In some instances, the interacting face of a peptide variant can be the same (e.g., substantially the same) as an unmodified peptide, e.g., to alter (e.g., increase or decrease), preserve, or maintain the binding properties of the peptide variant relative to the unmodified peptide. Methods for identifying the interacting face of a peptide are known in the art (Gong et al., BMC: Bioinformatics, 6:1471-2105 (2007); Andrade and Wei et al., Pure and Appl. Chem., 64(11):1777-1781 (1992); Choi et al., Proteins: Structure, Function, and Bioinformatics, 77(1):14-25 (2009); Park et al., BMC: and Bioinformatics, 10:1471-2105 (2009).

Those of skill in the art readily understand how to determine the identity of two polypeptides (e.g., an unmodified peptide and a peptide variant). For example, identity can be calculated after aligning the two sequences so that the identity is at its highest level. Another way of calculating identity can be performed by published algorithms. Optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman, Adv. Appl. Math, 2:482 (1981), by the identity alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by inspection.

The same types of identity can be obtained for nucleic acids by, for example, the algorithms disclosed in Zuker, Science 244:48-52 (1989); Jaeger et al., Proc. Natl. Acad. Sci. USA 86:7706-10 (1989); Jaeger et al., Methods Enzymol. 183:281-306 (1989), ~~which are herein incorporated by reference for at least material related to nucleic acid alignment~~. It is understood that any of the methods typically can be used and that in certain instances the results of these various methods may differ, but the skilled artisan understands if identity is found with at least one of these methods, the sequences would be said to have the stated identity and to be disclosed herein.

In some instances, as described in more detail under the methods section below, therapeutic compositions disclosed herein can be produced using genetic material (e.g., DNA and/or mRNA) isolated and/or purified from immune cells (e.g., B cells, including

a human subject, e.g., following an event. Exemplary events can include, but are not limited to, detection of diseases, infection; administration of a therapeutic composition disclosed herein, administration of a therapeutic agent or treatment regimen, administration of a vaccine, induction of an immune response. Such methods can be used clinically and/or for research.

EXAMPLES

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

Methods are described herein that allow sensitive, specific, and reliable detection of rare memory B cells, with defined antigen specificity, from limited quantities of peripheral blood. