaCl, 5 mM calcium chloride, 0.2 mM-5 mM histidine, 0.01-10 mM lysine hydrochloride and up to 10% maltose, 10% sucrose, or 5% mannitol.

[00150] U.S. Patent No. 5,605,884 (incorporated herein by reference in its entirety) teaches the use of formulations with relatively high concentrations of sodium chloride. These formulations include 0.35 M-1.2 M NaCl, 1.5-40 mM calcium chloride, 1 mM-50 mM histidine, and up to 10% sugar such as mannitol, sucrose, or maltose. A formulation comprising 0.45 M NaCl, 2.3 mM calcium chloride, and 1.4 mM histidine is exemplified.

[00151] International Patent Application WO 96/22107 (incorporated herein by reference in its entirety) describes formulations which include the sugar trehalose, for example formulations comprising: (1) 0.1 M NaCl, 15 mM calcium chloride, 15 mM histidine, and 1.27 M (48%) trehalose; or (2) 0.011% calcium chloride, 0.12% histidine, 0.002% TRIS, 0.002% Tween 80, 0.004% PEG 3350, 7.5% trehalose; and either 0.13% or 1.03% NaCl.

[00152] U.S. Patent No. 5,328,694 (incorporated herein by reference in its entirety) describes a formulation which includes 100-650 mM disaccharide and 100 mM-1.0 M amino acid, for example (1) 0.9 M sucrose, 0.25 M glycine, 0.25 M lysine, and 3 mM calcium chloride; and (2) 0.7 M sucrose, 0.5 M glycine, and 5 mM calcium chloride. Pharmaceutical compositions can be optionally prepared as lyophilized product, which may then be formulated for oral administration or reconstituted to a liquid form for parenteral administration.

[00153] In certain embodiments, the composition stimulates a T-cell response against a cell expressing or displaying a polypeptide comprising one or more of the MHC-binding epitopes in a subject to whom the composition is administered. The cell expressing the polypeptide may be a cell comprising a polynucleotide encoding the polypeptide, wherein the polynucleotide is in the genome of the cell, in an episomal vector, or in the genome of a virus that has infected the cell. The cell displaying the polypeptide may not comprise a polynucleotide encoding the polypeptide, and may be produced by contacting the cell with the polypeptide or a derivative thereof.

[00154] In certain embodiments, the composition induces *in vitro* activation of T cells in peripheral blood mononuclear cells (PBMCs) isolated from a subject. The *in vitro* activation of T cells includes, without limitation, *in vitro* proliferation of T cells, production of cytokines (*e.g.*, IFNγ) from T cells, and increased surface expression of activation markers (*e.g.*, CD25, CD45RO) on T cells.

5.4.2 Preparation of complexes of polypeptides and stress proteins

[00155] In another aspect, the instant disclosure provides a method of making a vaccine, the method comprising mixing one or more polypeptides as disclosed herein with a purified stress protein *in vitro* under suitable conditions such that the purified stress protein binds to at least one of the polypeptides. The method is also referred to as a complexing reaction herein. In certain embodiments, two or more purified stress proteins are employed, wherein each purified stress protein binds to at least one of the polypeptides.

[00156] The stress protein may be bound to the polypeptide non-covalently or covalently. In certain embodiments, the stress protein is non-covalently bound to the polypeptide. In various embodiments, the complexes formed *in vitro* are optionally purified. Purified complexes of stress proteins and polypeptides are substantially free of materials that are associated with such complexes in a cell, or in a cell extract. Where purified stress proteins and purified polypeptides are used in an *in vitro* complexing reaction, the term "purified complex(es)" does not exclude a composition that also comprises free stress proteins and conjugates or peptides not in complexes.

[00157] Any stress proteins described *supra* may be employed in the method of the invention. In certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, a mutant thereof, and combinations of two or more thereof. In one embodiment, the stress protein is an Hsc70, *e.g.*, a human Hsc70. In another embodiment, the stress protein is an Hsp70, *e.g.*, a human Hsp70.

In certain embodiments, the stress protein (*e.g.*, human Hsc70 or human Hsp70) is a recombinant protein.

[00158] Prior to complexing, HSPs can be pretreated with ATP or exposed to acidic conditions to remove any peptides that may be non-covalently associated with the HSP of interest. Acidic conditions are any pH levels below pH 7, including the ranges pH 1-pH 2, pH 2-pH 3, pH 3-pH 4, pH 4-pH 5, pH 5-pH 6, and pH 6-pH 6.9. When the ATP procedure is used, excess ATP is removed from the preparation by the addition of apyranase as described by Levy, et al., 1991, Cell 67:265-274 (incorporated herein by reference in its entirety). When acidic conditions are used, the buffer is readjusted to neutral pH by the addition of pH modifying reagents.

[00159] The molar ratio of total polypeptide(s) to total stress protein(s) can be any ratio from 0.01:1 to 100:1, including but not limited to 0.01:1, 0.02:1, 0.05:1. 0.1:1. 0.2:1, 0.5:1, 1:1, 1.5:1, 2:1, 2.5:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1. In certain embodiments, the composition to be prepared comprises a plurality of complexes each comprising a polypeptide disclosed herein and a stress protein, and the complexing reaction comprises mixing the polypeptides with the stress proteins, wherein the molar ratio of the polypeptide to the stress protein in each complex is at least 1:1 (*e.g.*, about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1).

[00160] In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 0.5:1 to 5:1. In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1 to 2:1. In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1, 1.25:1, or 1.5:1. Such ratios, particularly the ratios close to 1:1, are advantageous in that the composition does not comprise a great excess of free peptide(s) that is not bound to a stress protein. Since many antigenic peptides comprising MHC-binding epitopes tend to comprise hydrophobic regions, an excess amount of free peptide(s) may tend to aggregate during preparation and storage of the composition. Substantial complexation with a stress protein at a molar ratio of total polypeptide(s) to total stress protein(s) close to 1:1 (*e.g.*, 1:1, 1.25:1, 1.5:1, or 2:1) is enabled by a high binding affinity of the polypeptide to the stress protein. Accordingly, in certain embodiments, the polypeptide used in the complexing reaction binds to an HSP (*e.g.*, Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin) with a K_d lower than 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M. In certain embodiments, the polypeptide binds to

Hsc70 (*e.g.*, human Hsc70) with a K_d of 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, or lower.

[00161] The method disclosed herein can be used to prepare a composition (*e.g.*, a pharmaceutical composition or a vaccine) in bulk (*e.g.*, greater than or equal to 30 mg, 50 mg, 100 mg, 200 mg, 300 mg, 500 mg, or 1 g of total peptide and protein). The prepared composition can then be transferred to single-use or multi-use containers, or apportioned to unit dosage forms. Alternatively, method disclosed herein can be used to prepare a composition (*e.g.*, a pharmaceutical composition or a vaccine) in a small amount (*e.g.*, less than or equal to 300 μg, 1 mg, 3 mg, 10 mg, 30 mg, or 100 mg of total peptide and protein). In certain embodiments, the composition is prepared for single use, optionally in a unit dosage form.

[00162] In certain embodiments, the total amount of the polypeptide(s) and stress protein in the pharmaceutical composition is about 10 μg to 600 μg (*e.g.*, about 50 μg, 100 μg, 200 μg, 300 μg, 400 μg, or 500 μg). In certain embodiments, the total amount of the polypeptide(s) and stress protein in the pharmaceutical composition is about 300 μg. Amounts of the stress protein(s) and polypeptide(s) in a unit dosage form are disclosed *infra*.

[00163] An exemplary protocol for noncovalent complexing of a population of polypeptides to a stress protein *in vitro* is provided herein. The population of polypeptides can comprise a mixture of the different polypeptide species of the invention. Then, the mixture is incubated with the purified and/or pretreated stress protein for from 15 minutes to 3 hours (*e.g.*, 1 hour) at from 4° to 50° C (*e.g.*, 37° C) in a suitable binding buffer, such as phosphate buffered saline pH 7.4 optionally supplemented with 0.01% Polysorbate 20; a buffer comprising 9% sucrose in potassium phosphate buffer; a buffer comprising 2.7 mM Sodium Phosphate Dibasic, 1.5 mM Potassium Phosphate Monobasic, 150 mM NaCl, pH 7.2; a buffer containing 20 mM sodium phosphate, pH 7.2-7.5, 350-500 mM NaCl, 3 mM $MgCl_2$ and 1 mM phenyl methyl sulfonyl fluoride (PMSF); and the buffer optionally comprising 1 mM ADP. Any buffer may be used that is compatible with the stress protein. The preparations are then optionally purified by centrifugation through a Centricon 10 assembly (Millipore; Billerica, MA) to remove any unbound peptide. The non-covalent association of the proteins/peptides with the HSPs can be assayed by High Performance Liquid Chromatography (HPLC), Mass Spectrometry (MS), mixed lymphocyte target cell assay (MLTC), or enzyme-linked immunospot (ELISPOT) assay (Taguchi T, et al., J Immunol Methods 1990; 128: 65-73, incorporated herein by reference in its entirety). Once the complexes have been isolated and diluted, they can be optionally characterized further in

animal models using the administration protocols and excipients described herein (see, *e.g.*, Example 2 *infra*).

[00164] Complexes of stress proteins and polypeptides from separate covalent and/or non-covalent complexing reactions can be prepared to form a composition before administration to a subject. In certain embodiments, the composition is prepared within 1, 2, 3, 4, 5, 6, or 7 days before administration to a subject. In certain embodiments, the composition is prepared within 1, 2, 3, 4, 5, 6, 7, or 8 weeks before administration to a subject. In certain embodiments, the composition is prepared within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months before administration to a subject. The composition can optionally be stored at about 4 °C, -20 °C, or -80 °C after preparation and before use.

[00165] In certain embodiments, the complexes prepared by the method disclosed herein are mixed with an adjuvant at bedside just prior to administration to a patient. In certain embodiments, the adjuvant comprises a saponin or an immunostimulatory nucleic acid. In certain embodiments, the adjuvant comprises QS-21. In certain embodiments, the dose of QS-21 is 10 μg, 25 μg, or 50 μg. In certain embodiments, the dose of QS-21 is 50 μg. In certain embodiments, the adjuvant comprises a TLR agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[00166] As an alternative to making non-covalent complexes of stress proteins and polypeptides, the polypeptides can be covalently attached to stress proteins, *e.g.*, by chemical crosslinking or UV crosslinking. Any chemical crosslinking or UV crosslinking methods known in the art (see, *e.g.*, Wong, 1991, Chemistry of Protein Conjugation and Cross-Linking, CRC Press, incorporated herein by reference in its entirety) can be employed. For example, glutaraldehyde crosslinking (see, *e.g.*, Barrios et al., 1992, Eur. J. Immunol. 22: 1365-1372, incorporated herein by reference in its entirety) may be used. In an exemplary protocol, 1-2 mg of HSP-peptide complex is cross-linked in the presence of 0.002% glutaraldehyde for 2 hours. Glutaraldehyde is removed by dialysis against phosphate buffered saline (PBS) overnight (Lussow et al., 1991, Eur. J. Immunol. 21: 2297-2302, incorporated herein by reference in its entirety).

5.4.3 Vaccines

[00167] The compositions disclosed herein are useful as vaccines. Accordingly, in another aspect, the instant disclosure provides a vaccine formulation. The vaccine formulation may be prepared by any method that results in a stable, sterile, preferably injectable formulation.

[00168] In certain embodiments, the vaccine comprises one or more compositions disclosed herein and one or more adjuvants. A variety of adjuvants may be employed, including, for example, systemic adjuvants and mucosal adjuvants. A systemic adjuvant is an adjuvant that can be delivered parenterally. Systemic adjuvants include adjuvants that create a depot effect, adjuvants that stimulate the immune system, and adjuvants that do both.

[00169] An adjuvant that creates a depot effect is an adjuvant that causes the antigen to be slowly released in the body, thus prolonging the exposure of immune cells to the antigen. This class of adjuvants includes alum (*e.g.*, aluminum hydroxide, aluminum phosphate); or emulsion-based formulations including mineral oil, non-mineral oil, water-in-oil or oil-in-water-in oil emulsion, oil-in-water emulsions such as Seppic ISA series of Montanide adjuvants (*e.g.*, Montanide ISA 720, AirLiquide, Paris, France); MF-59 (a squalene-in-water emulsion stabilized with Span 85 and Tween 80; Chiron Corporation, Emeryville, Calif.; and PROVAX (an oil-in-water emulsion containing a stabilizing detergent and a micelle-forming agent; IDEC, Pharmaceuticals Corporation, San Diego, Calif.).

[00170] Other adjuvants stimulate the immune system, for instance, cause an immune cell to produce and secrete cytokines or IgG. This class of adjuvants includes immunostimulatory nucleic acids, such as CpG oligonucleotides; saponins purified from the bark of the *Q. saponaria* tree, such as QS-21; poly[di(carboxylatophenoxy)phosphazene (PCPP polymer; Virus Research Institute, USA); RNA mimetics such as polyinosinic:polycytidylic acid (poly I:C) or poly I:C stabilized with poly-lysine (poly-ICLC [Hiltonol®; Oncovir, Inc.]; derivatives of lipopolysaccharides (LPS) such as monophosphoryl lipid A (MPL; Ribi ImmunoChem Research, Inc., Hamilton, Mont.), muramyl dipeptide (MDP; Ribi) and threonyl-muramyl dipeptide (t-MDP; Ribi); OM-174 (a glucosamine disaccharide related to lipid A; OM Pharma SA, Meyrin, Switzerland); and Leishmania elongation factor (a purified Leishmania protein; Corixa Corporation, Seattle, Wash.).

[00171] Other systemic adjuvants are adjuvants that create a depot effect and stimulate the immune system. These compounds have both of the above-identified functions of systemic adjuvants. This class of adjuvants includes but is not limited to ISCOMs (Immunostimulating complexes which contain mixed saponins, lipids and form virus-sized particles with pores that can hold antigen; CSL, Melbourne, Australia); AS01 which is a liposome based formulation containing MPL and QS-21 (GlaxoSmithKline, Belgium); AS02 (GlaxoSmithKline , which is an oil-in-water emulsion containing MPL and QS-21: GlaxoSmithKline, Rixensart, Belgium); AS04 (GlaxoSmithKline, which contains alum and MPL; GSK, Belgium); AS15 which is a liposome based formulation containing CpG

oligonucleotides, MPL and QS-21 (GlaxoSmithKline, Belgium); non-ionic block copolymers that form micelles such as CRL 1005 (these contain a linear chain of hydrophobic polyoxypropylene flanked by chains of polyoxyethylene; Vaxcel, Inc., Norcross, Ga.); and Syntex Adjuvant Formulation (SAF, an oil-in-water emulsion containing Tween 80 and a nonionic block copolymer; Syntex Chemicals, Inc., Boulder, Colo.).

[00172] The mucosal adjuvants useful according to the invention are adjuvants that are capable of inducing a mucosal immune response in a subject when administered to a mucosal surface in conjunction with complexes of the invention. Mucosal adjuvants include CpG nucleic acids (*e.g.* PCT published patent application WO 99/61056, incorporated herein by reference in its entirety), bacterial toxins: *e.g.*, Cholera toxin (CT), CT derivatives including but not limited to CT B subunit (CTB); CTD53 (Val to Asp); CTK97 (Val to Lys); CTK104 (Tyr to Lys); CTD53/K63 (Val to Asp, Ser to Lys); CTH54 (Arg to His); CTN107 (His to Asn); CTE114 (Ser to Glu); CTE112K (Glu to Lys); CTS61F (Ser to Phe); CTS 106 (Pro to Lys); and CTK63 (Ser to Lys), Zonula occludens toxin (zot), Escherichia coli heat-labile enterotoxin, Labile Toxin (LT), LT derivatives including but not limited to LT B subunit (LTB); LT7K (Arg to Lys); LT61F (Ser to Phe); LT112K (Glu to Lys); LT118E (Gly to Glu); LT146E (Arg to Glu); LT192G (Arg to Gly); LTK63 (Ser to Lys); and LTR72 (Ala to Arg), Pertussis toxin, PT. including PT-9K/129G; Toxin derivatives (see below); Lipid A derivatives (*e.g.*, monophosphoryl lipid A, MPL); Muramyl Dipeptide (MDP) derivatives; bacterial outer membrane proteins (*e.g.*, outer surface protein A (OspA) lipoprotein of *Borrelia burgdorferi*, outer membrane protein of *Neisseria meningitidis*); oil-in-water emulsions (*e.g.*, MF59; aluminum salts (Isaka et al., 1998, 1999); and Saponins (*e.g.*, QS-21, *e.g.*, QS-21 Stimulon®, Antigenics LLC, Lexington, Mass.), ISCOMs, MF-59 (a squalene-in-water emulsion stabilized with Span 85 and Tween 80; Chiron Corporation, Emeryville, Calif.); the Seppic ISA series of Montanide adjuvants (*e.g.*, Montanide ISA 720; AirLiquide, Paris, France); PROVAX (an oil-in-water emulsion containing a stabilizing detergent and a micelle-forming agent; IDEC Pharmaceuticals Corporation, San Diego, Calif.); Syntext Adjuvant Formulation (SAF; Syntex Chemicals, Inc., Boulder, Colo.); poly[di(carboxylatophenoxy)]phosphazene (PCPP polymer; Virus Research Institute, USA) and Leishmania elongation factor (Corixa Corporation, Seattle, Wash.).

[00173] In certain embodiments, the adjuvant added to the compositions disclosed herein comprises a saponin and/or an immunostimulatory nucleic acid. In certain embodiments, the adjuvant added to the composition comprises or further comprises QS-21.

[00174] In certain embodiments, the adjuvant added to the compositions disclosed herein comprises a Toll-like receptor (TLR) agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[00175] The compositions of the invention described herein may be combined with an adjuvant in several ways. For example, different polypeptides may be mixed together first to form a mixture and then complexed with stress protein(s) and/or adjuvant(s) to form a composition. As another example, different polypeptides may be complexed individually with a stress protein and/or adjuvant(s), and the resulting batches of complexes may then be mixed to form a composition.

[00176] The adjuvant can be administered prior to, during, or following administration of the compositions comprising complexes of stress protein and polypeptides. Administration of the adjuvant and the compositions can be at the same or different administration sites.

5.4.4 Unit dosage forms

[00177] In another aspect, the instant disclosure provides a unit dosage form of a pharmaceutical composition or vaccine disclosed herein.

[00178] The amounts and concentrations of the polypeptides, stress proteins, and/or adjuvants at which the efficacy of a vaccine formulation of the invention may vary depending on the chemical nature and the potency of the polypeptides, stress proteins, and/or adjuvants. Typically, the starting amounts and concentrations in the vaccine formulation are the ones conventionally used for eliciting the desired immune response, using the conventional routes of administration, *e.g.*, intramuscular injection. The amounts and concentrations of the peptides, conjugates, stress proteins, and/or adjuvants can then be adjusted, *e.g.*, by dilution using a diluent, so that an effective protective immune response is achieved as assessed using standard methods known in the art (*e.g.*, determined by the antibody or T-cell response to the vaccine formulation relative to a control formulation).

[00179] In certain embodiments, the total amount of the polypeptides and stress protein in the pharmaceutical composition is about 10 μg to 600 μg (*e.g.*, about 50 μg, 100 μg, 200 μg, 300 μg, 400 μg, or 500 μg). In certain embodiments, the total amount of the polypeptides and stress protein in the pharmaceutical composition is about 300 μg. In certain embodiments, the amount of the stress protein in the composition is about 250 μg to 290 μg.

[00180] In certain embodiments, the amount of the stress protein in the pharmaceutical composition is about 10 μg to 600 μg (*e.g.*, about 50 μg, 100 μg, 200 μg, 300 μg, 400 μg, or

500 μg). In certain embodiments, the amount of the stress protein in the pharmaceutical composition is about 300 μg. The amount of the polypeptide is calculated based on a designated molar ratio and the molecular weight of the polypeptides.

[00181] In certain embodiments, the total molar amount of the polypeptides in the unit dosage form of the pharmaceutical composition is about 0.1 to 10 nmol (*e.g.*, about 0.1 nmol, 0.5 nmol, 1 nmol, 2 nmol, 3 nmol, 4 nmol, 5 nmol, 6 nmol, 7 nmol, 8 nmol, 9 nmol, or 10 nmol). In certain embodiments, the total molar amount of the polypeptides in the unit dosage form of the pharmaceutical composition is about 4 nmol. In certain embodiments, the total molar amount of the polypeptides in the unit dosage form of the pharmaceutical composition is about 5 nmol.

[00182] The molar ratio of total polypeptides to total stress proteins can be any ratio from about 0.01:1 to about 100:1, including but not limited to about 0.01:1, 0.02:1, 0.05:1. 0.1:1. 0.2:1, 0.5:1, 1:1, 1.5:1, 2:1, 2.5:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1. In certain embodiments, the composition comprises a plurality of complexes each comprising a polypeptide and a stress protein, wherein the molar ratio of the polypeptide to the stress protein in each complex is at least about 1:1 (*e.g.*, about 1.5:1, 2:1, 2.5:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 11:1, 12:1, 13:1, 14:1, 15:1, 16:1, 17:1, 18:1, 19:1, 20:1, 30:1, 40:1, 49:1, up to 100:1). In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 0.5:1 to 5:1.

[00183] In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1 to 2:1. In certain embodiments, the molar ratio of total polypeptide(s) to total stress protein(s) is about 1:1, 1.25:1, or 1.5:1. Such ratios, particularly the ratios close to 1:1, are advantageous in that the composition does not comprise a great excess of free peptide(s) that is not bound to a stress protein. Since many antigenic peptides comprising MHC-binding epitopes tend to comprise hydrophobic regions, an excess amount of free peptide(s) may tend to aggregate during preparation and storage of the composition. Substantial complexation with a stress protein at a molar ratio of total polypeptide(s) to total stress protein(s) close to 1:1 (*e.g.*, 1:1, 1.25:1, 1.5:1, or 2:1) is enabled by a high binding affinity of the polypeptide to the stress protein. Accordingly, in certain embodiments, the polypeptide binds to an HSP (*e.g.*, Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin) with a K_d lower than 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M. In certain embodiments, the polypeptide binds to Hsc70 (*e.g.*, human Hsc70) with a K_d of 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, or lower.

[00184] Methods of calculating the amounts of components in the unit dosage form are provided. For example, in certain embodiments, the polypeptides have an average molecular weight of about 3 kD, and the molecular weight of Hsc70 is about 71 kD. Assuming in one embodiment that the total amount of the polypeptides and stress protein in the pharmaceutical composition is 300 μg, and the molar ratio of the polypeptides to hsc70 is 1.5:1. The molar amount of Hsc70 can be calculated as 300 μg divided by 71 kD + 1.5 × 3 kD, resulting in about 4.0 nmol, and the mass amount of Hsc70 can be calculated by multiplying the molar amount with 71 kD, resulting in about 280 kD. The total molar amount of the polypeptides can be calculated as 1.5 × 4.0 nmol, resulting in 6.0 nmol. If 10 different polypeptides are employed, the molar amount of each polypeptide is 0.60 nmol. Assuming in another embodiment that a 300 μg dose of Hsc70 is intended to be included in a unit dosage form, and the molar ratio of polypeptides to Hsc70 is 1.5:1. The total molar amount of the polypeptides can be calculated as 300 μg divided by 71 kD then times 1.5, resulting in 6.3 nmol. If 10 different polypeptides are employed, the molar amount of each polypeptide is 0.63 nmol. In cases where one or more of the variables are different from those in the examples, the quantities of the stress proteins and of the polypeptides are scaled accordingly.

[00185] It is further appreciated that the unit dosage form can optionally comprise one or more adjuvants as disclosed *supra*. In certain embodiments, the adjuvant comprises a saponin and/or an immunostimulatory nucleic acid. In certain embodiments, the adjuvant comprises or further comprises QS-21. In certain embodiments, the amount of QS-21 in the unit dosage form of pharmaceutical composition is 10 μg, 25 μg, or 50 μg. In certain embodiments, the amount of QS-21 in the unit dosage form of pharmaceutical composition is 50 μg. In certain embodiments, the adjuvant comprises a Toll-like receptor (TLR) agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

5.5 Methods of Use

[00186] The compositions (*e.g.*, pharmaceutical compositions), vaccine formulations, and unit dosage forms disclosed herein are useful for inducing a cellular immune response. Stress proteins can deliver immunogenic peptides through the cross-presentation pathway in antigen presenting cells (APCs) (*e.g.*, macrophages and dendritic cells (DCs) via membrane receptors (mainly CD91) or by binding to Toll-like receptors, thereby leading to activation of $CD8^+$ and $CD4^+$ T cells. Internalization of a stress protein-peptide complex results in functional

maturation of the APCs with chemokine and cytokine production leading to activation of natural killer cells (NK), monocytes and Th1 and Th-2-mediated immune responses.

[00187] Accordingly, in one aspect, the instant disclosure provides a method of inducing a cellular immune response to an antigenic peptide in a subject, the method comprising administering to the subject an effective amount of a composition, vaccine formulations, or unit dosage form as disclosed herein. In another aspect, the instant disclosure provides a method of treating a disease (*e.g.*, cancer or infection) in a subject, the method comprising administering to the subject an effective amount of a composition, vaccine formulations, or unit dosage form as disclosed herein. The compositions (*e.g.*, pharmaceutical compositions), vaccine formulations, and unit dosage forms disclosed herein can also be used in preparing a medicament or vaccine for the treatment of a subject.

[00188] In various embodiments, such subjects can be an animal, *e.g.*, a mammal, a non-human primate, and a human. The term "animal" includes companion animals, such as cats and dogs; zoo animals; wild animals, including deer, foxes and raccoons; farm animals, livestock and fowl, including horses, cattle, sheep, pigs, turkeys, ducks, and chickens, and laboratory animals, such as rodents, rabbits, and guinea pigs. In certain embodiments, the subject has cancer. In certain embodiments, the subject has infection of a pathogenic microbe.

5.5.1 Treatment of cancer

[00189] The compositions, vaccine formulations, or unit dosage forms of the invention can be used alone or in combination with other therapies for the treatment of cancer. One or more of the MHC-binding epitopes in the HSP-binding antigenic conjugate(s) or peptide(s) can be present in the subject's cancer cells. In certain embodiments, one or more of the MHC-binding epitopes are common to or frequently found in the type and/or stage of the cancer. As used herein, the term "frequently found in cancers" refers to one or more mutant MHC-binding epitopes that are found in greater than 5% of cancers. In certain embodiments, one or more of the MHC-binding epitopes are specific to the cancer of the subject.

[00190] Cancers that can be treated using the compositions, vaccine formulations, or unit dosage forms of the invention include, without limitation, a solid tumor, a hematological cancer (*e.g.*, leukemia, lymphoma, myeloma, *e.g.*, multiple myeloma), and a metastatic lesion. In one embodiment, the cancer is a solid tumor. Examples of solid tumors include malignancies, *e.g.*, sarcomas and carcinomas, *e.g.*, adenocarcinomas of the various organ systems, such as those affecting the lung, breast, ovarian, lymphoid, gastrointestinal (*e.g.*, colon), anal, genitals and genitourinary tract (*e.g.*, renal, urothelial, bladder cells, prostate),

pharynx, CNS (*e.g.*, brain, neural or glial cells), head and neck, skin (*e.g.*, melanoma), and pancreas, as well as adenocarcinomas which include malignancies such as colon cancers, rectal cancer, renal-cell carcinoma, liver cancer, lung cancer (*e.g.*, non-small cell lung cancer or small cell lung cancer), cancer of the small intestine and cancer of the esophagus. The cancer may be at an early, intermediate, late stage or metastatic cancer. In certain embodiments, the cancer is associated with elevated PD-1 activity (*e.g.*, elevated PD-1 expression).

[00191] In one embodiment, the cancer is chosen from a lung cancer (*e.g.*, lung adenocarcinoma or a non-small cell lung cancer (NSCLC) (*e.g.*, a NSCLC with squamous and/or non-squamous histology, or a NSCLC adenocarcinoma)), a melanoma (*e.g.*, an advanced melanoma), a renal cancer (*e.g.*, a renal cell carcinoma), a liver cancer (*e.g.*, hepatocellular carcinoma or intrahepatic cholangiocellular carcinoma), a myeloma (*e.g.*, a multiple myeloma), a prostate cancer, a breast cancer (*e.g.*, a breast cancer that does not express one, two or all of estrogen receptor, progesterone receptor, or Her2/neu, *e.g.*, a triple negative breast cancer), an ovarian cancer, a colorectal cancer, a pancreatic cancer, a head and neck cancer (*e.g.*, head and neck squamous cell carcinoma (HNSCC), anal cancer, gastro-esophageal cancer (*e.g.*, esophageal squamous cell carcinoma), mesothelioma, nasopharyngeal cancer, thyroid cancer, cervical cancer, epithelial cancer, peritoneal cancer, or a lymphoproliferative disease (*e.g.*, a post-transplant lymphoproliferative disease). In one embodiment, the cancer is NSCLC. In one embodiment, the cancer is a renal cell carcinoma. In one embodiment, the cancer is an ovarian cancer, optionally wherein the ovarian cancer is associated with human papillomavirus (HPV) infection. In a specific embodiment, the ovarian cancer is a platinum-refractory ovarian cancer.

[00192] In one embodiment, the cancer is a hematological cancer, for example, a leukemia, a lymphoma, or a myeloma. In one embodiment, the cancer is a leukemia, for example, acute lymphoblastic leukemia (ALL), acute myelogenous leukemia (AML), acute myeloblastic leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloid leukemia (CML), chronic myelomonocytic leukemia (CMML), chronic lymphocytic leukemia (CLL), or hairy cell leukemia. In one embodiment, the cancer is a lymphoma, for example, B cell lymphoma, diffuse large B-cell lymphoma (DLBCL), activated B-cell like (ABC) diffuse large B cell lymphoma, germinal center B cell (GCB) diffuse large B cell lymphoma, mantle cell lymphoma, Hodgkin lymphoma, non-Hodgkin lymphoma, relapsed non-Hodgkin lymphoma, refractory non-Hodgkin lymphoma, recurrent follicular non-Hodgkin lymphoma, Burkitt lymphoma, small lymphocytic

lymphoma, follicular lymphoma, lymphoplasmacytic lymphoma, or extranodal marginal zone lymphoma. In one embodiment the cancer is a myeloma, for example, multiple myeloma.

[00193] In another embodiment, the cancer is chosen from a carcinoma (*e.g.*, advanced or metastatic carcinoma), melanoma or a lung carcinoma, *e.g.*, a non-small cell lung carcinoma.

[00194] In one embodiment, the cancer is a lung cancer, *e.g.*, a lung adenocarcinoma, non-small cell lung cancer or small cell lung cancer.

[00195] In one embodiment, the cancer is a melanoma, *e.g.*, an advanced melanoma. In one embodiment, the cancer is an advanced or unresectable melanoma that does not respond to other therapies. In other embodiments, the cancer is a melanoma with a BRAF mutation (*e.g.*, a BRAF V600 mutation). In yet other embodiments, the compositions, vaccine formulations, or unit dosage forms disclosed herein is administered after treatment with an anti-CTLA-4 antibody (*e.g.*, ipilimumab) with or without a BRAF inhibitor (*e.g.*, vemurafenib or dabrafenib).

[00196] In another embodiment, the cancer is a hepatocarcinoma, *e.g.*, an advanced hepatocarcinoma, with or without a viral infection, *e.g.*, a chronic viral hepatitis.

[00197] In another embodiment, the cancer is a prostate cancer, *e.g.*, an advanced prostate cancer.

[00198] In yet another embodiment, the cancer is a myeloma, *e.g.*, multiple myeloma.

[00199] In yet another embodiment, the cancer is a renal cancer, *e.g.*, a renal cell carcinoma (RCC) (*e.g.*, a metastatic RCC, clear cell renal cell carcinoma (CCRCC) or kidney papillary cell carcinoma).

[00200] In yet another embodiment, the cancer is chosen from a lung cancer, a melanoma, a renal cancer, a breast cancer, a colorectal cancer, a leukemia, or a metastatic lesion of the cancer.

[00201] The compositions, vaccine formulations, or unit dosage forms of the invention may be administered when a cancer is detected, or prior to or during an episode of recurrence.

[00202] Administration can begin at the first sign of cancer or recurrence, followed by boosting doses until at least symptoms are substantially abated and for a period thereafter.

[00203] In some embodiments, the compositions can be administered to a subject with cancer who has undergone tumor resection surgery that results in an insufficient amount of resected tumor tissue (*e.g.*, less than 7 g, less than 6 g, less than 5 g, less than 4 g, less than 3 g, less than 2 g, or less than 1 g of resected tumor tissue) for production of a therapeutically effective amount of an autologous cancer vaccine comprising a representative set of antigens

collected from the resected tumor tissue. See, for example, cancer vaccines described in Expert Opin. Biol. Ther. 2009 Feb;9(2):179-86; incorporated herein by reference.

[00204] The compositions, vaccine formulations, and unit dosage forms of the invention can also be used for immunization against recurrence of cancers. Prophylactic administration of a composition to an individual can confer protection against a future recurrence of a cancer.

5.5.2 Treatment of infection

[00205] The compositions, vaccine formulations, or unit dosage forms of the invention can be used alone or in combination with other therapies for the treatment of a microbial infection (*e.g.*, a pathogenic microbial infection). One or more of the MHC-binding epitopes in the HSP-binding antigenic conjugate(s) or peptide(s) can be identified from the microbe. In certain embodiments, one or more of the MHC-binding epitopes are present at the surface of the microbe or a cell infected with the microbe.

[00206] Infections that can be treated using the compositions, vaccine formulations, or unit dosage forms of the invention include, without limitation, a viral infection, a bacterial infection, a fungal infection, a protozoal infection, or a parasitic infection.

[00207] Viral infections that can be treated by the compositions, vaccine formulations, or unit dosage forms disclosed herein include, but are not limited to, those caused by hepatitis type A, hepatitis type B, hepatitis type C, influenza (*e.g.*, influenza A or influenza B), varicella, adenovirus, herpes simplex type I (HSV-I), herpes simplex type II (HSV-II), rinderpest, rhinovirus, echovirus, rotavirus, respiratory syncytial virus, papilloma virus (*e.g.*, human papillomavirus (HPV)), papova virus, cytomegalovirus, echinovirus, arbovirus, hantavirus, coxsackie virus, mumps virus, measles virus, rubella virus, polio virus, Epstein Barr virus (EBV), human immunodeficiency virus type I (HIV-I), human immunodeficiency virus type II (HIV-II), dengue virus, smallpox virus, rabies virus, rabies virus, and Zika virus. Viral diseases caused by any of these viruses that can be treated in accordance with the methods described herein include, but are not limited to, fever, immunodeficiency, viral meningitis, and encephalitis.

[00208] Bacterial infections that can be treated by the compositions, vaccine formulations, or unit dosage forms disclosed herein include, but are not limited to, infections caused by *Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Enterococcus faecalis, Proteus vulgaris, Staphylococcus viridans,* and *Pseudomonas aeruginosa.* Bacterial diseases caused by any of these bacteria that can be treated in accordance with the methods described herein include, but are not limited to, Mycobacteria rickettsia, Mycoplasma, Neisseria, S.

pneumonia, Borrelia burgdorferi (Lyme disease), Bacillus antracis (anthrax), tetanus, Streptococcus, Staphylococcus, mycobacterium, pertissus, cholera, plague, diptheria, chlamydia, S. aureus and legionella.

[00209] Fungal infections that can be treated by the compositions, vaccine formulations, or unit dosage forms disclosed herein include, but are not limited to, infections caused by *Candida* (*e.g.*, *Candida glabrata*), *Pneumocystis carinii*, *Fusarium keratitis*, *coccidioidal*, *Aspergillus niger*, *Cryptococcus neoformans*, and *Curvularia geniculata*. Fungal diseases caused by any of these bacteria that can be treated in accordance with the methods described herein include, but are not limited to, zygomycosis, *Candida* mastitis, progressive disseminated trichosporonosis with latent trichosporonemia, disseminated candidiasis, pulmonary paracoccidioidomycosis, pulmonary aspergillosis, *Pneumocystis carinii* pneumonia, cryptococcal meningitis, *coccidioidal* meningoencephalitis and cerebrospinal vasculitis, paranasal sinus mycoses, *Aspergillus fumigatus* endocarditis, tibial dyschondroplasia, *Candida glabrata* vaginitis, oropharyngeal candidiasis, X-linked chronic granulomatous disease, tinea pedis, cutaneous candidiasis, mycotic placentitis, disseminated trichosporonosis, allergic bronchopulmonary aspergillosis, mycotic keratitis, fungal peritonitis, staphylococcal endophthalmitis, sporotrichosis, and dermatophytosis.

[00210] Protozoal infections that can be treated by the compositions, vaccine formulations, or unit dosage forms disclosed herein include, but are not limited to, infections caused by leishmania, coccidiosis, trypanosoma schistosoma, and malaria.

[00211] Parasitic infections that can be treated by the compositions, vaccine formulations, or unit dosage forms disclosed herein include, but are not limited to, infections caused by chlamydia and rickettsia.

[00212] The compositions, vaccine formulations, and unit dosage forms of the invention can be used for immunization against subjects who have been diagnosed, by any medical methods known in the art, to have infections. They can be used for immunization against subjects who have been exposed to a pathogenic microbe, will be exposed to a pathogenic microbe, or are otherwise at a high risk of contracting an infectious disease, for prophylaxis.

5.5.3 Combination Therapy

[00213] Combination therapy refers to the use of compositions, vaccine formulations, or unit dosage forms of the invention, as a first modality, with a second modality to treat cancer or infections. Accordingly, in certain embodiments, the instant disclosure provides a method of inducing a cellular immune response to an antigenic peptide in a subject as disclosed herein, or a method of treating a disease in a subject as disclosed herein, the method

comprising administering to the subject an effective amount of (a) a composition, vaccine formulations, or unit dosage form as disclosed herein and (b) a second modality.

[00214] In one embodiment, the second modality is a non-HSP modality, *e.g.*, a modality that does not comprise HSP as a component. This approach is commonly termed combination therapy, adjunctive therapy or conjunctive therapy (the terms are used interchangeably). With combination therapy, additive potency or additive therapeutic effect can be observed. Synergistic outcomes are sought where the therapeutic efficacy is greater than additive. The use of combination therapy can also provide better therapeutic profiles than the administration of either the first or the second modality alone.

[00215] The additive or synergistic effect may allow for a reduction in the dosage and/or dosing frequency of either or both modalities to mitigate adverse effects. In certain embodiments, the second modality administered alone is not clinically adequate to treat the subject (*e.g.*, the subject is non-responsive or refractory to the single modality), such that the subject needs an additional modality. In certain embodiments, the subject has responded to the second modality, yet suffers from side effects, relapses, develops resistance, etc., such that the subject needs an additional modality. Methods of the invention comprising administration of the compositions, vaccine formulations, or unit dosage forms of the invention to such subjects to improve the therapeutic effectiveness of the second modality. The effectiveness of a treatment modality can be assayed *in vivo* or *in vitro* using methods known in the art.

[00216] In one embodiment, a lesser amount of the second modality is required to produce a therapeutic benefit in a subject. In specific embodiments, a reduction of about 10%, 20%, 30%, 40% and 50% of the amount of second modality can be achieved. The amount of the second modality, including amounts in a range that does not produce any observable therapeutic benefits, can be determined by dose-response experiments conducted in animal models by methods well known in the art.

[00217] In certain embodiments, the second modality comprises a TCR, *e.g.*, a soluble TCR or a cell expressing a TCR. In certain embodiments, the second modality comprises a cell expressing a chimeric antigen receptor (CAR). In certain embodiments, the cell expressing the TCR or CAR is a T cell. In a particular embodiment, the TCR or CAR binds to (*e.g.*, specifically binds to) at least one MHC-binding epitope in the composition, vaccine formulation, or unit dosage form of the invention.

[00218] In certain embodiments, the second modality comprises a TCR mimic antibody. In certain embodiments, the TCR mimic antibody is an antibody that specifically binds to a

peptide-MHC complex. Non-limiting examples of TCR mimic antibodies are disclosed in U.S. Patent No. 9,074,000, U.S. Publication Nos. US 2009/0304679 A1 and US 2014/0134191 A1, all of which are incorporated herein by reference in their entireties. In a particular embodiment, the TCR mimic antibody binds to (*e.g.*, specifically binds to) at least one MHC-binding epitope in the composition, vaccine formulation, or unit dosage form of the invention.

[00219] In certain embodiments, the second modality comprises a checkpoint targeting agent. In certain embodiments, the checkpoint targeting agent is selected from the group consisting of an antagonist anti-CTLA-4 antibody, an antagonist anti-PD-L1 antibody, an antagonist anti-PD-L2 antibody, an antagonist anti-PD-1 antibody, an antagonist anti-TIM-3 antibody, an antagonist anti-LAG-3 antibody, an antagonist anti-CEACAM1 antibody, an agonist anti-CD137 antibody, an antagonist anti-TIGIT antibody, an antagonist anti-VISTA antibody, an agonist anti-GITR antibody, and an agonist anti-OX40 antibody.

[00220] In certain embodiments, an anti-PD-1 antibody is used as the second modality in methods disclosed herein. In certain embodiments, the anti-PD-1 antibody is nivolumab, also known as BMS-936558 or MDX1106, developed by Bristol-Myers Squibb. In certain embodiments, the anti-PD-1 antibody is pembrolizumab, also known as lambrolizumab or MK-3475, developed by Merck & Co. In certain embodiments, the anti-PD-1 antibody is pidilizumab, also known as CT-011, developed by CureTech. In certain embodiments, the anti-PD-1 antibody is MEDI0680, also known as AMP-514, developed by Medimmune. In certain embodiments, the anti-PD-1 antibody is PDR001 developed by Novartis Pharmaceuticals. In certain embodiments, the anti-PD-1 antibody is REGN2810 developed by Regeneron Pharmaceuticals. In certain embodiments, the anti-PD-1 antibody is PF-06801591 developed by Pfizer. In certain embodiments, the anti-PD-1 antibody is BGB-A317 developed by BeiGene. In certain embodiments, the anti-PD-1 antibody is TSR-042 developed by AnaptysBio and Tesaro. In certain embodiments, the anti-PD-1 antibody is SHR-1210 developed by Hengrui.

[00221] Further non-limiting examples of anti-PD-1 antibodies that may be used in treatment methods disclosed herein are disclosed in the following patents and patent applications, all of which are herein incorporated by reference in their entireties for all purposes: U.S. Patent No. 6,808,710; U.S. Patent No. 7,332,582; U.S. Patent No. 7,488,802; U.S. Patent No. 8,008,449; U.S. Patent No. 8,114,845; U.S. Patent No. 8,168,757; U.S. Patent No. 8,354,509; U.S. Patent No. 8,686,119; U.S. Patent No. 8,735,553; U.S. Patent No. 8,747,847; U.S. Patent No. 8,779,105; U.S. Patent No. 8,927,697; U.S. Patent No.

8,993,731; U.S. Patent No. 9,102,727; U.S. Patent No. 9,205,148; U.S. Publication No. US 2013/0202623 A1; U.S. Publication No. US 2013/0291136 A1; U.S. Publication No. US 2014/0044738 A1; U.S. Publication No. US 2014/0356363 A1; U.S. Publication No. US 2016/0075783 A1; and PCT Publication No. WO 2013/033091 A1; PCT Publication No. WO 2015/036394 A1; PCT Publication No. WO 2014/179664 A2; PCT Publication No. WO 2014/209804 A1; PCT Publication No. WO 2014/206107 A1; PCT Publication No. WO 2015/058573 A1; PCT Publication No. WO 2015/085847 A1; PCT Publication No. WO 2015/200119 A1; PCT Publication No. WO 2016/015685 A1; and PCT Publication No. WO 2016/020856 A1.

[00222] In certain embodiments, an anti-PD-L1 antibody is used as the second modality in methods disclosed herein. In certain embodiments, the anti-PD-L1 antibody is atezolizumab developed by Genentech. In certain embodiments, the anti-PD-L1 antibody is durvalumab developed by AstraZeneca, Celgene and Medimmune. In certain embodiments, the anti-PD-L1 antibody is avelumab, also known as MSB0010718C, developed by Merck Serono and Pfizer. In certain embodiments, the anti-PD-L1 antibody is MDX-1105 developed by Bristol-Myers Squibb. In certain embodiments, the anti-PD-L1 antibody is AMP-224 developed by Amplimmune and GSK.

[00223] Non-limiting examples of anti-PD-L1 antibodies that may be used in treatment methods disclosed herein are disclosed in the following patents and patent applications, all of which are herein incorporated by reference in their entireties for all purposes: US Patent No. 7,943,743; US Patent No. 8,168,179; US Patent No. 8,217,149; U.S. Patent No. 8,552,154; U.S. Patent No. 8,779,108; U.S. Patent No. 8,981,063; U.S. Patent No. 9,175,082; U.S. Publication No. US 2010/0203056 A1; U.S. Publication No. US 2003/0232323 A1; U.S. Publication No. US 2013/0323249 A1; U.S. Publication No. US 2014/0341917 A1; U.S. Publication No. US 2014/0044738 A1; U.S. Publication No. US 2015/0203580 A1; U.S. Publication No. US 2015/0225483 A1; U.S. Publication No. US 2015/0346208 A1; U.S. Publication No. US 2015/0355184 A1; and PCT Publication No. WO 2014/100079 A1; PCT Publication No. WO 2014/022758 A1; PCT Publication No. WO 2014/055897 A2; PCT Publication No. WO 2015/061668 A1; PCT Publication No. WO 2015/109124 A1; PCT Publication No. WO 2015/195163 A1; PCT Publication No. WO 2016/000619 A1; and PCT Publication No. WO 2016/030350 A1.

[00224] In certain embodiments, a compound that targets an immunomodulatory enzyme(s) such as IDO (indoleamine-(2,3)-dioxygenase) and/or TDO (tryptophan 2,3-dioxygenase) is used as the second modality in methods disclosed herein. Therefore, in one

embodiment, the compound targets an immunomodulatory enzyme(s), such as an inhibitor of indoleamine-(2,3)-dioxygenase (IDO). In certain embodiments, such compound is selected from the group consisting of epacadostat (Incyte Corp; see, *e.g.*, WO 2010/005958 which is herein incorporated by reference in its entirety), F001287 (Flexus Biosciences/Bristol-Myers Squibb), indoximod (NewLink Genetics), and NLG919 (NewLink Genetics). In one embodiment, the compound is epacadostat. In another embodiment, the compound is F001287. In another embodiment, the compound is indoximod. In another embodiment, the compound is NLG919. In a specific embodiment, an anti-TIM-3 (*e.g.*, human TIM-3) antibody disclosed herein is administered to a subject in combination with an IDO inhibitor for treating cancer. The IDO inhibitor as described herein for use in treating cancer is present in a solid dosage form of a pharmaceutical composition such as a tablet, a pill or a capsule, wherein the pharmaceutical composition includes an IDO inhibitor and a pharmaceutically acceptable excipient. As such, the antibody as described herein and the IDO inhibitor as described herein can be administered separately, sequentially or concurrently as separate dosage forms. In one embodiment, the antibody is administered parenterally, and the IDO inhibitor is administered orally. In particular embodiments, the inhibitor is selected from the group consisting of epacadostat (Incyte Corporation), F001287 (Flexus Biosciences/Bristol-Myers Squibb), indoximod (NewLink Genetics), and NLG919 (NewLink Genetics). Epacadostat has been described in PCT Publication No. WO 2010/005958, which is herein incorporated by reference in its entirety for all purposes. In one embodiment, the inhibitor is epacadostat. In another embodiment, the inhibitor is F001287. In another embodiment, the inhibitor is indoximod. In another embodiment, the inhibitor is NLG919.

[00225] In certain embodiments, the second modality comprises a different vaccine (*e.g.*, a peptide vaccine, a DNA vaccine, or an RNA vaccine) for treating cancer or infection. In certain embodiments, the vaccine is a heat shock protein based tumor vaccine or a heat shock protein based pathogen vaccine (*e.g.*, a vaccine as described in WO 2016/183486, which is incorporated herein by reference in its entirety). In a specific embodiment, the second modality comprises a stress protein-based vaccine. For example, in certain embodiments, the second modality comprises a composition, vaccine formulation, or unit dosage form as disclosed herein that is different from the first modality. In certain embodiments, the second modality comprises a composition, vaccine formulation, or unit dosage form analogous to those disclosed herein except for having a different sequence of the HSP-binding peptide. In certain embodiments, the stress protein-based vaccine is derived from a tumor preparation,

such that the immunity elicited by the vaccine is specifically directed against the unique antigenic peptide repertoire expressed by the cancer of each subject.

[00226] In certain embodiments, the second modality comprises one or more adjuvants, such as the ones disclosed *supra* that may be included in the vaccine formulation disclosed herein. In certain embodiments, the second modality comprises a saponin, an immunostimulatory nucleic acid, and/or QS-21. In certain embodiments, the second modality comprises a Toll-like receptor (TLR) agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[00227] In certain embodiments, the second modality comprises one or more of the agents selected from the group consisting of lenalidomide, dexamethasone, interleukin-2, recombinant interferon alfa-2b, and peginterferon alfa-2b.

[00228] In certain embodiments, where the pharmaceutical composition, vaccine formulation, or unit dosage form is used for treating a subject having cancer, the second modality comprises a chemotherapeutic or a radiotherapeutic. In certain embodiments, the chemotherapeutic agent is a hypomethylating agent (*e.g.*, azacitidine).

[00229] In certain embodiments, where the pharmaceutical composition, vaccine formulation, or unit dosage form is used for treating a subject having infection of a pathogenic microbe, the second modality comprises one or more anti-infective interventions (*e.g.*, antivirals, antibacterials, antifungals, or anti-helminthics) for the treatment of the infectious disease.

[00230] The composition, vaccine formulation, or unit dosage form of the invention can be administered separately, sequentially, or concurrently from the second modality (*e.g.*, chemotherapeutic, radiotherapeutic, checkpoint targeting agent, IDO inhibitor, vaccine, adjuvant, soluble TCR, cell expressing a TCR, cell expressing a CAR, and/or TCR mimic antibody), by the same or different delivery routes.

5.5.4 Dosage regimen

[00231] The dosage of the compositions or vaccine formulations disclosed herein, and the dosage of any additional treatment modality if combination therapy is to be administered, depends to a large extent on the weight and general state of health of the subject being treated, as well as the frequency of treatment and the route of administration. Amounts effective for this use will also depend on the stage and severity of the disease and the judgment of the prescribing physician, but generally range for the initial immunization (that

is, for therapeutic administration) from about 1.0 μg to about 1000 μg (1 mg) (including, for example, 10, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 240, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, or 1000 μg) of any one of the compositions disclosed herein for a 70 kg patient, followed by boosting dosages of from about 1.0 μg to about 1000 μg of the composition (including, for example, 10, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, or 1000 μg) pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific CTL activity in the patient's blood. Regimens for continuing therapy, including site, dose and frequency may be guided by the initial response and clinical judgment. Dosage ranges and regimens for adjuvants are known to those in the art, see, *e.g.*, Vogel and Powell, 1995, A Compendium of Vaccine Adjuvants and Excipients; M. F. Powell, M. J. Newman (eds.), Plenum Press, New York, pages 141-228.

[00232] Preferred adjuvants include QS-21, *e.g.*, QS-21 Stimulon®, and CpG oligonucleotides. Exemplary dosage ranges for QS-21 are 1 μg to 200 μg per administration. In other embodiments, dosages for QS-21 can be 10, 25, and 50 μg per administration. In certain embodiments, the adjuvant comprises a Toll-like receptor (TLR) agonist. In certain embodiments, the TRL agonist is an agonist of TLR4. In certain embodiments, the TRL agonist is an agonist of TLR7 and/or TLR8. In certain embodiments, the TRL agonist is an agonist of TLR9. In certain embodiments, the TRL agonist is an agonist of TLR5.

[00233] In certain embodiments, the administered amount of compositions depends on the route of administration and the type of HSPs in the compositions. For example, the amount of HSP in the compositions can range, for example, from 5 to 1000 μg (1 mg) per administration. In certain embodiments, the administered amount of compositions comprising Hsc70-, Hsp70- and/or Gp96-polypeptide complexes is, for example, 5, 10, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 200, 250, 300, 400, 500, 600, 700, 750, 800, 900, or 1000 μg. In certain embodiments, the administered amount of the composition is in the range of about 10 to 600 μg per administration and about 5 to 100 μg if the composition is administered intradermally. In certain embodiments, the administered amount of the composition is about 5 μg to 600 μg, about 5 μg to 300 μg, about 5 μg to 150 μg, or about 5 μg to 60 μg. In certain embodiments, the administered amount of the composition is less than 100 μg. In certain embodiments, the administered amount of the composition is about 5 μg, 25 μg, 50 μg, or 240 μg. In certain embodiments, the compositions comprising complexes of stress proteins and polypeptides are purified.

[00234] In one embodiment of a therapeutic regimen, a dosage substantially equivalent to that observed to be effective in smaller non-human animals (*e.g.*, mice or guinea pigs) is effective for human administration, optionally subject to a correction factor not exceeding a fifty fold increase, based on the relative lymph node sizes in such mammals and in humans. Specifically, interspecies dose-response equivalence for stress proteins (or HSPs) noncovalently bound to or mixed with antigenic molecules for a human dose is estimated as the product of the therapeutic dosage observed in mice and a single scaling ratio, not exceeding a fifty fold increase. In certain embodiment, the dosages of the composition can be much smaller than the dosage estimated by extrapolation.

[00235] The doses recited above can be given once or repeatedly, such as daily, every other day, weekly, biweekly, or monthly, for a period up to a year or over a year. Doses are preferably given once every 28 days for a period of about 52 weeks or more.

[00236] In one embodiment, the compositions are administered to a subject at reasonably the same time as an additional treatment modality or modalities. This method provides that the two administrations are performed within a time frame of less than one minute to about five minutes, or up to about sixty minutes from each other, for example, at the same doctor's visit.

[00237] In another embodiment, the compositions and an additional treatment modality or modalities are administered at exactly the same time.

[00238] In yet another embodiment the compositions and an additional treatment modality or modalities are administered in a sequence and within a time interval such that the complexes of the invention and the additional treatment modality or modalities can act together to provide an increased benefit than if they were administered alone.

[00239] In another embodiment, the compositions and an additional treatment modality or modalities are administered sufficiently close in time so as to provide the desired therapeutic or prophylactic outcome. Each can be administered simultaneously or separately, in any appropriate form and by any suitable route. In one embodiment, the complexes of the invention and the additional treatment modality or modalities are administered by different routes of administration. In an alternate embodiment, each is administered by the same route of administration. The compositions can be administered at the same or different sites, *e.g.* arm and leg. When administered simultaneously, the compositions and an additional treatment modality or modalities may or may not be administered in admixture or at the same site of administration by the same route of administration.

[00240] In various embodiments, the compositions and an additional treatment modality or modalities are administered less than 1 hour apart, at about 1 hour apart, 1 hour to 2 hours apart, 2 hours to 3 hours apart, 3 hours to 4 hours apart, 4 hours to 5 hours apart, 5 hours to 6 hours apart, 6 hours to 7 hours apart, 7 hours to 8 hours apart, 8 hours to 9 hours apart, 9 hours to 10 hours apart, 10 hours to 11 hours apart, 11 hours to 12 hours apart, no more than 24 hours apart or no more than 48 hours apart. In other embodiments, the compositions and a vaccine composition are administered 2 to 4 days apart, 4 to 6 days apart, 1 week a part, 1 to 2 weeks apart, 2 to 4 weeks apart, one month apart, 1 to 2 months apart, or 2 or more months apart. In preferred embodiments, the compositions and an additional treatment modality or modalities are administered in a time frame where both are still active. One skilled in the art would be able to determine such a time frame by determining the half-life of each administered component.

[00241] In certain embodiments, the compositions are administered to the subject weekly for at least four weeks. In certain embodiments, after the four weekly doses, at least 2 (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) further doses of the compositions are administered biweekly to the subject. In certain embodiments, the compositions administered as a booster three months after the final weekly or biweekly dose. The three monthly booster can be administered for the life of the subject (*e.g.*, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 40, 50, or more years). In certain embodiments, the total number of doses of the compositions administered to the subject is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20.

[00242] In one embodiment, the compositions and an additional treatment modality or modalities are administered within the same patient visit. In certain embodiments, the compositions are administered prior to the administration of an additional treatment modality or modalities. In an alternate specific embodiment, the compositions are administered subsequent to the administration of an additional treatment modality or modalities.

[00243] In certain embodiments, the compositions and an additional treatment modality or modalities are cyclically administered to a subject. Cycling therapy involves the administration of the compositions for a period of time, followed by the administration of a modality for a period of time and repeating this sequential administration. Cycling therapy can reduce the development of resistance to one or more of the therapies, avoid or reduce the side effects of one of the therapies, and/or improve the efficacy of the treatment. In such embodiments, the disclosure contemplates the alternating administration of the compositions followed by the administration of a modality 4 to 6 days later, preferable 2 to 4 days, later,

more preferably 1 to 2 days later, wherein such a cycle may be repeated as many times as desired. In certain embodiments, the compositions and the modality are alternately administered in a cycle of less than 3 weeks, once every two weeks, once every 10 days or once every week. In certain embodiments, the compositions are administered to a subject within a time frame of one hour to twenty four hours after the administration of a modality. The time frame can be extended further to a few days or more if a slow- or continuous-release type of modality delivery system is used.

5.5.5 Routes of Administration

[00244] The compositions disclosed herein may be administered using any desired route of administration. Many methods may be used to introduce the compositions described above, including but not limited to, oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, mucosal, intranasal, intra-tumoral, and intra-lymph node routes. Non-mucosal routes of administration include, but are not limited to, intradermal and topical administration. Mucosal routes of administration include, but are not limited to, oral, rectal and nasal administration. Advantages of intradermal administration include use of lower doses and rapid absorption, respectively. Advantages of subcutaneous or intramuscular administration include suitability for some insoluble suspensions and oily suspensions, respectively. Preparations for mucosal administrations are suitable in various formulations as described below.

[00245] Solubility and the site of the administration are factors which should be considered when choosing the route of administration of the compositions. The mode of administration can be varied between multiple routes of administration, including those listed above.

[00246] If the compositions are water-soluble, then it may be formulated in an appropriate buffer, for example, phosphate buffered saline or other physiologically compatible solutions, preferably sterile. Alternatively, if a composition has poor solubility in aqueous solvents, then it may be formulated with a non-ionic surfactant such as Tween, or polyethylene glycol. Thus, the compositions may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral, or rectal administration.

[00247] For oral administration, the composition may be in liquid form, for example, solutions, syrups or suspensions, or may be presented as a drug product for reconstitution with water or other suitable vehicle before use. Such a liquid preparation may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents

(*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-p-hydroxybenzoates or sorbic acid). The compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pre-gelatinized maize starch, polyvinyl pyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well-known in the art.

[00248] The compositions for oral administration may be suitably formulated to be released in a controlled and/or timed manner.

[00249] For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

[00250] The preparation may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The preparation may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

[00251] The preparation may also be formulated in a rectal preparation such as a suppository or retention enema, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides.

[00252] In addition to the formulations described above, the preparation may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example, subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the preparation may be formulated with suitable polymeric or hydrophobic materials (for example, as emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophilic drugs.

[00253] For administration by inhalation, the compositions are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized

aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

5.5.6 Patient (Subject) Evaluation

[00254] Patients treated with the compositions disclosed herein may be tested for an anti-tumor immune response. In this regard, peripheral blood from patients may be obtained and assayed for markers of anti-tumor immunity. Using standard laboratory procedures, leukocytes may be obtained from the peripheral blood and assayed for frequency of different immune cell phenotypes, HLA subtype, and function of anti-tumor immune cells.

[00255] The majority of effector immune cells in the anti-tumor response is $CD8^+$ T cells and thus is HLA class I restricted. Using immunotherapeutic strategies in other tumor types, expansion of CD8+ cells that recognize HLA class I restricted antigens is found in a majority of patients. However, other cell types are involved in the anti-tumor immune response, including, for example, CD4+ T cells, and macrophages and dendritic cells, which may act as antigen-presenting cells. Populations of T cells (CD4+, CD8+, and Treg cells), macrophages, and antigen presenting cells may be determined using flow cytometry. HLA typing may be performed using routine methods in the art, such as methods described in Boegel et al. Genome Medicine 2012, 4:102 (seq2HLA), or using a TruSight® HLA sequencing panel (Illumina, Inc.). The HLA subtype of CD8+ T cells may be determined by a complement-dependent microcytotoxicity test.

[00256] To determine if there is an increase in anti-tumor T cell response, an enzyme linked immunospot assay may be performed to quantify the IFNγ-producing peripheral blood mononuclear cells (PBMC). This technique provides an assay for antigen recognition and immune cell function. In some embodiments, subjects who respond clinically to the vaccine may have an increase in tumor-specific T cells and/or IFNγ-producing PBMCs. In some embodiments, immune cell frequency is evaluated using flow cytometry. In some embodiments, antigen recognition and immune cell function is evaluated using enzyme linked immunospot assays.

[00257] In some embodiments, a panel of assays may be performed to characterize the immune response generated to the composition alone or given in combination with standard of care (*e.g.*, maximal surgical resection, radiotherapy, and concomitant and adjuvant chemotherapy with temozolomide for glioblastoma multiforme). In some embodiments, the panel of assays includes one or more of the following tests: whole blood cell count, absolute

lymphocyte count, monocyte count, percentage of $CD4^+CD3^+$ T cells, percentage of $CD8^+CD3^+$ T cells, percentage of $CD4^+CD25^+FoxP3^+$ regulatory T cells and other phenotyping of PBL surface markers, intracellular cytokine staining to detect proinflammatory cytokines at the protein level, qPCR to detect cytokines at the mRNA level and CFSE dilution to assay T cell proliferation.

[00258] In evaluating a subject, a number of other tests may be performed to determine the overall health of the subject. For example, blood samples may be collected from subjects and analyzed for hematology, coagulation times and serum biochemistry. Hematology for CBC may include red blood cell count, platelets, hematocrit, hemoglobin, white blood cell (WBC) count, plus WBC differential to be provided with absolute counts for neutrophils, eosinophils, basophils, lymphocytes, and monocytes. Serum biochemistry may include albumin, alkaline phosphatase, aspartate amino transferase, alanine amino transferase, total bilirubin, BUN, glucose, creatinine, potassium and sodium. Protime (PT) and partial thromboplastin time (PTT) may also be tested. One or more of the following tests may also be conducted: anti-thyroid (anti-microsomal or thyroglobulin) antibody tests, assessment for anti-nuclear antibody, and rheumatoid factor. Urinalysis may be performed to evaluated protein, RBC, and WBC levels in urine. Also, a blood draw to determine histocompatibility leukocyte antigen (HLA) status may be performed.

[00259] In some embodiments, radiologic tumor evaluations are performed one or more times throughout a treatment to evaluate tumor size and status. For example, tumor evaluation scans may be performed within 30 days prior to surgery, within 48 hours after surgery (*e.g.*, to evaluate percentage resection), 1 week (maximum 14 days) prior to the first vaccination (*e.g.*, as a baseline evaluation), and approximately every 8 weeks thereafter for a particular duration. MRI or CT imaging may be used. Typically, the same imaging modality used for the baseline assessment is used for each tumor evaluation visit.

5.6 Kits

[00260] Kits are also provided for carrying out the prophylactic and therapeutic methods disclosed herein. The kits may optionally further comprise instructions on how to use the various components of the kits.

[00261] In certain embodiments, the kit comprises a first container containing the composition disclosed herein, and a second container containing one or more adjuvants. The adjuvant can be any adjuvant disclosed herein, *e.g.*, a saponin, an immunostimulatory nucleic acid, or QS-21 (*e.g.*, QS-21 Stimulon®). In certain embodiments, the kit further comprises a third container containing an additional treatment modality. The kit can further comprise an

instruction on the indication, dosage regimen, and route of administration of the composition, adjuvant, and additional treatment modality, *e.g.*, as disclosed in Section 5.5 herein.

[00262] Alternatively, the kit can comprise the stress protein(s) and polypeptide(s) of a composition disclosed herein in separate containers. In certain embodiments, the kit comprises a first container containing one or more polypeptides disclosed herein, and a second container containing a purified stress protein capable of binding to the polypeptide.

[00263] The first container can contain any number of different polypeptides. For example, in certain embodiments, the first container contains no more than 100 different polypeptides, *e.g.*, 2-50, 2-30, 2-20, 5-20, 5-15, 5-10, or 10-15 different polypeptides. In certain embodiments, each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide. In certain embodiments, the total amount of the polypeptide(s) in the first container is a suitable amount for a unit dosage. In certain embodiments, the total amount of the polypeptide(s) in the first container is about 0.1 to 20 nmol (*e.g.*, 3, 4, 5, or 6 nmol).

[00264] The second container can contain any stress protein disclosed herein. In certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, or Calreticulin, and a mutant or fusion protein thereof. In certain embodiments, the stress protein is Hsc70 (*e.g.*, human Hsc70). In certain embodiments, the stress protein is a recombinant protein. In certain embodiments, the total amount of the stress protein(s) in the second container is about 10 μg to 600 μg (*e.g.*, 250 μg to 290 μg). In certain embodiments, the total amount of the stress protein(s) in the second container is about 50 μg, 100 μg, 200 μg, 300 μg, 400 μg, or 500 μg. In certain embodiments, the amount of the stress protein in the pharmaceutical composition is about 300 μg. In certain embodiments, the total molar amount of the stress protein(s) in the second container is calculated based on the total molar amount of the polypeptide(s) in the first container, such that the molar ratio of the polypeptide(s) to the stress protein(s) is about 0.5:1 to 5:1 (*e.g.*, about 1:1 to 2:1, *e.g.*, about 1:1, 1.25:1, or 1.5:1). In certain embodiments, the total amount of the stress protein(s) in the second container is an amount for multiple administrations (*e.g.*, less than or equal to 1 mg, 3 mg, 10 mg, 30 mg, or 100 mg).

[00265] In certain embodiments, the kit further comprises an instruction for preparing a composition from the polypeptide(s) in the first container and the stress protein(s) in the second container (*e.g.*, an instruction for the complexing reaction as disclosed in Section 5.4.2 herein).

[00266] In certain embodiments, the kit further comprises a third container containing one or more adjuvants. The adjuvant can be any adjuvant disclosed herein, *e.g.*, a saponin, an immunostimulatory nucleic acid, or QS-21 (*e.g.*, QS-21 Stimulon®). In certain embodiments, the kit further comprises a fourth container containing an additional treatment modality. The kit can further comprise an instruction on the indication, dosage regimen, and route of administration of the composition prepared from the polypeptide(s) and stress protein(s), the adjuvant, and the additional treatment modality, *e.g.*, as disclosed in Section 5.5 herein.

[00267] In certain embodiments, the composition, polypeptide(s), stress protein(s), adjuvant(s), and additional treatment modality in the containers are present in pre-determined amounts effective to treat cancers or infections. If desired, the compositions can be presented in a pack or dispenser device which may contain one or more unit dosage forms of the compositions. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

5.7 HPV Peptides

[00268] In another aspect, the instant disclosure provides a polypeptide comprising an HSP-binding peptide and an amino acid sequence from a human papillomavirus (HPV) (*e.g.*, HPV16 or HPV18). Such amino acid sequence is also referred to as an HPV peptide herein.

[00269] The HPV peptide can comprise any amino acid sequence as disclosed in Table 3. In certain embodiments, the amino acid sequence from HPV comprises the amino acid sequence of SEQ ID NO: 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, or 53.

Table 3. Amino acid sequences of antigenic HPV peptides

Peptide Name	Amino Acid Sequence	SEQ ID NO:
PEP087	MHQKRTAMFQDPQERPRKLPQLCTELQTTI	38
PEP088	PRKLPQLCTELQTTIHDIILECVYCKQQLL	39
PEP089	HDIILECVYCKQQLLRREVYDFAFRDLCIV	40
PEP090	RREVYDFAFRDLCIVYRDGNPYAVCDKCLKF	41
PEP091	RDGNPYAVCDKCLKFYSKISEYRHYCYSLY	42
PEP092	YSKISEYRHYCYSLYGTTLEQQYNKPLCDL	43
PEP093	GTTLEQQYNKPLCDLLIRCINCQKPLCP	44
PEP094	DLLIRCINCQKPLCPEEKQRHLDKKQRFH	45
PEP095	PEEKQRHLDKKQRFHNIRGRWTG	46
PEP096	DKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL	47
PEP097	MHGDTPTLHEYMLDLQPETTDLYCYEQLN	48
PEP098	LQPETTDLYCYEQLNDSSEEEDEIDGP	49
PEP099	QLNDSSEEEDEIDGPAGQAEPDRAHYNIV	50
PEP100	PAGQAEPDRAHYNIVTFCCKCDSTLRLCV	51

Peptide Name	Amino Acid Sequence	SEQ ID NO:
PEP101	VTFCCKCDSTLRLCVQSTHVDIRTLEDLL	52
PEP102	VQSTHVDIRTLEDLLMGTLGIVCPICSQKP	53

[00270] The HSP-binding peptide can be any HSP-binding peptide disclosed in Section 5.2, or any HSP-binding peptide known in the art (*see*, *e.g.*, US20160331821A1 and US7309491B2, each of which is incorporated by reference herein in its entirety). In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 1, 2, 3, 4, or 232. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 5, 6, 7, 8, 9, 10, 11, 12, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 204, 205, 207, 208, 209, 210, 211, 212, 213, 214, or 215. In certain embodiments, the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 6.

[00271] The HPV peptide can be linked to the HSP-binding peptide via any linker disclosed herein (*e.g.*, in Section 5.3). In certain embodiments, the HPV peptide is linked to the HSP-binding peptide via a peptide linker. In certain embodiments, the peptide linker comprises the amino acid sequence of FR or FFRK (SEQ ID NO: 13).

[00272] In certain embodiments, the HPV peptide comprises the amino acid sequence of SEQ ID NO: 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, or 69.

Table 4. Amino acid sequences of HSP-binding antigenic HPV peptides

Peptide Name	Description	Amino Acid Sequence	SEQ ID NO:
PEP071	HPV16 E6 1-30 linked to PEP006	MHQKRTAMFQDPQERPRKLPQLCT ELQTTIFFRKNWLRLTW	54
PEP072	HPV16 E6 16-45 linked to PEP006	PRKLPQLCTELQTTIHDIILECVYCK QQLLFFRKNWLRLTW	55
PEP073	HPV16 E6 31-60 linked to PEP006	HDIILECVYCKQQLLRREVYDFAFR DLCIVFFRKNWLRLTW	56
PEP074	HPV16 E6 46-76 linked to PEP006	RREVYDFAFRDLCIVYRDGNPYAVC DKCLKFFFRKNWLRLTW	57
PEP075	HPV16 E6 62-91 linked to PEP006	RDGNPYAVCDKCLKFYSKISEYRHY CYSLYFFRKNWLRLTW	58
PEP076	HPV16 E6 77-106 linked to PEP006	YSKISEYRHYCYSLYGTTLEQQYNK PLCDLFFRKNWLRLTW	59
PEP077	HPV16 E6 92-119 linked to PEP006	GTTLEQQYNKPLCDLLIRCINCQKPL CPFFRKNWLRLTW	60
PEP078	HPV16 E6 105-133 linked to PEP006	DLLIRCINCQKPLCPEEKQRHLDKKQ RFHFFRKNWLRLTW	61

Peptide Name	Description	Amino Acid Sequence	SEQ ID NO:
PEP079	HPV16 E6 119-141 linked to PEP006	PEEKQRHLDKKQRFHNIRGRWTGFF RKNWLRLTW	62
PEP080	HPV16 E6 127-158 linked to PEP006	DKKQRFHNIRGRWTGRCMSCCRSS RTRRETQLFFRKNWLRLTW	63
PEP081	HPV16 E7 1-29 linked to PEP006	MHGDTPTLHEYMLDLQPETTDLYC YEQLNFFRKNWLRLTW	64
PEP082	HPV16 E7 15-41 linked to PEP006	LQPETTDLYCYEQLNDSSEEEDEIDG PFFRKNWLRLTW	65
PEP083	HPV16 E7 27-55 linked to PEP006	QLNDSSEEEDEIDGPAGQAEPDRAH YNIVFFRKNWLRLTW	66
PEP084	HPV16 E7 41-69 linked to PEP006	PAGQAEPDRAHYNIVTFCCKCDSTL RLCVFFRKNWLRLTW	67
PEP085	HPV16 E7 55-83 linked to PEP006	VTFCCKCDSTLRLCVQSTHVDIRTLE DLLFFRKNWLRLTW	68
PEP086	HPV16 E7 69-98 linked to PEP006	VQSTHVDIRTLEDLLMGTLGIVCPIC SQKPFFRKNWLRLTW	69

[00273] In another aspect, the instant disclosure provides a composition (*e.g.*, pharmaceutical composition) comprising a plurality of different polypeptides, wherein each polypeptide comprises an HSP-binding peptide and an HPV peptide. In certain embodiments, the amino acid sequence of at least one HPV peptide is selected from the group consisting of SEQ ID NOs: 38-53. In certain embodiments, the amino acid sequence of each HPV peptide is selected from the group consisting of SEQ ID NOs: 38-53. In certain embodiments, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different HPV peptides.

[00274] In certain embodiments, the amino acid sequence of at least one polypeptide is selected from the group consisting of SEQ ID NOs: 54-69. In certain embodiments, the amino acid sequence of each polypeptide is selected from the group consisting of SEQ ID NOs: 54-69. In certain embodiments, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different polypeptides.

[00275] In certain embodiments, the composition further comprises a purified stress protein. Any stress protein disclosed herein (*e.g.*, in Section 5.4) can be used. For example, in certain embodiments, the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant or fusion protein thereof. In certain embodiments, the stress protein is Hsc70 (*e.g.*, human Hsc70).

[00276] The ratio of polypeptide to stress protein can be any ratio disclosed herein, *e.g.*, about 0.5:1 to 5:1. In certain embodiments, the ratio of polypeptide to stress protein is about 1:1 to 2:1. In certain embodiments, the ratio of polypeptide to stress protein is about 1:1, 1.25:1, or 1.5:1. Also, the amounts of the polypeptide(s) and of the stress protein(s) can be any amounts disclosed in Section 5.4 herein. In certain embodiments, the composition is in a unit dosage form.

[00277] In another aspect, the instant disclosure provides a kit comprising the composition disclosed herein either in a single container or in separate containers, optionally further comprising containers containing one or more adjuvants and additional treatment modalities, as disclosed in Section 5.6 herein.

[00278] In another aspect, the instant disclosure provides a method of inducing a cellular immune response to an HPV peptide in a subject, the method comprising administering to the subject an effective amount of a composition as disclosed in this section. In another aspect, the instant disclosure provides a method of treating an HPV-associated disease in a subject, the method comprising administering to the subject an effective amount of a composition as disclosed this section. In certain embodiments, the HPV-associated disease is a cancer (*e.g.*, cervical cancer). In certain embodiments, the HPV is HPV16 or HPV18. Any dosage regimen as disclosed in Section 5.5.4 herein and any route of administration as disclosed in Section 5.5.5 herein can be used. The method can further comprise an additional treatment modality as disclosed in Section 5.5.3 herein, and can further comprise a patient evaluation step as disclosed in Section 5.5.6 herein.

6. EXAMPLES

[00279] The examples in this Section (i.e., Section 6) are offered by way of illustration, and not by way of limitation.

6.1 Example 1: Identification of peptides that bind to Hsc70 with high affinity

[00280] This example describes the design of heat shock protein (HSP)-binding peptide with improved binding to HSPs as compared to a heat shock protein-binding peptide having the amino acid sequence of NLLRLTG (SEQ ID NO: 70) (*see* U.S. patent application published as US20160331821A1, incorporated herein by reference in its entirety).

6.1.1 Binding of peptides to Hsc70

[00281] To identify peptides that bind to human Hsc70 with high affinity, variants of the NLLRLTG (SEQ ID NO: 70) sequence were designed, and a linker having the amino acid

sequence of FFRK (SEQ ID NO: 13) was added to the N-terminus. The amino acid sequences of the peptides synthesized and tested are provided in Table 5.

Table 5. Amino acid sequences of HSP-binding peptides

Peptide Name	Amino Acid Sequence	SEQ ID NO:
PEP001	FFRKNLLRLTG	71
PEP006	FFRKNWLRLTW	18
PEP012	FFRKNWLKLTW	19
PEP055	FFRKNWLKLKW	72
PEP056	FFRKNWLKLKW amide*	73
PEP057	FFRKNWLKLRW	74
PEP058	FFRKNWLKLWK	75

*amidation of C-terminal carboxyl group

[00282] The peptides were synthesized using standard Fmoc solid-phase chemical synthesis with pre-loaded polystyrene wang (PS-Wang) resin in a Symphony-X automatic synthesizer (Gyros Protein Technologies Inc). Fmoc protected L-amino acids were applied with standard HCTU/NMM activation chemistry. With respect to resin substitution, 5-fold excess of amino acid, 5-fold excess of activating reagent (HCTU) and 10-fold excess of N-methyl morpholine was used for coupling the amino acid to make the peptide bond. The reaction was performed for 6 min with double coupling cycle for any incomplete coupling throughout the synthesis. These steps were repeated until the desired sequence was obtained. At the end of the synthesis, resin was washed with dichloromethane (DCM) and dried. Upon completion of peptide assembly, the resin was transferred to another cleavage vessel for cleaving the peptide from the resin. A cleavage cocktail reagent Trifluoroacetic acid: Dithiothreitol water: Triisopropylsilane (88:5:5:2 v/w/v/v) was mixed with the resin and stirred for 4 hours at 25°C. The crude peptides were isolated from the resin by filtration and evaporated with N_2 gas followed by precipitation with chilled diethyl ether and stored at -20°C for 12 hours. The precipitated peptides were centrifuged and washed 2X with ether, dried, dissolved in the choice of solvent, and lyophilized to produce a crude dry powder. The crude peptides were purified by prep-HPLC with a C18 column (Ultimate 3000, Thermo Scientific) using a water (0.1% TFA)-acetonitrile (0.1% TFA) gradient. Peptide purity was tested using an analytical C18-column. Further characterization was confirmed by 6550 Q-TOF (Agilent Technologies) mass spectrometry.

[00283] Individual peptides were solubilized in 100% DMSO at 10 mg/ml followed by a second dilution step to 320 µM in 75% DMSO. To form a peptide-Hsc70 complex, Hsc70

was mixed at a concentration of 7 μM (0.5 mg/ml) with the appropriate concentration of peptide in 1X PBS with a final volume of 25 μl. The mixed samples were then incubated at 37°C for 1 hour and cooled down on ice for 10 min. To evaluate the quantity of the complex in the solution, 20 μl (10 μg) of the sample was loaded on a size exclusion chromatography (SEC) column TSKgel SuperSW3000 (Tosoh Bioscience) at a flow rate of 0.2 ml/min with 1X PBS as a running buffer. The data was collected by measuring the absorbance at both 280 and 214 nm.

[00284] In a separate experiment, further variants of the peptide NLLRLTG (SEQ ID NO: 70) were generated and the ability of these peptides to form a peptide-Hsc70 complex was analyzed. Peptides were again synthesized using standard Fmoc solid-phase chemical synthesis, as described above. Individual peptides were solubilized in pH adjusted water at a concentration of 250μM, and spiked with polysorbate 20 to a final concentration of 0.1%. To form a peptide-Hsc70 complex, Hsc70 (1 mg/ml, 0.1% polysorbate) was mixed with peptide at peptide:Hsc70 molar ratios of, 0.25:1, 0.5:1, 1:1, 2:1, and 4:1, for 60 minutes at 30°C. Following incubation, samples were cooled for 5 minutes at room temperature and transferred to HPLC vials for analysis. To evaluate the quantity of the complex in the solution, 20 μl (10 μg) of the sample was loaded on a size exclusion chromatography column TSKgel SuperSW3000 (Tosoh Bioscience) at a flow rate of 0.2 ml/min with 1X PBS as a running buffer. The data was collected by measuring the absorbance at 214 nm.

[00285] The percent of Hsc70 bound to peptide was calculated by SEC. As shown in the SEC chromatogram depicted in Figure 1, recombinant human heat shock cognate 71 kDa protein (Hsc70) appeared as monomer (M), dimer (D), trimer (T), and higher order high molecular weight (HMW) oligomeric species when subjected to SEC chromatography. Resolution and evaluation of the extent to which peptide-Hsc70 complex was formed with a given peptide or peptide mixture was complicated by the close elution of a complex of Hsc70 monomer with peptide (Msh). The peaks corresponding to monomer and complex overlap and were not fully resolved by conventional SEC media. In order to more accurately calculate the extent of complex formation, the following data analytical method was used. A central feature of this method was based on the observation that trimeric and dimeric forms of Hsc70 were observed to be recruited to the formation of monomeric peptide complexes. Peak area integrations of these protein species were well resolved from the complex and monomer. Further, the extent to which complex was formed appeared to be inversely proportional to the extent to which trimer and dimer were recruited to complex formation. Because of this observation, changes in trimer and dimer reflected the extent to which

monomer was recruited to the formation of complex. Thus, the progression of changes in the level of trimer and dimer was used to calculate expected changes in the peak areas of overlapping complex and monomer species, and these calculated peak areas were used to calculate net formation of complex. This data analysis method is described below.

[00286] Terms used for various chromatographic fractions include: High Molecular Weight (HMW), Trimer and other mid-order oligomer (T), Dimer (D), Complex (C), Monomer shoulder (Msh), and Monomer (M) (see Figure 1). Peak areas of the various fractions were extracted from SEC data and the percentage of peptide-Hsc70 complex formation was calculated using the following set of equations:

$$\% \text{ Complex} = (\text{AREA}_{\text{Complex}} / \text{AREA}_{\text{Total}}) \text{ X } 100$$

$$\text{AREA}_{\text{Complex}} = \text{AREA}_{\text{Total}} - (\text{Area}_{\text{T+D}} + \text{Area}_{\text{Mshx}} + \text{Area}_{\text{Mx}})$$

$$\text{AREA}_{\text{Total}} = \text{AREA}_{\text{T+D, C, Msh, M}} + (\text{AREA}_{\text{HDW-x}} - \text{AREA}_{\text{HDW-0}})$$

$$\text{AREA}_{\text{Mshx}} = \text{AREA}_{\text{Msh0}} \text{ X } (\text{AREA}_{(\text{T+D})x})/(\text{AREA}_{(\text{T+D})0})$$

$$\text{AREA}_{\text{Mx}} = \text{AREA}_{\text{M0}} \text{ X } (\text{AREA}_{(\text{T+D})x})/(\text{AREA}_{(\text{T+D})0})$$

[00287] $\text{AREA}_{\text{Total}}$ is the sum of total integrated peak areas from trimer/oligomer region through the monomer peak and excludes the initial HMW peak area but includes the excess increase of the HMW peak area that was observed when peptide was added. The HMW peak was excluded from the complexation calculation on the basis that it was aggregated protein that was not functional for complexation. This correction took into account $\text{Area}_{\text{Total}}$ factors in the minor increase in HMW area, adding it back to base total area used to calculate area of complex. Including this adjustment resulted in a more stable $\text{Area}_{\text{Total}}$ across the range of peptide concentrations used to form complexes.

[00288] The foregoing method was applied to the SEC chromatogram for each complexation reaction by applying vertical lines to the chromatogram to produce HMW, T, C, D, and M segments (as shown in Figure 1), calculating the area under the curve for of each of the indicated HMW, T, C, D, and M segments, and inputting the values into the equations described above. The results of this analysis are show in Table 6.

Table 6. Percent complexation of peptides with Hsc70

Peptide Name	SEQ ID NO:	Sequence	0.25:1	0.5:1	1:1	2:1	4:1
PEP001	71	FFRKNLLRLTG	23.4	44.7	68.1	82.5	90.1
PEP002	165	FFRKNRLLLTG	19.2	32.0	48.7	64.8	78.8
PEP003	166	FFRKNWLLLTW	26.8	45.6	67.2	81.3	87.6
PEP004	167	FFRKNLLRWTG	15.4	29.0	46.8	62.5	75.3

PEP005	168	FFRKNRLWLTG	16.0	32.7	54.8	67.6	77.6
PEP006	18	FFRKNWLRLTW	25.4	53.4	81.5	88.3	91.8
PEP027	21	FFRKNFLRLTF	19.1	49.0	77.0	85.6	90.0
PEP008	169	FFRKFWLRLTW	24.4	38.3	61.8	79.1	81.6
PEP009	170	FFRKNWLRLLW	32.8	63.5	81.0	85.3	89.0
PEP010	171	FFRKNWLRLFW	19.1	42.2	64.9	79.3	86.5
PEP011	172	FFRKNWLRLKW	31.2	58.2	81.6	87.8	90.4
PEP012	19	FFRKNWLKLTW	29.9	58.2	79.2	86.2	89.5
PEP013	173	FFRKNWIRITW	25.6	48.3	69.6	81.9	87.7
PEP014	174	FFRKQWLRLTW	29.3	54.4	80.9	88.1	90.3
PEP028	22	FRNWLRLTW	24.0	46.4	75.6	84.1	87.5
PEP055	72	FFRKNWLKLKW	24.1	52.2	75.9	83.7	86.3
PEP057	74	FFRKNWLKLRW	24.9	50.0	72.2	82.8	88.3
PEP058	75	FFRKNWLKLWK	22.7	43.5	66.5	78.8	83.9
PEP155	164	FFRKNLLRLTW	22.5	48.1	75.6	82.9	86.6

[00289] PEP006 was selected for further characterization.

6.1.2 Complexation of Hsc70 with PEP006

[00290] This example demonstrates the ability of PEP006 to bind to Hsc70 at a range of molar ratios from 0.25:1 to 3:1, as determined by size exclusion chromatography.

[00291] Briefly, PEP006 peptide was reconstituted in water for injection (WFI) to a concentration of 645 µM. Recombinant human Hsc70 (rhHsc70) was diluted at a concentration of 1.66 mg/mL. Both solutions were pre-warmed in a 37 °C incubator for 10 minutes, and were combined and incubated at 37 °C for 60 minutes. The final concentration of rhHsc70 was 1 mg/mL (about 14.1 µM), and the molar ratio of PEP006 to rhHsc70 was 0.25:1, 0.5:1, 1:1, 1.5:1, 2:1, 2.5:1, and 3:1. A negative control containing only rhHsc70 at 1 mg/mL was also prepared.

[00292] A quantity of 10 µg of each sample was injected neat in triplicate for resolution by size exclusion HPLC (Alliance HPLC, Waters Model #2695 Separations Module; Dual Wavelength UV Detector, Waters Model 2487) using a chromatography column TSKgel SuperSW3000 (Tosoh Bioscience, Catalog # 18675). The column temperature was controlled at 25°C ± 5°C, and the autosampler temperature was controlled at 5°C ± 3°C. The mobile phase was composed of 10mM sodium phosphate with 300mM sodium chloride, pH

7.2, and was delivered at a flow rate of 0.2mL/min for 30 minutes. UV absorbance of PEP006 peptide and rhHsc70 protein was measured at the wavelengths of 214 nm and 280nm. The absorbance data was processed by Waters Empower (V2) software.

[00293] Figure 2 shows a chromatogram of the PEP006-Hsc70 complexation products, wherein the column retention time became shorter when rhHsc70 bound to PEP006.

6.1.3 Complexation of Hsc70 with polypeptides comprising PEP006

[00294] This example describes characterization of the binding of Hsc70 to the polypeptide LGVVRPRALHRELDLVDDSPTPGSPGSFFRKNWLRLTW (SEQ ID NO: 77), which comprises PEP006 and a peptide observed from a patient's tumor (LGVVRPRALHRELDLVDDSPTPGSPGS (SEQ ID NO: 76)). The molar ratios of polypeptide to Hsc70 tested in this example were 0.125:1, 0.25:1, 0.5:1, 1:1, 1.5:1, 2:1, 2.5:1, 3:1, 3.5:1, and 4:1.

[00295] Figure 3A shows a chromatogram of the polypeptide-Hsc70 complexation products, wherein the column retention time became shorter when rhHsc70 bound to the polypeptide. Figure 3B is a graph showing percent complexation of a polypeptide comprising PEP006 with HSC70 over a range of polypeptide:Hsc70 molar ratios from 0.125:1 to 4:1, as calculated from size exclusion chromatography traces similar to those in Figure 3A, using the methods described Example 6.1.1. Three independent experiments are shown.

[00296] To further characterize binding of Hsc70 to polypeptides comprising C-terminal PEP006 or PEP001, a range of polypeptides was generated with C-terminal PEP001, PEP006, and in some cases, the same polypeptide without a C-terminal HSC70 binding peptide. The peptides used are shown in Table 7 below. Polypeptides were synthesized, complexation was performed, and SEC data was analyzed according to the methods described in Example 6.1.1, above.

Table 7. Polypeptides

Peptide Name	Sequence	SEQ ID NO:
PEP165	AKFVAAWTLKAAA	184
PEP166	AKFVAAWTLKAAAFFRKNLLRLTG	185
PEP167	AKFVAAWTLKAAAFFRKNWLRLTW	186
PEP168	PLLPFYPPDEALEIGLELNSSALPPTE	187
PEP169	PLLPFYPPDEALEIGLELNSSALPPTEF FRKNLLRLTG	188
PEP170	PLLPFYPPDEALEIGLELNSSALPPTEF FRKNWLRLTW	189

PEP171	EHIHRAGGLFVADAIQVGFGRIGKHFW	190
PEP172	EHIHRAGGLFVADAIQVGFGRIGKHFWFFRKNLLRLTG	191
PEP173	EHIHRAGGLFVADAIQVGFGRIGKHFWFFRKNWLRLTW	192
PEP174	DKPLRRNNSYTSYIMAICGMPLDSFRA	193
PEP175	DKPLRRNNSYTSYIMAICGMPLDSFRAFFRKNLLRLTG	194
PEP176	DKPLRRNNSYTSYIMAICGMPLDSFRAFFRKNWLRLTW	195
PEP177	EVIQTSKYYMRDVIAIESAWLLELAPH	196
PEP178	EVIQTSKYYMRDVIAIESAWLLELAPH FFRKNLLRLTG	197
PEP179	EVIQTSKYYMRDVIAIESAWLLELAPHFFRKNWLRLTW	198
PEP180	VILPQAPSGPSYATYLQPAQAQMLTPP	199
PEP181	VILPQAPSGPSYATYLQPAQAQMLTPPFFRKNLLRLTG	200
PEP182	VILPQAPSGPSYATYLQPAQAQMLTPPFFRKNWLRLTW	201

[00297] Figure 4A is a graph showing percent complexation for five different peptides, where each of the five different peptides comprised, C-terminal PEP001, C-terminal PEP006, or no C-terminal HSC70 binding peptide. Figure 4B is a graph showing percent complexation for six different peptides, where each of the six different peptides comprised either, C-terminal PEP001, or C-terminal PEP006.

6.2 Example 2: Enhancement of cellular immunity by HSP-binding peptides

[00298] This example demonstrates immunogenicity and tumor-suppressing activity of polypeptides comprising HPV E6-E7 peptides and PEP001 or PEP006 in two animal models.

6.2.1 Increase of antigenic peptide immunogenicity by HSP-binding peptides

[00299] In this example, immunogenicity of a pool of four polypeptides, each comprising an immunogenic HPV E6 or E7 peptide linked to PEP001 or PEP006, or not linked to an HSP-binding peptide, was analyzed in an immunogenicity animal model.

[00300] Briefly, four HPV E6 or E7 peptides either alone or linked to PEP001 or PEP006, having the amino acid sequences provided in Table 8, were chemically synthesized and dissolved in 100% DMSO at concentrations ranging from 25 to 100 mg/ml. These HPV E6 and E7 peptides were known to be immunogenic in C57BL/6 mice (*see* Bartkowiak et al.

(2015) Proc Natl Acad Sci U S A. 112(38); and Manuri et al. (2007) Vaccine 25(17):3302-10, each of which is incorporated by reference herein in its entirety). The known epitope sequence of PEP059 and PEP060 was RAHYNIVTF (SEQ ID NO: 78), and the known epitope sequence of PEP061 and PEP062 was VYDFAFRDL (SEQ ID NO: 79).

Table 8. Amino acid sequences of HPV peptides*

Peptide pool	Peptide Name	Description	Amino Acid Sequence	SEQ ID NO:
Naked peptides	PEP059	HPV16 E7 44–62 Q19D	QAEPDRAHYNIVTFCCKCD	80
	PEP060	HPV16 E7 49–57 R9F	RAHYNIVTF	81
	PEP061	HPV16 E6 43–57 Q15L	QLLRREVYDFAFRDL	82
	PEP062	HPV16 E6 49–58 V10C	VYDFAFRDLC	83
PEP001-linked peptides	PEP067	PEP059 linked to C-terminal PEP001	QAEPDRAHYNIVTFCCKCDFFRKNLLRLTG	84
	PEP068	PEP060 linked to C-terminal PEP001	RAHYNIVTFFFRKNLLRLTG	85
	PEP069	PEP061 linked to C-terminal PEP001	QLLRREVYDFAFRDLFFRKNLLRLTG	86
	PEP070	PEP062 linked to C-terminal PEP001	VYDFAFRDLCFFRKNLLRLTG	87
PEP006-linked peptides	PEP063	PEP059 linked to C-terminal PEP006	QAEPDRAHYNIVTFCCKCDFFRKNWLRLTW	88
	PEP064	PEP060 linked to C-terminal PEP006	RAHYNIVTFFFRKNWLRLTW	89
	PEP065	PEP061 linked to C-terminal PEP006	QLLRREVYDFAFRDLFFRKNWLRLTW	90
	PEP066	PEP062 linked to C-terminal PEP006	VYDFAFRDLCFFRKNWLRLTW	91

*The PEP001 and PEP006 sequences in the polypeptides are underlined

[00301] Recombinant human Hsc70 (rhHsc70) protein was purified from rhHsc70-expressing *E. coli* by chromatography using, sequentially, a weak anionic Q Sepharose column, an ATP agarose affinity column, and a DEAE-FF weak anion exchange column. The purified rhHsc70 protein was diluted in filtered PBS supplemented with 0.01% Polysorbate 20.

[00302] For vaccines preparation, an equimolar pool of four polypeptides was prepared in 75% DMSO at a total concentration of 320 μM. The purified rhHsc70 protein was pre-incubated at 37°C for 30 minutes, and the polypeptide pool was added to the rhHsc70 protein

solution at 2:1 or 1:1 molar ratio to reach an rhHsc70 protein concentration of 0.5 mg/ml. The mixture was incubated for 1 hour at 37°C and filtered sequentially through a 0.8 μm and a 0.2 μm filter. The mixture was then placed on ice for 30 min and stored at -80 °C.

[00303] For vaccination, six-week-old female C57BL/6J mice purchased from the Jackson Laboratory were maintained in a specific pathogen-free environment. The mice were immunized by subcutaneous injection of the vaccine. Each injection contained a total of 30 μg (about 0.42 nmol) Hsc70 complexed to the peptide pool (0.42 nmol for 1:1 ratio or 0.84 nmol for 2:1 ratio), supplemented with 10 μg of QS-21 Stimulon®, diluted in BioXcell InVivoPure pH 7.0 Dilution Buffer to a final volume of 200 μl. For each injection in the free peptide groups (without complexation with Hsc70), an equimolar pool of the four polypeptides at a total concentration of 10 nmol, supplemented with 10 μg of the adjuvant QS-21 Stimulon®, was diluted in filtered PBS with 0.1% Polysorbate 20 to a final volume of 200 μl. One week after the initial immunization, a boosting dose containing the same amount of vaccine was injected subcutaneously to each mouse.

[00304] One week after the second immunization, an IFNγ ELISpot assay was performed. Briefly, immunized mice were euthanized, splenocytes were gently isolated, and 5×10^5 to 1×10^6 live cells from each mouse were seeded on a plate previously coated with a murine IFNγ capture antibody. The cells were re-stimulated overnight using the naked peptides (PEP059-062). The cells were removed by lysis, and the IFNγ bound to the capture antibody was detected using a detection antibody couple to horseradish peroxidase (HRP). The number of spots in each well, representing the number of IFNγ-producing cells in this well, was counted using CTL S6 ImmunoSpot® analyzer and software.

[00305] As shown in Figure 5A, HPV vaccines containing PEP001- or PEP006-linked peptides complexed with Hsc70 demonstrated increased immunogenicity as compared to the naked HPV peptides. With these particular HPV peptides, the vaccines containing PEP006-linked peptides complexed with Hsc70 showed a greater immunogenicity than the vaccines containing PEP001-linked peptides complexed with Hsc70 under the conditions used.

[00306] To compare the immunogenicity of PEP001- and PEP006-containing vaccines with vaccines employing naked peptides at the same peptide dose, an additional experiment was performed using the same procedure as described above, except that in the absence of Hsc70, the amounts of free peptides were 0.84 nmol and 0.42 nmol in the 2:1 ratio group and 1:1 ratio group, respectively.

[00307] As shown in Figure 5B, HPV vaccines containing PEP001- or PEP006-linked peptides complexed with Hsc70 elicited a greater number of IFNγ-producing splenocytes

than the equivalent doses of naked peptide complexed with Hsc70 at mole ratios of 1:1 and 2:1. The vaccines containing PEP001- and PEP006-linked peptides complexed with Hsc70 also elicited a greater response than an equivalent dose of free peptides not complexed with Hsc70 at mole ratios of 1:1 and 2:1. With these particular HPV peptides, the vaccines containing PEP006-linked peptides complexed with Hsc70 showed a greater immunogenicity than the vaccines containing PEP001-linked peptides complexed with Hsc70 under the conditions used.

[00308] In related experiments, the immunogenicity of three pools of three different MC38 peptides was assessed using the immunogenicity animal model and protocol described above for the HPV E6 or E7 peptides. The details of the MC38 peptide pools are set forth in Table 9. As shown in Figure 6, all of the peptide pools elicited some level of immune response.

Table 9. MC38 peptide vaccine pools*

Vaccine pool	Peptide Name	Description	Amino Acid Sequence	SEQ ID NO:
Naked peptides	PEP156	MC38 Peptide	GRVLELFRAAQLANDVVLQI MELCGATR	165
	PEP157	MC38 Peptide	GIPVHLELASMTNMELMSSI VHQQVFPT	166
	PEP158	MC38 Peptide	EAGQSLVISASIIVFNLLELEG DYR	167
PEP001-linked peptides	PEP159	PEP156 linked to C-terminal PEP001	GRVLELFRAAQLANDVVLQI MELCGATRFFRKNLLRLTG	168
	PEP160	PEP157 linked to C-terminal PEP001	GIPVHLELASMTNMELMSSI VHQQVFPTFFRKNLLRLTG	169
	PEP161	PEP158 linked to C-terminal PEP001	EAGQSLVISASIIVFNLLELEG DYRFFRKNLLRLTG	170
PEP006-linked peptides	PEP162	PEP156 linked to C-terminal PEP006	GRVLELFRAAQLANDVVLQI MELCGATRFFRKNWLRLTW	171
	PEP163	PEP157 linked to C-terminal PEP006	GIPVHLELASMTNMELMSSI VHQQVFPTFFRKNWLRLTW	172
	PEP164	PEP158 linked to C-terminal PEP006	EAGQSLVISASIIVFNLLELEG DYRFFRKNWLRLTW	173

*The PEP001 and PEP006 sequences in the polypeptides are underlined.

6.2.2 Increase of tumor vaccine efficacy by HSP-binding peptides

[00309] This example demonstrates therapeutic efficacy of the HPV vaccine described in Section 6.2.1, using a TC1 HPV16 E6/E7 syngeneic mouse tumor model.

[00310] TC1 cells express the oncogenes HRAS, HPV16 E6 and E7 as disclosed in Lin et al. (1996) Cancer Res. 56(1):21-26, which is hereby incorporated by reference in its entirety. Low passage TC1 cells were washed in serum-free PBS and re-suspend in PBS at a concentration of 2×10^6 cells/ml. C57BL/6 mice shaved on the flank three days prior to use were injected subcutaneously in the shaved area with 2×10^5 cells in 100 µl volume. Vaccines were prepared according to the methods described in Section 6.2.1. The naked peptides, PEP001-linked peptides, and PEP006-linked peptides were complexed with rhHsc70 protein at the ratios of 1:1, 4:1, and 2:1, respectively. The vaccines were administered to the mice subcutaneously at days 5, 10, and 15 post TC1 cell implantation.

[00311] Tumors were measured every 3-4 days with a caliper. Tumor volume was calculated using the formula of $1/2 \times D \times d^2$, where D is the major axis and d is the minor axis. Any palpable but non-measurable tumor was estimated as 0.5 mm^3, whereas absence of tumor was recorded as 0 mm^3. Mice were sacrificed when tumors reached 2000 mm^3 or upon ulceration, and survival curves were plotted.

[00312] As shown in Figures 7A-7E, tumor growth in the mice injected with the vaccine comprising PEP001- or PEP006-linked HPV peptides was slower than in the mice injected with the vaccine comprising naked HPV peptides or injected with PBS. Similar therapeutic effects of the vaccines comprising PEP001- and PEP006-linked HPV peptides were observed in the survival curve (Figure 7F).

[00313] The vaccine comprising PEP006-linked HPV peptides complexed with rhHsc70 was more potent in suppressing tumor growth than the vaccine comprising PEP001-linked HPV peptides complexed with rhHsc70 (Figures 7A, 7D, and 7E). Notably, this difference translated into substantial protection against mortality in these experiments (Figure 7F).

6.2.3 Efficacy of tumor vaccines comprising PEP006 and a novel set of HPV peptides

[00314] This example demonstrates therapeutic efficacy of an HPV vaccine comprising a novel set of HPV peptides. The sequences of the polypeptides used in the vaccine are provided in Table 4. Specifically, PEP073 and PEP074 comprised the amino acid sequence of EVYDFAFRDL (SEQ ID NO: 92), a murine H-2Db and a human HLA-A*24:02 epitope. PEP081 comprised the amino acid sequences of YMLDLQPET (SEQ ID NO: 93) and MLDLQPETT (SEQ ID NO: 94), human HLA-A*02:01 epitopes. PEP084 comprised the amino acid sequence of RAHYNIVTF (SEQ ID NO: 78), a murine H-2Db epitope. PEP086 comprised the amino acid sequence of LLMGTLGIVC (SEQ ID NO: 95), a human HLA-A*02:01 epitope. Each peptide also comprised the amino acid sequence of PEP006.

[00315] The vaccine was prepared by the method described in Section 6.2.2, and the ratio of peptide to rhHsc70 protein was 2:1 for the HPV peptide pool. The efficacy of the vaccine was assessed using the same mouse model as described in Section 6.2.2, and the vaccine comprising the pool of PEP063-066 was used as a comparator.

[00316] As shown in Figures 8A and 8B, the vaccine containing Hsc70 and PEP071-086 reduced tumor growth and improved survival as compared to PBS control in the TC1 HPV16 E6/E7 syngeneic tumor model.

6.2.4 Efficacy of two formulations of tumor vaccine comprising PEP006

[00317] This example demonstrates therapeutic efficacy of a vaccine using two different formulations, one in which all peptides were initially reconstituted in DMSO and one in which only peptides which were not soluble in neutral, acidic, or basic water, were initially reconstituted in DMSO. The sequences of the polypeptides used in the vaccine, which contain tumor associated antigens from HPV E6 and E7 oncoproteins, are provided in Table 4. Specifically, the vaccine used in this example comprised sixteen peptides, PEP071-PEP086. Each peptide comprises the amino acid sequence PEP006 at the C-terminus.

[00318] Two formulations of vaccine were generated for evaluation. In Formulation A, each of the 16 HPV peptides was initially reconstituted from powder in 100% DMSO. Specifically, the peptides were resuspended in 100% DMSO at 25 mg/ml and then equimolar amounts of each peptide were pooled in a solution of 75% DMSO diluted in sterile water at final pool concentration of 320 μM (each peptide @ ≅ 20 μM). In Formulation B, each peptide was tested for solubility in neutral water followed by pH-adjusted (*i.e.* acidic, containing HCl, or basic, containing NaOH) water if necessary. DMSO was used only if the peptide was not soluble in water. Specifically, the 16 peptides were solubilized at 500 μM in neutral water solution, pH adjusted water, or in 100% DMSO (when peptides could not be resuspended in aqueous solutions). The peptides were then mixed at equal volume to make a 500 μM working pool (each peptide @ ≅ 31 μM). For both vaccine formulations, the peptides were subsequently diluted in aqueous buffer to the concentration desired for complexation to Hsc70.

[00319] For complexation to HSC70, rh-Hsc70 was incubated for 0.5 hour at 37°C, then further incubated for 1 hour at 37° C with the pool of 16 peptides at 2:1 molar ratio of total peptide:protein, following sterile procedures. Complexes were then incubated on ice for 15 min. The complexes were filtered and aliquoted.

[00320] C57BL/6 mice (n=13/group) were injected subcutaneously with $2x10^5$ live TC-1 tumor cells in the flank followed by treatment with the two formulations of vaccine, both

comprising the same 16 overlapping long synthetic peptides covering the full length of the E6 and E7 HPV oncoproteins or PBS control. On days 5, 10, and 15 after tumor challenge mice were administered (a) 30 μg Hsc70-based vaccine (either Formulation A or Formulation B) + 10 μg QS-21 or (b) PBS subcutaneously at the diagonally opposite brachial lymph node area from the tumor site. Each dose of vaccine contained 30 μg Hsc70 and ~4 μg total peptide (~250 ng each peptide) along with QS-21 adjuvant. Injections were carried out with a 1mL BD Syringe with a Sub-Q 26G x 5/8 inch needle.

[00321] Tumor growth kinetics and survival were monitored. Tumor volumes were measured by caliper every 3-4 days of the study starting on day 5 after tumor challenge. Tumor length was based on the longest linear distance. Width was based on the longest linear distance perpendicular to the length. Mice were euthanized when tumor volumes reached 2000 mm^3. Tumor volumes (mm^3) were calculated as length x $width^2$ x 0.5. For mice with two tumors, each was measured independently and the volumes summed. Mice were distributed to each treatment group randomly on day 5 post tumor inoculation. Mice without early measurable tumors were excluded from the study. Ten mice per group were followed for survival using the Kaplan-Meier method and Log-rank test ($p \leq 0.0001$ survival in mice treated with either vaccine formulation vs. survival in mice treated with PBS). Tumor size was assessed every 2-3 days and each group's mean tumor volume was plotted as function of time.

[00322] Tumors grew rapidly in control mice treated with PBS (Figures 9A and 9B). In contrast, a significant delay in the rate of tumor growth was observed in mice treated with either vaccine formulation (Figures 9A and 9B) (tumor growth in mice treated with Formulation A compared to tumor growth in mice treated with PBS **$p \leq 0.01$ and tumor growth mice treated with Formulation B compared to tumor growth in mice treated with PBS ****$p \leq 0.0001$: Wilcoxon Rank Sum Test). Tumor growth kinetics of individual mice were plotted as a function of time. Prolonged survival was observed in mice treated with either Formulation A or Formulation B as compared to mice treated with PBS (Figure 9C).

[00323] The TC-1 tumor is known to develop a resistance phenotype to antigen targeting therapies which can be driven by immune editing and loss of epitopes expressed by the tumor (Smahel et al., 2007) which likely explains the eventual progression of tumors beginning on ~d. 28 for both vaccine formulations. Together, these data demonstrate that an efficient vaccine-induced immune response against tumor associated antigens such as HPV E6 and E7 oncoproteins can translate into significant tumor control and prolonged survival.

6.3 Example 3: Improvement of peptide synthesis by Hsc70-binding peptides

[00324] This example demonstrates the ability of PEP001 and PEP006 to improve crude purity of peptides during synthesis.

6.3.1 Improvement of crude purity of Ova antigen peptide by addition of PEP001 or PEP006

[00325] An Ova antigen peptide comprising the amino acid sequence of EVSGLEQLESIINFEKLTEWTSSNVME (PEP053, SEQ ID NO: 97), either naked or linked to PEP001 (PEP052, SEQ ID NO: 230, EVSGLEQLESIINFEKLTEWTSSNVMEFFRKNLLRLTG) or PEP006 (PEP054, SEQ ID NO: 231, EVSGLEQLESIINFEKLTEWTSSNVMEFFRKNWLRLTW), were synthesized by the method described in Section 6.1.1. This Ova antigen peptide comprised an MHC-binding epitope having the amino acid sequence of SIINFEKL (SEQ ID NO: 96). Peptide purity was determined by reverse phase chromatography using the Vanquish Bioanalytical and Ultimate 3000 Dionex workstation, following the procedure provided in the *Vanquish/Ultimate 3000 User's Guide and Data Explorer User's Guide* included with the Chromeleon 7.0 software package.

[00326] After cycles of amino acid residue addition, the synthesized peptides were cleaved from the resin and dissolved in 1:1 acetonitrile:water (v/v) at 1 mg/mL concentration. The dissolved sample was analyzed by analytical HPLC using a Phenomenex Luna C18 10µm 4.6 x 250mm column. A volume of 20 µL of sample was injected, and was subject to gradient elution using a mixture of solution A (0.1% TFA in water) and solution B (0.1% TFA in acetonitrile) as mobile phase, following the gradient of Table 10. The column temperature was maintained at 37°C ± 5°C. The peptides were detected by UV absorbance at the wavelengths of 214 nm and 280 nm.

Table 10. Gradient table for HPLC mobile phase

Time (min)	Flow (mL/min)	% Solution A	% Solution B	Curve
0	1	95	5	5
0.01	1	95	5	5
25	1	35	65	5
25.01	1	5	95	5
31	1	5	95	5
31	1	95	5	5
40	1	95	5	5

[00327] In an elution curve, each peak represented a peptide with a specific retention time, and the area under the peak reflected the amount of this peptide. The peak of the correct peptide was confirmed by mass spectrometry. The crude purity of the peptide was calculated as the area under the peak of the correct peptide divided by the total area under the entire curve.

[00328] As shown in Figure 10A, the naked Ova peptide (middle panel) had a heterogeneous signal. By contrast, the Ova-PEP001 (upper panel) and Ova-PEP006 (lower panel) preparations showed nearly a single peak at the expected retention time. Quantification of the chromatograms also indicated that Ova-PEP001 and Ova-PEP006 had substantially increased crude purity (Figure 10B). This result was contrary to the general rule that longer peptides were more difficult to synthesize and purify, and suggested that PEP001 and PEP006 improved the crude purity in chemical synthesis of peptide.

6.3.2 Improvement of crude purity of a range of peptides by addition of PEP006

[00329] The 50 peptides shown below in Table 11 were synthesized by the method described in Section 6.1.1. This group of 50 peptides contains 25 unique peptide sequences (labelled A-Y) that were synthesized with or without ("naked peptide") the addition of a C-terminal PEP006 peptide sequence. Peptide purity was determined by reverse phase chromatography as described in section 6.3.1 above. As shown in Figure 11, addition of the PEP006 peptide sequence increased the crude purity for a majority of the peptides as compare to the corresponding naked peptide. Because of the sample complexity, many peptide separations were multi-dimensional. Three peptides were not detected in the C18 column under standard reverse phase gradient up to 95%. For these three peptides, there was no detectable peak to integrate throughout the gradient and crude purity was listed as zero. Possible causes of the lack of detection of the three peptides could include adherence of the sample to the C18 column or the storage vial, and/or the sample dropping out of solution.

Table 11. Peptides

	Naked Peptide Sequence			Peptide Sequence including PEP006		
	Sequence	**Peptide Name**	**SEQ ID NO:**	**Sequence**	**Peptide Name**	**SEQ ID NO:**
A	KFPLILYLGMAIVTVLYISLGSLGYLQ	PEP105	114	KFPLILYLGMAIVTVLYISLGSLGYLQFFRKNWLRLTW	PEP130	139

B	TMRGCGPCLRIAPSFSSMSNKYPQAVF	PEP106	115	TMRGCGPCLRIAPSFSSMSNKYPQAVFFFRKNWLRLTW	PEP131	140
C	RMKKENLMPREELARLFPNLPELIEIH	PEP107	116	RMKKENLMPREELARLFPNLPELIEIHFFRKNWLRLTW	PEP132	141
D	FSRTWIGIWSVLCFASTLFTVLTYLVD	PEP108	117	FSRTWIGIWSVLCFASTLFTVLTYLVDFFRKNWLRLTW	PEP133	142
E	TSLAIGTKSGYKLFSLSSVEQLDQVHG	PEP109	118	TSLAIGTKSGYKLFSLSSVEQLDQVHGFFRKNWLRLTW	PEP134	143
F	LFPTDCHSVPPHYTELLTFHSKEGTDH	PEP110	119	LFPTDCHSVPPHYTELLTFHSKEGTDHFFRKNWLRLTW	PEP135	144
G	PSRGSSSSSGYPVGVVFQPVGSGGVQP	PEP111	120	PSRGSSSSSGYPVGVVFQPVGSGGVQPFFRKNWLRLTW	PEP136	145
H	LSPGAAAPSGWALAPLGDTMKIYMELQ	PEP112	121	LSPGAAAPSGWALAPLGDTMKIYMELQFFRKNWLRLTW	PEP137	146
I	ELYRKLLRSQSVRFCFQGLLENSAHLI	PEP113	122	ELYRKLLRSQSVRFCFQGLLENSAHLIFFRKNWLRLTW	PEP138	147
J	AQVIILNHPGQISTGYAPVLDCHTAHI	PEP114	123	AQVIILNHPGQISTGYAPVLDCHTAHIFFRKNWLRLTW	PEP139	148
K	PVQLWVSATPPAGSPVRAMAIYKKSQH	PEP115	124	PVQLWVSATPPAGSPVRAMAIYKKSQHFFRKNWLRLTW	PEP140	149
L	NAFNPLNASASLPPAAMPITTADGRSD	PEP116	125	NAFNPLNASASLPPAAMPITTADGRSDFFRKNWLRLTW	PEP141	150
M	VGSVAGNKLLRAAWRRASLAATSLALG	PEP117	126	VGSVAGNKLLRAAWRRASLAATSLALGFFRKNWLRLTW	PEP142	151
N	AETSLLEAGASAASTAAALENLQVEAS	PEP118	127	AETSLLEAGASAASTAAALENLQVEASFFRKNWLRLTW	PEP143	152
O	NSVLQTLLQMRAAKSSVAPSREELLGT	PEP119	128	NSVLQTLLQMRAAKSSVAPSREELLGTFFRKNWLRLTW	PEP144	153
P	DFTHPEAREWFQGLLRRLRLRYNVTSF	PEP120	129	DFTHPEAREWFQGLLRRLRLRYNVTSFFFRKNWLRLTW	PEP145	154
Q	KKHDVRSIIGSPGLPFPALHPLDIMAD	PEP121	130	KKHDVRSIIGSPGLPFPALHPLDIMADFFRKNWLRLTW	PEP146	155

R	AGRPRPVLRSVNSLEPSQVIFCNRSPR	PEP122	131	AGRPRPVLRSVNSLEPSQVIFCNRSPRFFRKNWLRLTW	PEP147	156
S	TFFASDNAVDITTLTNSCLSNSDHSRD	PEP123	132	TFFASDNAVDITTLTNSCLSNSDHSRDFFRKNWLRLTW	PEP148	157
T	TLLRSSYVAQVPLLTLCTRGPPEEDAP	PEP124	133	TLLRSSYVAQVPLLTLCTRGPPEEDAPFFRKNWLRLTW	PEP149	158
U	MFSFNMFDHPIPLVFQNRFSTQYR	PEP125	134	MFSFNMFDHPIPLVFQNRFSTQYRFFRKNWLRLTW	PEP150	159
V	ATAAGSSTISQDTIHLTSGPVSALASG	PEP126	135	ATAAGSSTISQDTIHLTSGPVSALASGFFRKNWLRLTW	PEP151	160
W	ACSSSYNSAVMESSSVNVSMVHSSSKE	PEP127	136	ACSSSYNSAVMESSSVNVSMVHSSSKEFFRKNWLRLTW	PEP152	161
X	VLQEWKACDKLYDVATMRTTQLTYSME	PEP128	137	VLQEWKACDKLYDVATMRTTQLTYSMEFFRKNWLRLTW	PEP153	162
Y	RDPFRVRASAALLNKLYAMGLVPTRGS	PEP129	138	RDPFRVRASAALLNKLYAMGLVPTRGSFFRKNWLRLTW	PEP154	163

* * *

[00330] The invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[00331] All references (*e.g.*, publications or patents or patent applications) cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each individual reference (*e.g.*, publication or patent or patent application) was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. Other embodiments are within the following claims.

WHAT IS CLAIMED:

1. An isolated polypeptide comprising a heat shock protein (HSP)-binding peptide comprising the amino acid sequence of $X_1LX_2LTX_3$ (SEQ ID NO: 1), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G.

2. The isolated polypeptide of claim 1, wherein the HSP-binding peptide comprises the amino acid sequence of:
(a) $NX_1LX_2LTX_3$ (SEQ ID NO: 2), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;
(b) WLX_1LTX_2 (SEQ ID NO: 3), wherein X_1 is R or K; and X_2 is W or G; or
(c) $NWLX_1LTX_2$ (SEQ ID NO: 4), wherein X_1 is R or K; and X_2 is W or G.

3. The isolated polypeptide of claim 1 or 2, wherein the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12, 98-113, 207, and 212.

4. The isolated polypeptide of claim 3, wherein the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 5-12, 98-113, 207, and 212.

5. The isolated polypeptide of any one of the preceding claims, wherein the HSP-binding peptide comprises the amino acid sequence of SEQ ID NO: 6.

6. The isolated polypeptide of claim 5, wherein the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 6.

7. An isolated polypeptide comprising an HSP-binding peptide comprising the amino acid sequence of $NWX_1X_2X_3X_4X_5$ (SEQ ID NO: 232), wherein X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K.

8. The isolated polypeptide of claim 7, wherein the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 204, 208-211, and 213-215.

9. The isolated polypeptide of claim 8, wherein the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 204, 208-211, and 213-215.

10. An isolated polypeptide comprising an HSP-binding peptide comprising the amino acid sequence of SEQ ID NO: 205.

11. The isolated polypeptide of claim 10, wherein the amino acid sequence of the HSP-binding peptide consists of the amino acid sequence of SEQ ID NO: 205.

12. The isolated polypeptide of any one of the preceding claims, wherein the HSP-binding peptide is no more than 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, 49, or 50 amino acids in length.

13. The isolated polypeptide of any one of the preceding claims, further comprising an antigenic peptide comprising one or more major histocompatibility complex (MHC)-binding epitopes.

14. The isolated polypeptide of claim 13, wherein the MHC-binding epitope binds to an MHC I molecule with an IC_{50} of 500 nM or less.

15. The isolated polypeptide of claim 13 wherein the MHC-binding epitope binds to an MHC II molecule with an IC_{50} of 1000 nM or less.

16. The isolated polypeptide of any one of claims 13-15, wherein the MHC-binding epitope is from a cancer cell.

17. The isolated polypeptide of claim 16, wherein the MHC-binding epitope comprises an amino acid mutation or a gene fusion mutation of the cancer cell.

18. The isolated polypeptide of claim 17, wherein the amino acid mutation is a substitution, deletion, or insertion mutation.

19. The isolated polypeptide of claim 17 or 18, wherein the amino acid mutation or gene fusion mutation is at position 1, 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, 49, or 50 of the amino acid sequence of the antigenic peptide.

20. The isolated polypeptide of any one of claims 13-15, wherein the MHC-binding epitope is from a pathogenic microbe.

21. The isolated polypeptide of claim 20, wherein the pathogenic microbe is a virus.

22. The isolated polypeptide of claim 21, wherein the virus is a human papillomavirus (HPV).

23. The isolated polypeptide of claim 22, wherein the antigenic peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

24. The isolated polypeptide of any one of claims 13-21, wherein the antigenic peptide is 8 to 50 amino acids in length, optionally 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, 49, or 50 amino acids in length.

25. The isolated polypeptide of claim 24, wherein the antigenic peptide is 20 to 30 amino acids in length.

26. The isolated polypeptide of claim 24, wherein the antigenic peptide is 27 amino acids in length.

27. An isolated polypeptide comprising an HSP-binding peptide and an antigenic peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

28. The isolated polypeptide of claim 27, wherein the amino acid sequence of the antigenic peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

29. The isolated polypeptide of claim 27 or 28, wherein the HSP-binding peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-12, 98-113, 204, 205, 207-215, and 232.

30. The isolated polypeptide of claim 29, wherein the amino acid sequence of the HSP-binding peptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-12, 98-113, 204, 205, 207-215, and 232.

31. The isolated polypeptide of any one of claims 13-30, wherein the MHC-binding epitope comprises a modified amino acid residue.

32. The isolated polypeptide of claim 31, wherein the modified amino acid residue is a Tyr, Ser, Thr, Arg, Lys, or His that has been phosphorylated on a side chain hydroxyl or amine.

33. The isolated polypeptide of claim 31, wherein the modified amino acid residue is a mimetic of a Tyr, Ser, Thr, Arg, Lys, or His amino acid that has been phosphorylated on a side chain hydroxyl or amine.

34. The isolated polypeptide of claim 33, wherein the mimetic is a non-hydrolyzable analogue of a phosphorylated residue.

35. The isolated polypeptide of claim 31, wherein the modified amino acid residue is an Asn that has been glycosylated on a side chain amide, a Ser or Thr that has been glycosylated on a side chain hydroxyl, a Lys or Arg that has been methylated on a side chain amino, a Lys that has been acetylated on a side chain amino, an N-terminal residue that has been acetylated on the α-amino, or a C-terminal residue that has been amidated on the α-carboxyl.

36. The isolated polypeptide of any one of claims 31-35, wherein the modified amino acid residue is at position 1, 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, 49, or 50 of the amino acid sequence of the antigenic peptide.

37. The isolated polypeptide of any one of claims 13-36, wherein the HSP-binding peptide is linked to the antigenic peptide via a chemical linker.

38. The isolated polypeptide of any one of claims 13-36, wherein the HSP-binding peptide is linked to the antigenic peptide via a peptide linker.

39. The isolated polypeptide of claim 38, wherein the peptide linker comprises the amino acid sequence of FFRK (SEQ ID NO: 13) or FR.

40. The isolated polypeptide of claim 38 or 39, wherein the HSP-binding peptide is at the C-terminus of the polypeptide.

41. The isolated polypeptide of claim 40 comprising the amino acid sequence of:
(a) FFRKX_1LX_2LTX_3 (SEQ ID NO: 14), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;
(b) FFRKNX_1LX_2LTX_3 (SEQ ID NO: 15), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;
(c) FFRKWLX_1LTX_2 (SEQ ID NO: 16), wherein X_1 is R or K; and X_2 is W or G;
(d) FFRKNWLX_1LTX_2 (SEQ ID NO: 17), wherein X_1 is R or K; and X_2 is W or G; or
(e) FFRKNW$X_1X_2X_3X_4X_5$ (SEQ ID NO: 233), wherein X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K, at the C-terminus of the polypeptide.

42. The isolated polypeptide of claim 40, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 18-25, 71, 72, 74, 75, 166, 167, 173, and 174.

43. The isolated polypeptide of claim 38 or 39, wherein the HSP-binding peptide is at the N-terminus of the polypeptide.

44. The isolated polypeptide of claim 43, comprising the amino acid sequence of:
(a) X_1LX_2LTX_3FFRK (SEQ ID NO: 26), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;
(b) NX_1LX_2LTX_3FFRK (SEQ ID NO: 27), wherein X_1 is W or F; X_2 is R or K; and X_3 is W, F, or G;

(c) WLX_1LTX_2FFRK (SEQ ID NO: 28), wherein X_1 is R or K; and X_2 is W or G;
(d) $NWLX_1LTX_2FFRK$ (SEQ ID NO: 29), wherein X_1 is R or K; and X_2 is W or G; or
(e) $NWX_1X_2X_3X_4X_5FFRK$ (SEQ ID NO: 234), wherein X_1 is L or I; X_2 is L, R, or K; X_3 is L or I; X_4 is T, L, F, K, R, or W; and X_5 is W or K, at the N-terminus of the polypeptide.

45. The isolated polypeptide of claim 43, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 30-37, and 216-229.

46. The isolated polypeptide of any one the preceding claims, wherein the polypeptide is 12 to 50 amino acids in length, optionally 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, 49, or 50 amino acids in length.

47. The isolated polypeptide of any one the preceding claims, wherein the polypeptide is 20 to 40 amino acids in length.

48. The isolated polypeptide of any one the preceding claims, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69.

49. The isolated polypeptide of claim 48, wherein the amino acid sequence of the polypeptide consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69.

50. The isolated polypeptide of any one of the preceding claims, wherein the polypeptide is chemically synthesized.

51. A composition comprising a complex of the polypeptide of any one of claims 13-50 and a purified stress protein.

52. The composition of claim 51, wherein the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant or fusion protein thereof.

53. The composition of claim 52, wherein the stress protein is Hsc70.

54. The composition of claim 53, wherein the stress protein is human Hsc70.

55. The composition of any one of claims 51-54, wherein the stress protein is a recombinant protein.

56. A composition comprising a plurality of the polypeptides of any one of claims 13-50.

57. The composition of any one of claims 51-56, comprising 2-20 different polypeptides of any one of claims 13-50.

58. The composition of claim 57, wherein each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide.

59. The composition of any one of claims 56-58, wherein the antigenic peptide of each one of the polypeptides comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 38-53.

60. The composition of claim 59, wherein the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different antigenic peptides.

61. The composition of any one of claims 58-60, wherein each one of the polypeptides comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69.

62. The composition of any one of claims 58-61, wherein the amino acid sequence of each one of the polypeptides consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 54-69.

63. The composition of any one of claims 58-62, wherein the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 different polypeptides.

64. The composition of any one of claims 47-59, wherein the total amount of the polypeptide(s) in the composition is about 0.1 to 20 nmol.

65. The composition of claim 64, wherein the total amount of the polypeptide(s) in the composition is about 3, 4, 5, or 6 nmol.

66. The composition of any one of claims 51-55 and 57-65, wherein the amount of the stress protein in the composition is about 10 μg to 600 μg.

67. The composition of claim 66, wherein the amount of the stress protein in the composition is about 250 μg to 290 μg.

68. The composition of any one of claims 51-55 and 57-67, wherein the molar ratio of the polypeptide(s) to the stress protein is about 0.5:1 to 5:1.

69. The composition of claim 68, wherein the molar ratio of the polypeptide(s) to the stress protein is about 1:1 to 2:1.

70. The composition of claim 69, wherein the molar ratio of the polypeptide(s) to the stress protein is about 1:1, 1.25:1, or 1.5:1.

71. The composition of any one of claims 51-55 and 57-70, wherein the total amount of the polypeptide(s) and stress protein in the composition is about 10 μg to 600 μg.

72. The composition of claim 71, wherein the total amount of the polypeptide(s) and stress protein in the composition is about 300 μg.

73. The composition of any one of claims 51-72, wherein the composition further comprises an adjuvant.

74. The composition of claim 73, wherein the adjuvant comprises a saponin or an immunostimulatory nucleic acid.

75. The composition of claim 73, wherein the adjuvant comprises QS-21.

76. The composition of claim 75, wherein the amount of the QS-21 in the composition is about 10 μg, 25 μg, or 50 μg.

77. The composition of any one of claims 73-76, wherein the adjuvant comprises a TLR agonist, optionally a TLR4 agonist, TLR5 agonist, TLR7 agonist, TLR8 agonist, and/or TLR9 agonist.

78. The composition of any one of claims 51-77, which is a pharmaceutical composition comprising a pharmaceutically acceptable carrier or excipient.

79. The composition of any one of claims 51-78, wherein the composition is in a unit dosage form.

80. A method of inducing a cellular immune response to an antigenic peptide in a subject, the method comprising administering to the subject (a) an effective amount of a composition of any one of claims 51-78 or (b) a unit dosage form of claim 79.

81. The method of claim 80, wherein the subject has cancer.

82. The method of claim 80, wherein the subject has an infection of a pathogenic microbe.

83. A method of treating a disease in a subject, the method comprising administering to the subject (a) an effective amount of a composition of any one of claims 51-78 or (b) a unit dosage form of claim 79.

84. The method of claim 83, wherein the disease is cancer.

85. The method of claim 83, wherein the disease is an infection of a pathogenic microbe.

86. The method of claim 81 or 84, wherein the MHC-binding epitope is present in the subject's cancer cells.

87. The method of claim 82 or 85, wherein the MHC-binding epitope is present in the pathogenic microbe.

88. The method of any one of claims 80-87, wherein the composition or unit dosage form is administered to the subject weekly for four weeks.

89. The method of claim 88, wherein at least two further doses of the composition or unit dosage form are administered biweekly to the subject after the four weekly doses.

90. The method of claim 88 or 89, wherein at least one booster dose of the composition or unit dosage form is administered three months after the final weekly or biweekly dose.

91. The method of claim 90, wherein the composition or unit dosage form is further administered every three months for at least 1 year.

92. The method of any one of claims 80-91, further comprising administering to the subject lenalidomide, dexamethasone, interleukin-2, recombinant interferon alfa-2b, or PEG-interferon alfa-2b.

93. The method of any one of claims 80-92, further comprising administering to the subject an indoleamine dioxygenase-1 (IDO-1) inhibitor.

94. The method of claim 93, wherein the IDO-1 inhibitor is 4-amino-N-(3-chloro-4-fluorophenyl)-N'-hydroxy-1,2,5-oxadiazole-3-carboximidamide.

95. The method of any one of claims 80-94, further comprising administering to the subject an immune checkpoint antibody.

96. The method of claim 95, wherein the immune checkpoint antibody is selected from the group consisting of an agonistic anti-GITR antibody, an agonistic anti-OX40 antibody, an antagonistic anti-PD-1 antibody, an antagonistic anti-CTLA-4 antibody, an antagonistic anti-TIM-3 antibody, an antagonistic anti-LAG-3 antibody, an antagonistic anti-TIGIT antibody, an agonistic anti-CD96 antibody, an antagonistic anti-VISTA antibody, an antagonistic anti-CD73 antibody, an agonistic anti-CD137 antibody, an antagonist anti-

CEACAM1 antibody, an agonist anti-ICOS antibody, and or an antigen-binding fragment thereof.

97. A kit comprising a first container containing the polypeptide of any one of claims 13-51, and a second container containing a purified stress protein capable of binding to the polypeptide.

98. The kit of claim 97, wherein the first container contains 2-20 different polypeptides of any one of claims 13-51.

99. The kit of claim 98, wherein each of the different polypeptides comprises the same HSP-binding peptide and a different antigenic peptide.

100. The kit of any one of claims 97-99, wherein the total amount of the polypeptide(s) in the first container is about 0.1 to 20 nmol.

101. The kit of claim 100, wherein the total amount of the polypeptide(s) in the first container is about 3, 4, 5, or 6 nmol.

102. The kit of any one of claims 97-101, wherein the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant thereof.

103. The kit of claim 102, wherein the stress protein is Hsc70.

104. The kit of claim 103, wherein the stress protein is human Hsc70.

105. The kit of any one of claims 97-104, wherein the stress protein is a recombinant protein.

106. The kit of any one of claims 97-105, wherein the amount of the stress protein in the second container is about 10 μg to 600 μg.

107. The kit of claim 106, wherein the amount of the stress protein in the second container is about 250 μg to 290 μg.

108. The kit of any one of claims 97-107, wherein the molar ratio of the polypeptide to the stress protein is about 0.5:1 to 5:1.

109. The kit of claim 108, wherein the molar ratio of the polypeptide to the stress protein is about 1:1 to 2:1.

110. The kit of claim 109, wherein the molar ratio of the polypeptide to the stress protein is about 1:1, 1.25:1, or 1.5:1.

111. The kit of any one of claims 97-110, wherein the total amount of the polypeptide(s) in the first container and the stress protein in the second container is about 10 μg to 600 μg.

112. The kit of claim 111, wherein the total amount of the polypeptide(s) in the first container and the stress protein in the second container is 300 μg.

113. The kit of any one of claims 97-112, further comprising a third container containing an adjuvant.

114. The kit of claim 113, wherein the adjuvant comprises a saponin or an immunostimulatory nucleic acid.

115. The kit of claim 114, wherein the adjuvant comprises QS-21.

116. The kit of claim 115, wherein the amount of the QS-21 in the third container is about 10 μg, 25 μg, or 50 μg.

117. The kit of any one of claims 113-116, wherein the adjuvant comprises a TLR agonist, optionally a TLR4 agonist, TLR5 agonist, TLR7 agonist, TLR8 agonist, and/or TLR9 agonist.

118. A method of making a vaccine, the method comprising mixing one or more polypeptides of any one of claims 13-51 with a purified stress protein under suitable conditions such that the purified stress protein binds to at least one of the polypeptides.

119. The method of claim 118, wherein the stress protein is selected from the group consisting of Hsc70, Hsp70, Hsp90, Hsp110, Grp170, Gp96, Calreticulin, and a mutant thereof.

120. The method of claim 119, wherein the stress protein is Hsc70.

121. The method of claim 120, wherein the stress protein is human Hsc70.

122. The method of any one of claims 118-121, wherein the stress protein is a recombinant protein.

123. The method of any one of claims 118-122, wherein the molar ratio of the polypeptide to the stress protein is about 0.5:1 to 5:1.

124. The method of claim 123, wherein the molar ratio of the polypeptide to the stress protein is about 1:1 to 2:1.

125. The method of any one of claims 118-124, wherein the suitable conditions comprise a temperature of about 37 °C.

126. The method of any one of claims 118-125, wherein the molar ratio of the polypeptide to the stress protein is about 1:1, 1.25:1, or 1.5:1.

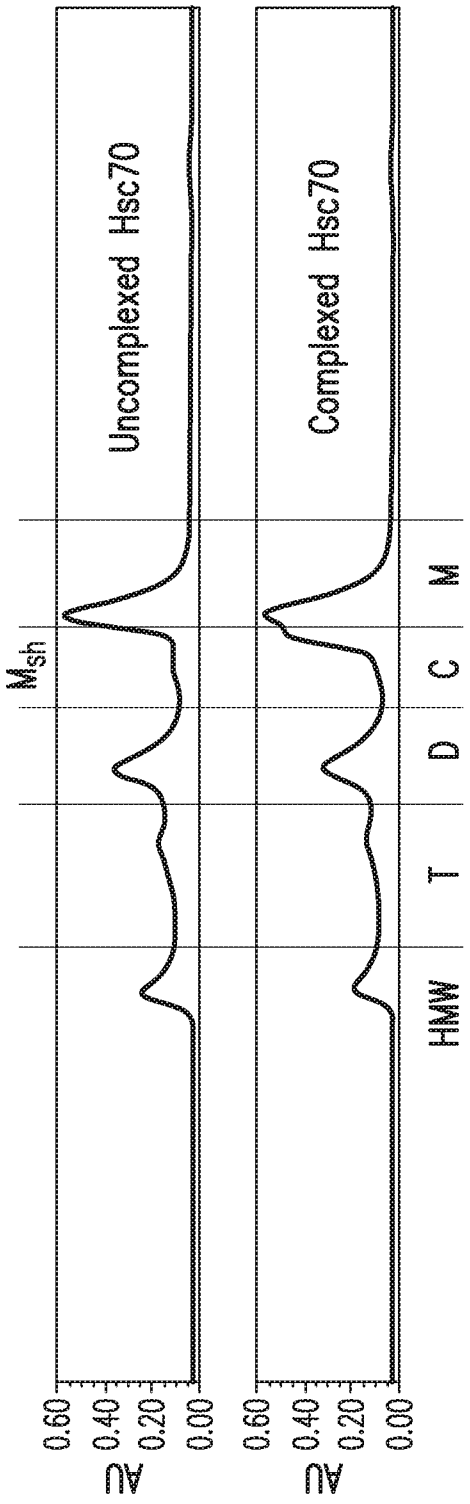
Uncomplexed Hsc70
Complexed Hsc70
M_{sh}
HMW
T
D
C
M
0.60
0.40
0.20
0.00
AU

FIG. 1

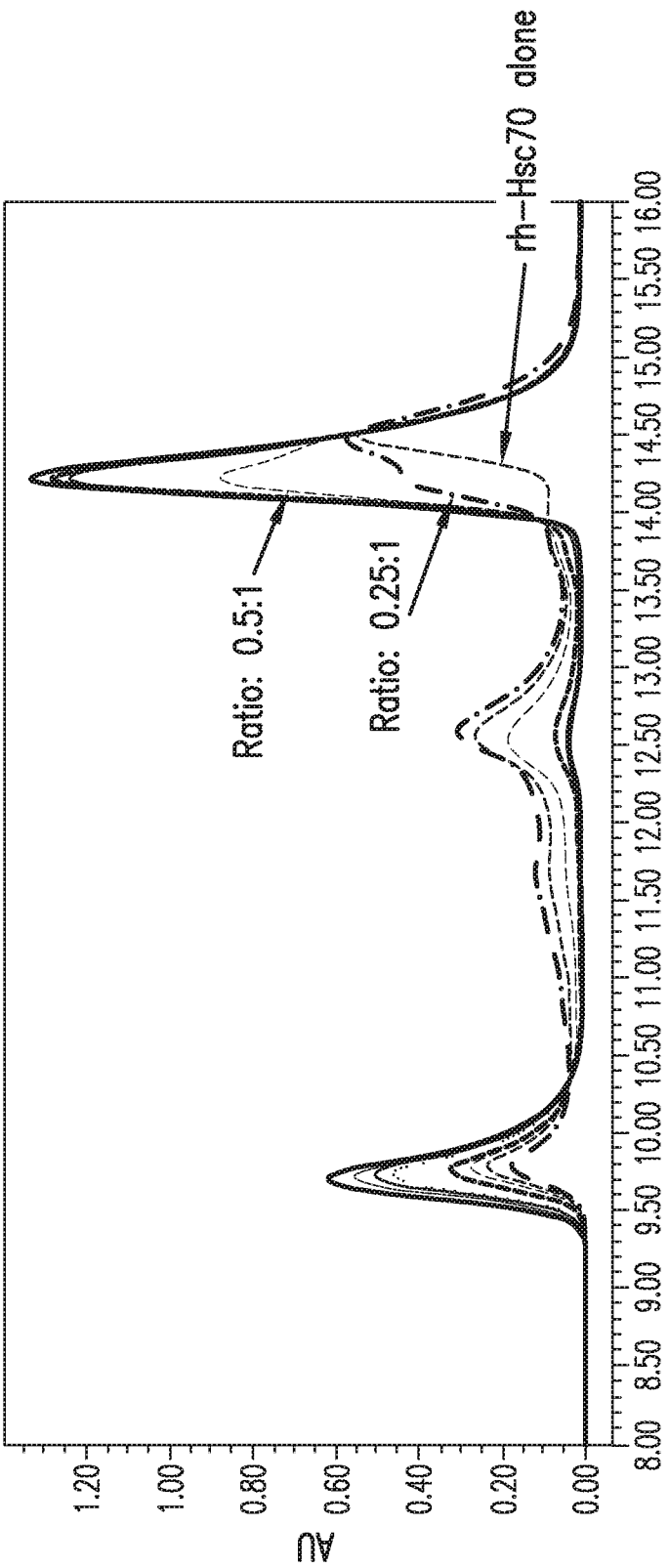
rh-Hsc70 alone
Ratio: 0.5:1
Ratio: 0.25:1
AU
1.20
1.00
0.80
0.60
0.40
0.20
0.00
8.00
8.50
9.00
9.50
10.00
10.50
11.00
11.50
12.00
12.50
13.00
13.50
14.00
14.50
15.00
15.50
16.00

FIG. 2

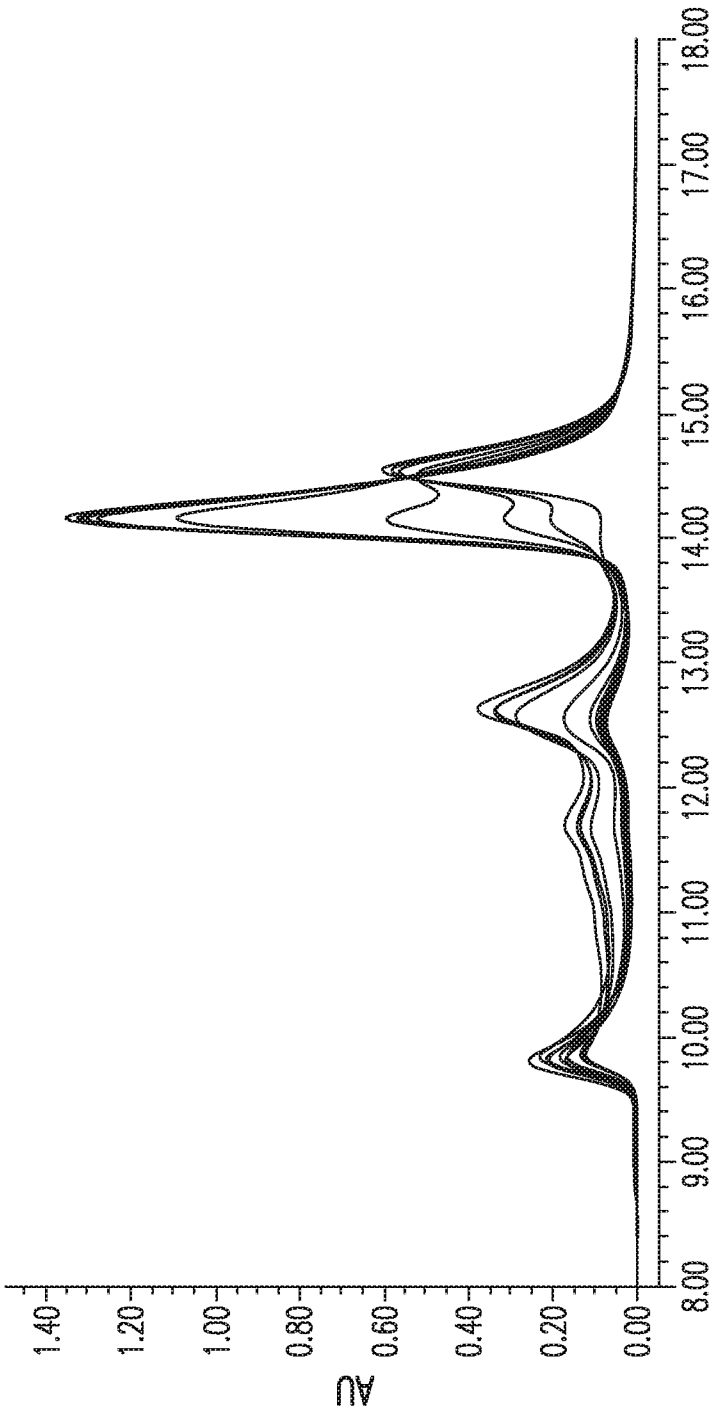
AU
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
8.00
9.00
10.00
11.00
12.00
13.00
14.00
15.00
16.00
17.00
18.00
Minutes

FIG.3A

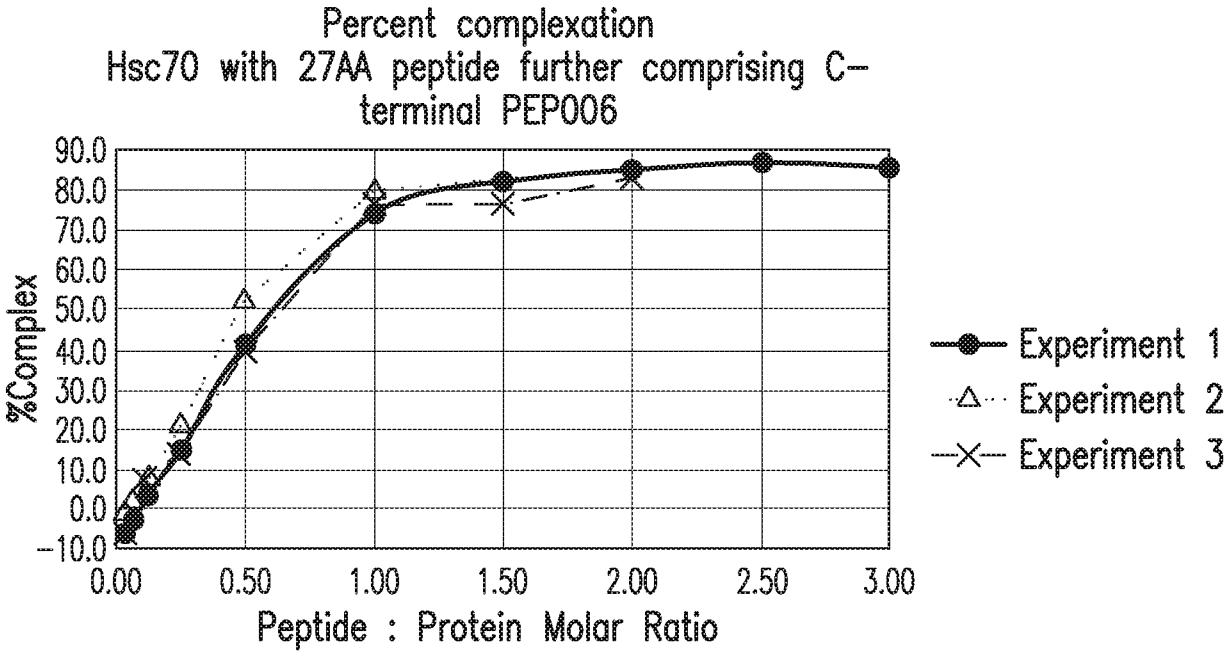
Percent complexation
Hsc70 with 27AA peptide further comprising C-terminal PEP006
%Complex
90.0
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
-10.0
0.00
0.50
1.00
1.50
2.00
2.50
3.00
Peptide : Protein Molar Ratio
Experiment 1
Experiment 2
Experiment 3

FIG.3B

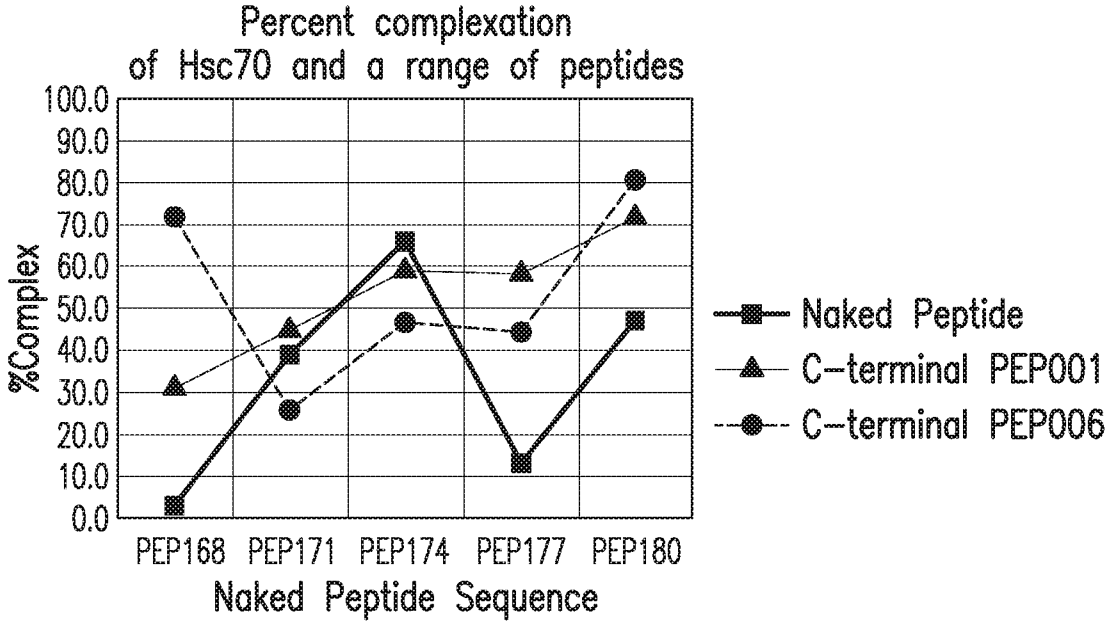
Percent complexation
of Hsc70 and a range of peptides
%Complex
100.0
90.0
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
PEP168
PEP171
PEP174
PEP177
PEP180
Naked Peptide Sequence
Naked Peptide
C-terminal PEP001
C-terminal PEP006

FIG.4A

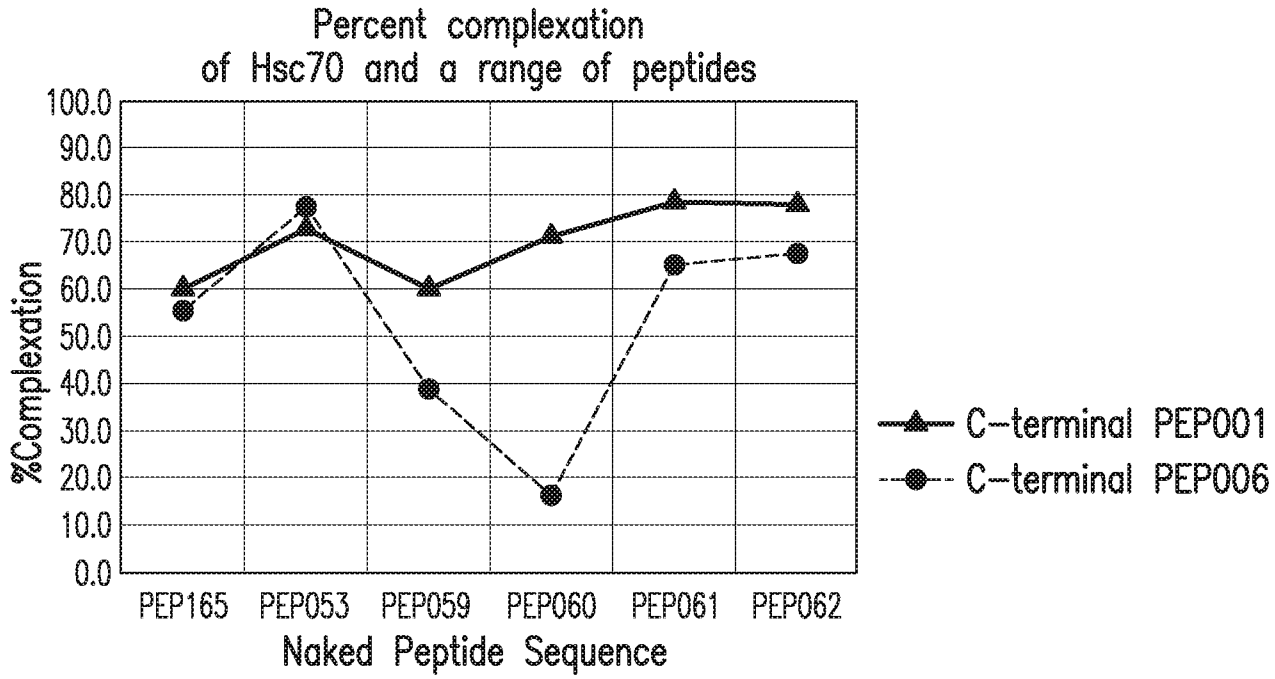
Percent complexation
of Hsc70 and a range of peptides
%Complexation
100.0
90.0
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
PEP165
PEP053
PEP059
PEP060
PEP061
PEP062
Naked Peptide Sequence
C-terminal PEP001
C-terminal PEP006

FIG.4B

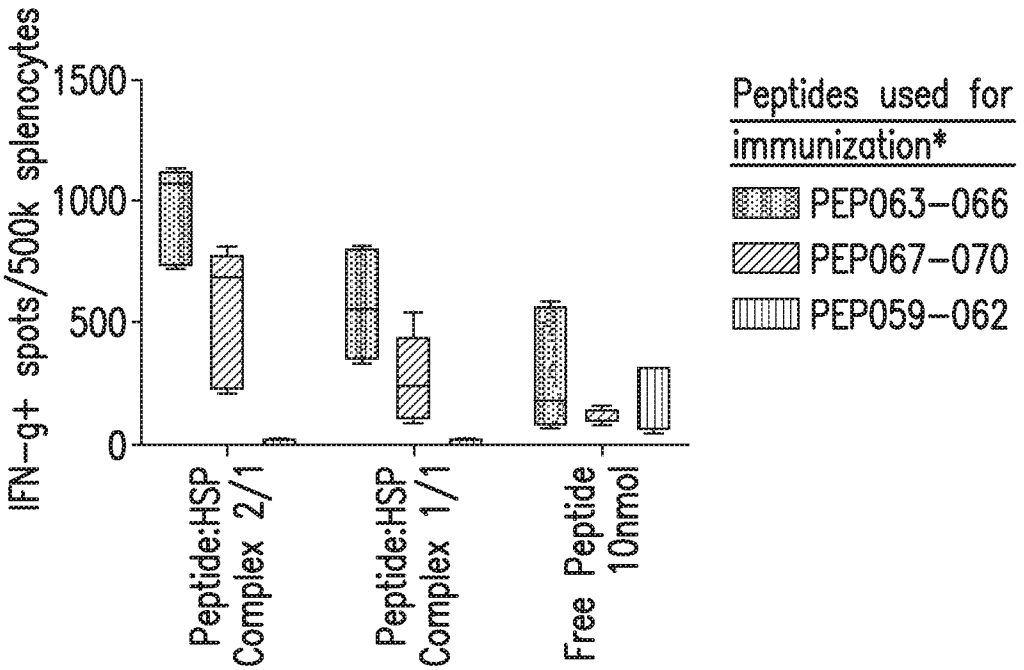
IFN-g+ spots/500k splenocytes
1500
1000
500
0
Peptide:HSP Complex 2/1
Peptide:HSP Complex 1/1
Free Peptide 10nmol
Peptides used for immunization*
PEP063-066
PEP067-070
PEP059-062

FIG.5A

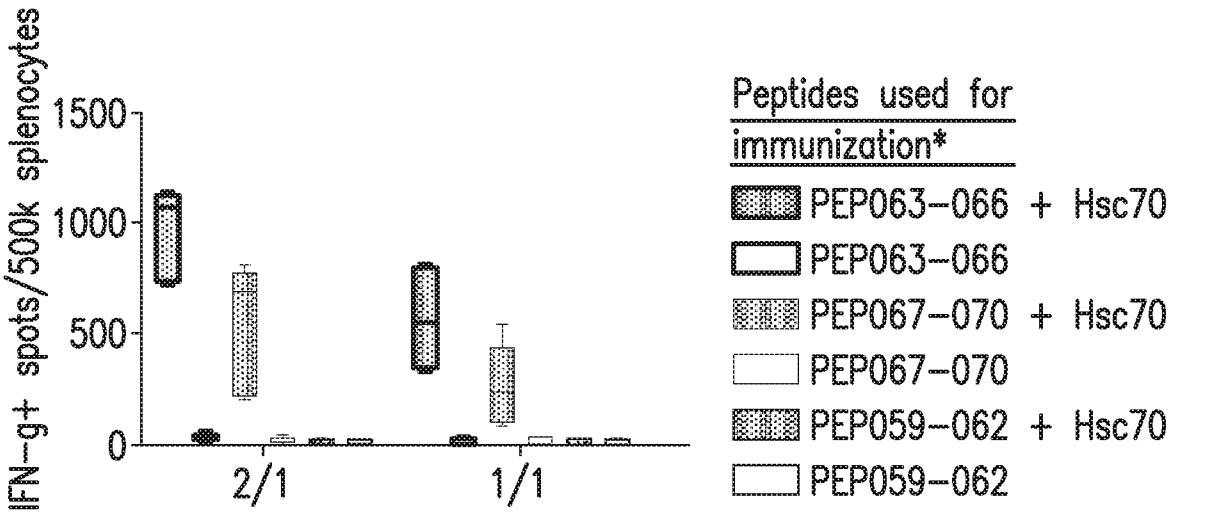
IFN-g+ spots/500k splenocytes
1500
1000
500
0
2/1
1/1
Peptides used for immunization*
PEP063-066 + Hsc70
PEP063-066
PEP067-070 + Hsc70
PEP067-070
PEP059-062 + Hsc70
PEP059-062
*Restimulation for all conditions was performed with naked peptides PEP059-062

FIG.5B

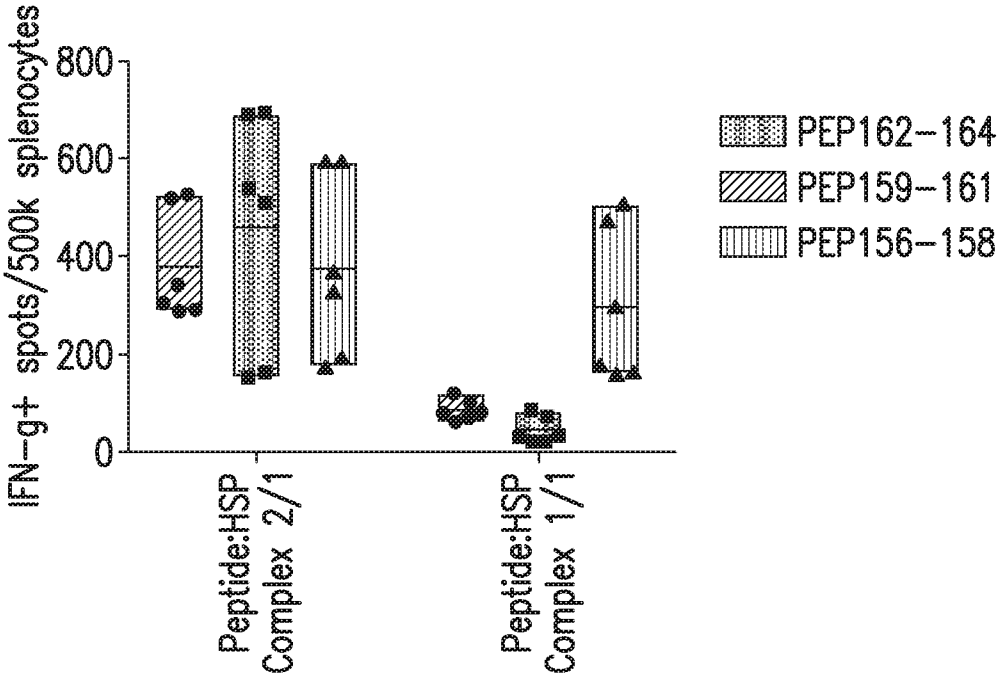
IFN-g+ spots/500k splenocytes
800
600
400
200
0
Peptide:HSP Complex 2/1
Peptide:HSP Complex 1/1
PEP162-164
PEP159-161
PEP156-158

FIG.6

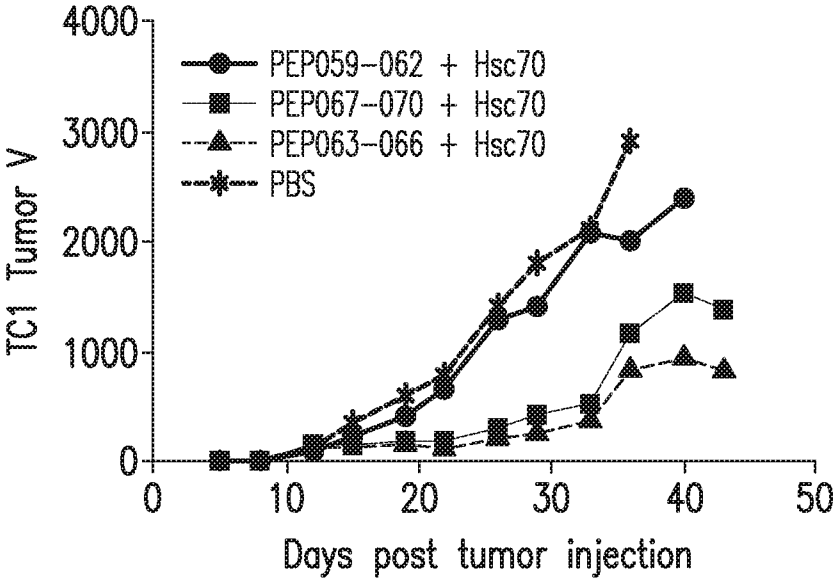

FIG.7A

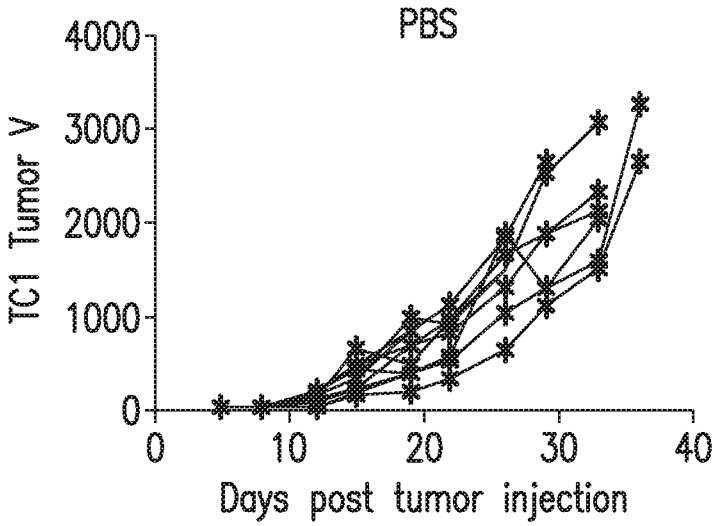

FIG.7B

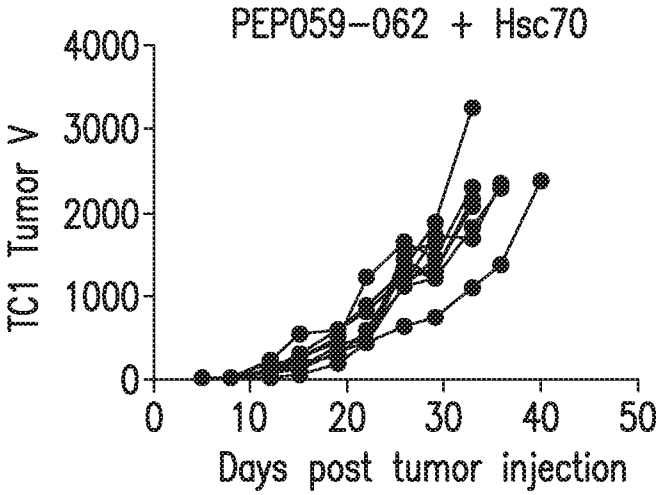

FIG.7C

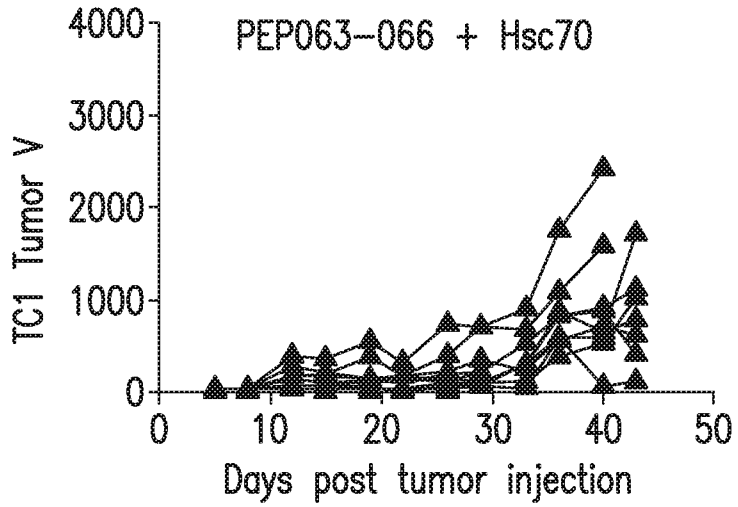

FIG.7D

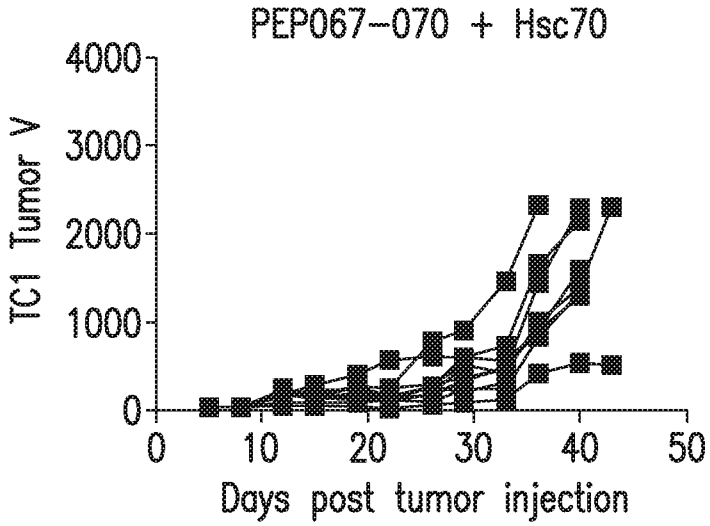

FIG.7E

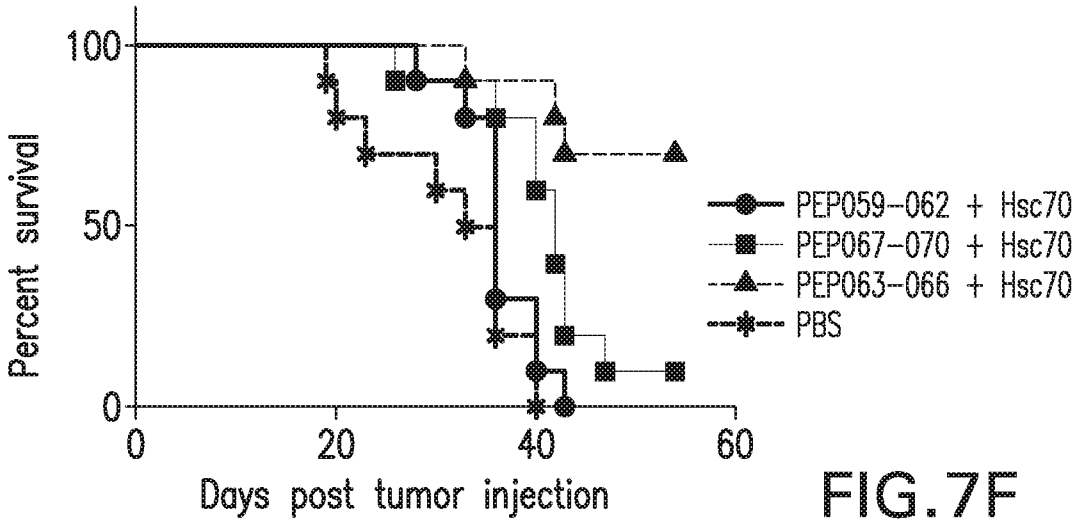

FIG.7F

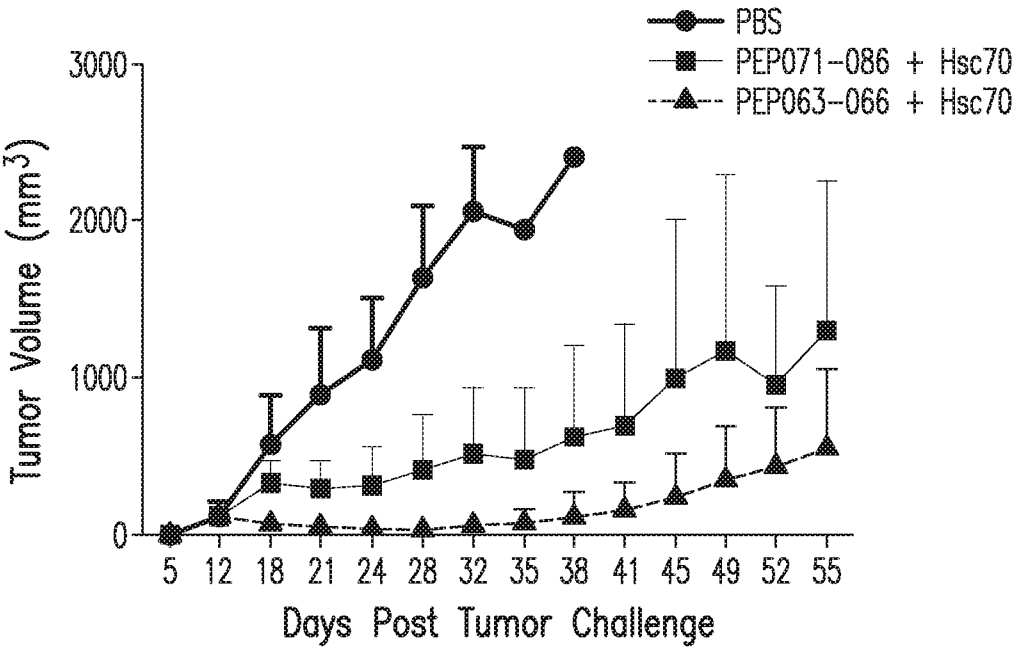
PBS
PEP071-086 + Hsc70
PEP063-066 + Hsc70
Tumor Volume (mm3)
3000
2000
1000
0
5 12 18 21 24 28 32 35 38 41 45 49 52 55
Days Post Tumor Challenge

FIG.8A

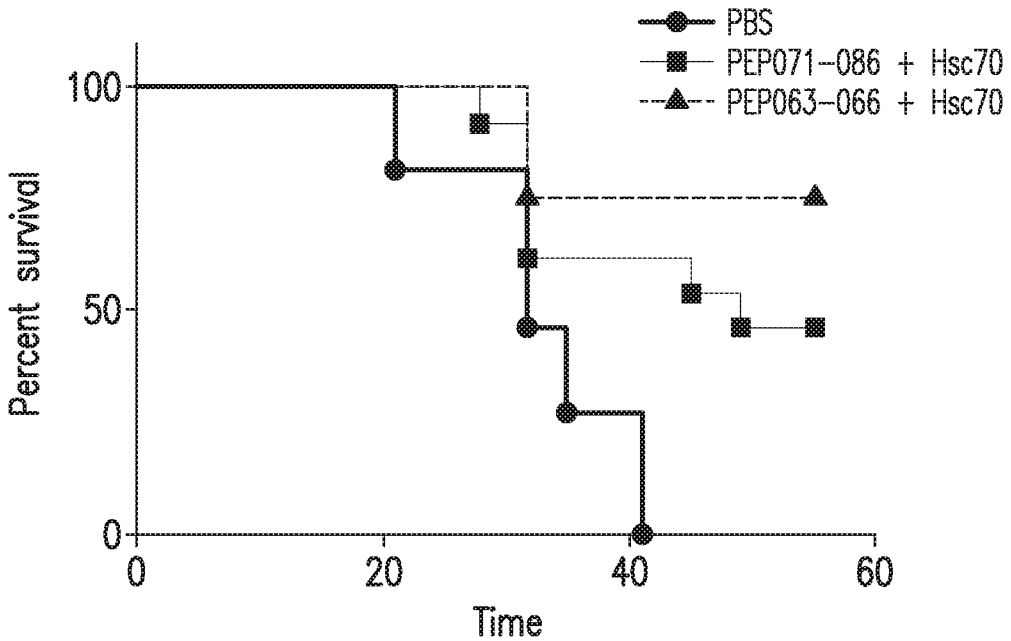
PBS
PEP071-086 + Hsc70
PEP063-066 + Hsc70
Percent survival
100
50
0
0 20 40 60
Time

FIG.8B

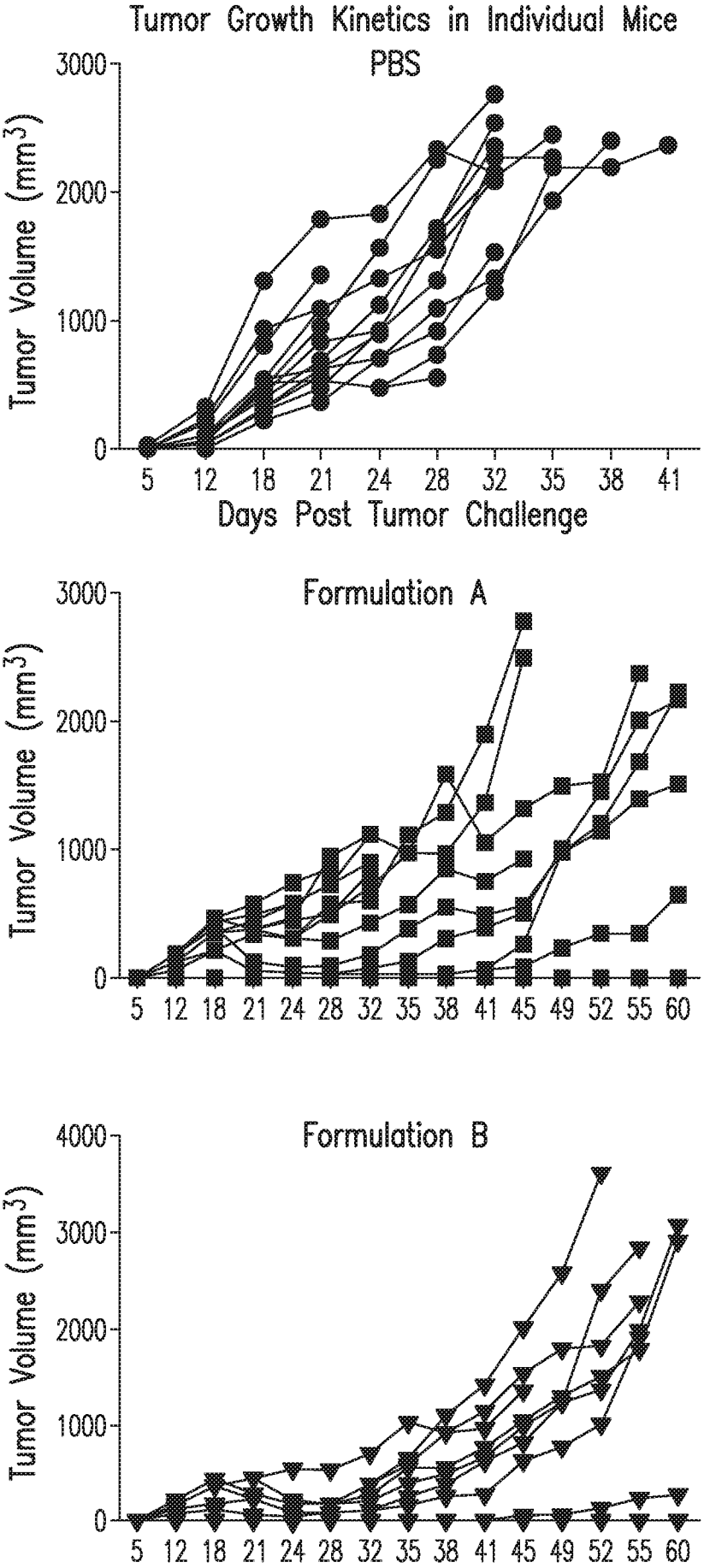
Tumor Growth Kinetics in Individual Mice
PBS
Tumor Volume (mm3)
3000
2000
1000
0
5 12 18 21 24 28 32 35 38 41
Days Post Tumor Challenge
Formulation A
Tumor Volume (mm3)
3000
2000
1000
0
5 12 18 21 24 28 32 35 38 41 45 49 52 55 60
Formulation B
Tumor Volume (mm3)
4000
3000
2000
1000
0
5 12 18 21 24 28 32 35 38 41 45 49 52 55 60

FIG.9A

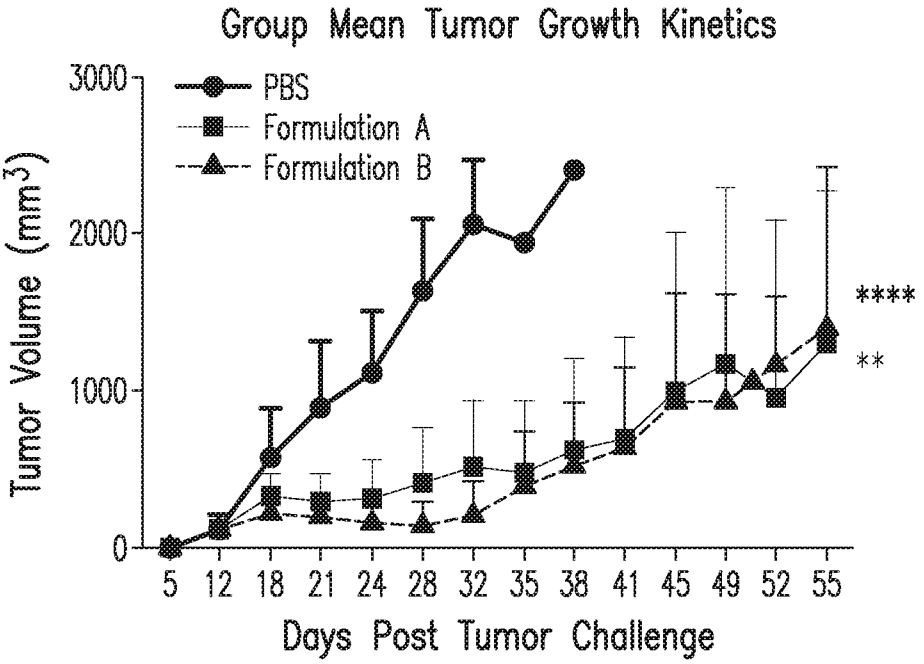
Group Mean Tumor Growth Kinetics
PBS
Formulation A
Formulation B
Tumor Volume (mm3)
3000
2000
1000
0
5 12 18 21 24 28 32 35 38 41 45 49 52 55
Days Post Tumor Challenge
****
**

FIG.9B

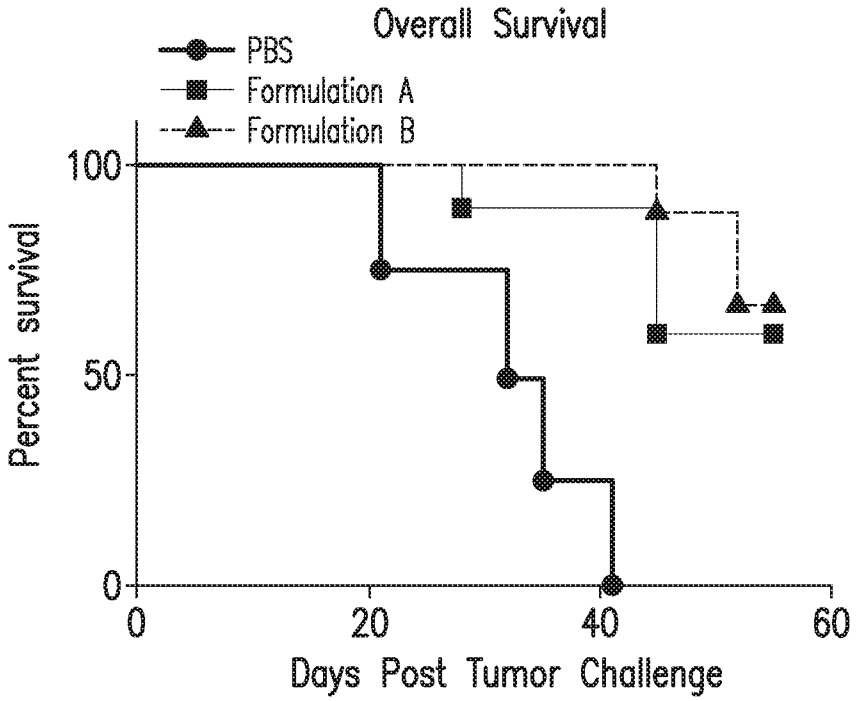
Overall Survival
PBS
Formulation A
Formulation B
Percent survival
100
50
0
0 20 40 60
Days Post Tumor Challenge

FIG.9C

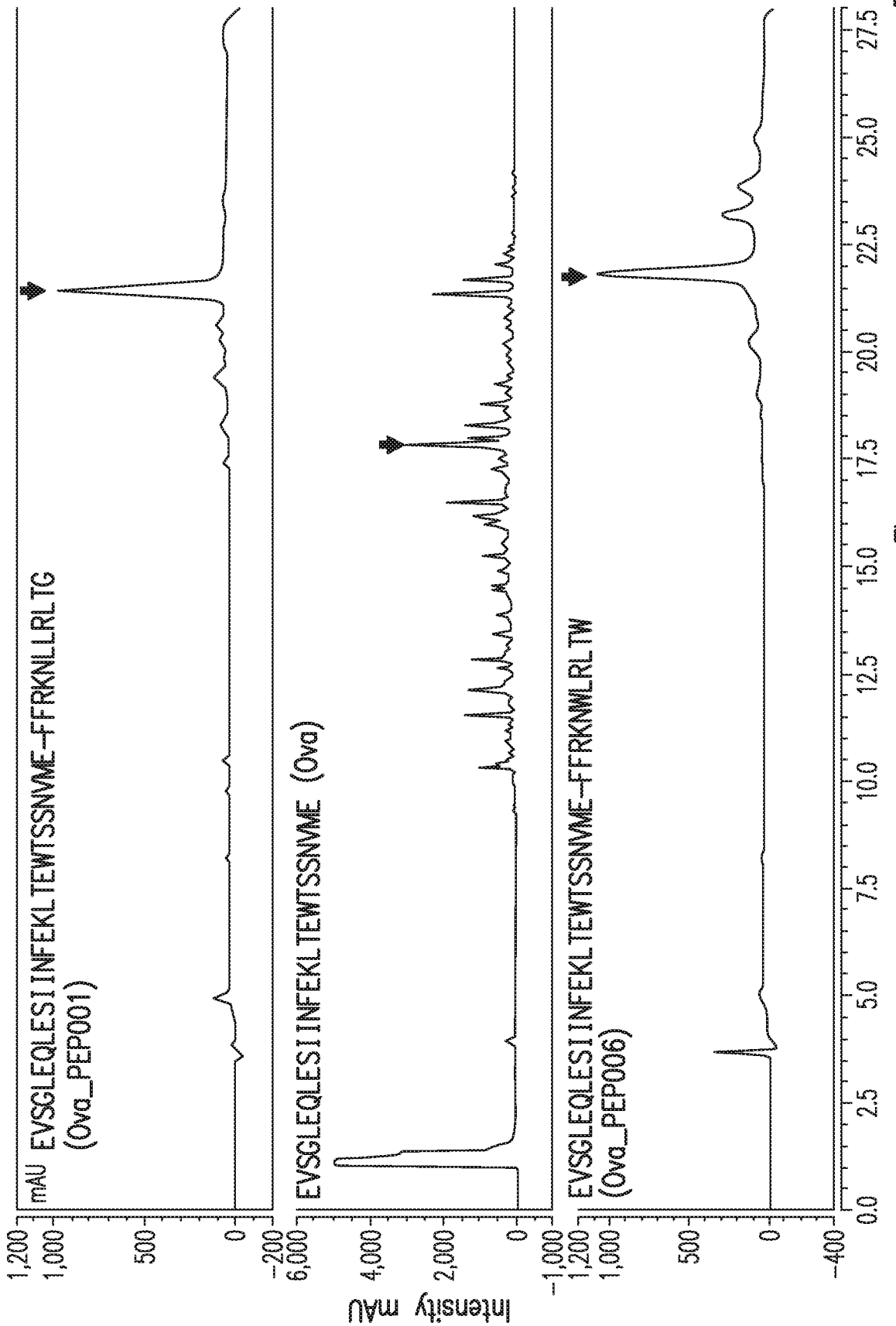
mAU
EVSGLEQLESIINFEKLTEWTSSNVME-FFRKNLLRLTG
(Ova_PEP001)
1,200
1,000
500
0
-200
EVSGLEQLESIINFEKLTEWTSSNVME (Ova)
6,000
4,000
2,000
0
-1,000
EVSGLEQLESIINFEKLTEWTSSNVME-FFRKNMLRLTW
(Ova_PEP006)
1,200
1,000
500
0
-400
Intensity mAU
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
25.0
27.5
Time

FIG. 10A

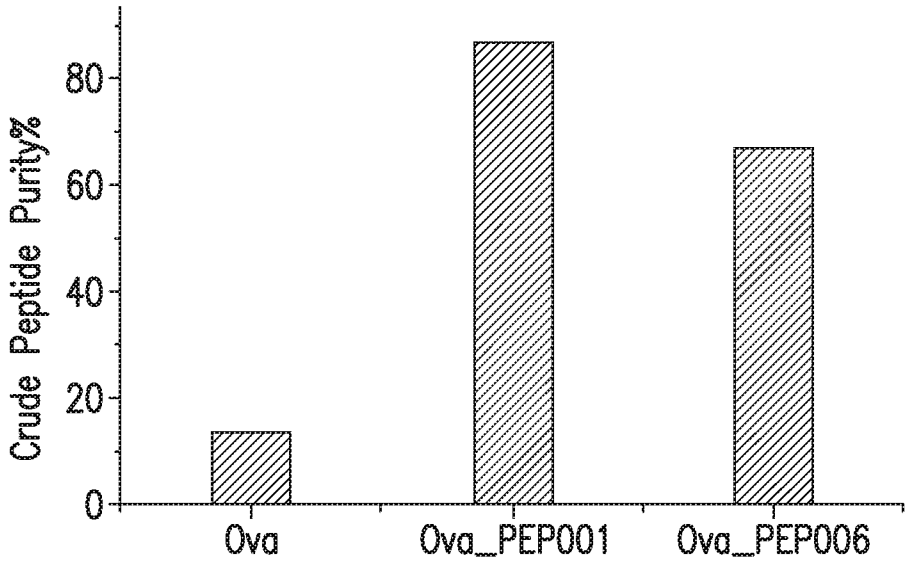

FIG.10B

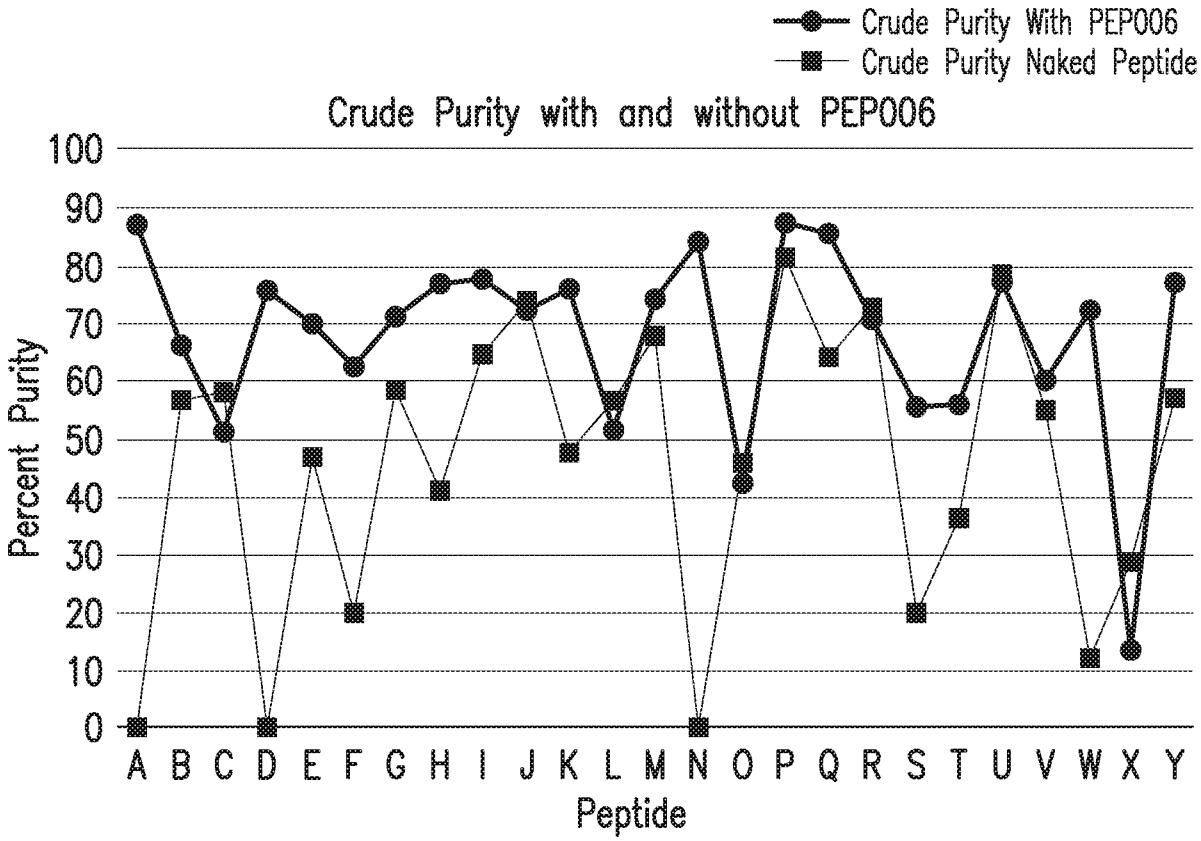

FIG.11

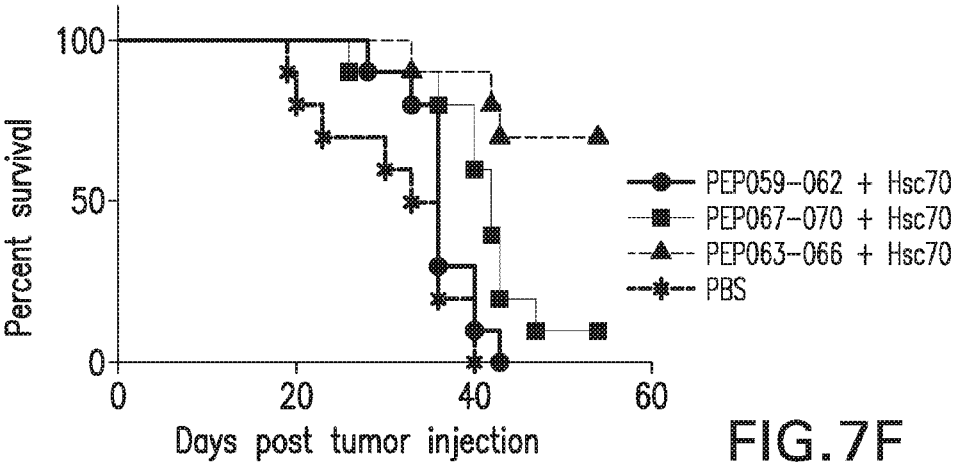
100
50
0
Percent survival
0
20
40
60
Days post tumor injection
PEP059-062 + Hsc70
PEP067-070 + Hsc70
PEP063-066 + Hsc70
PBS

FIG.7F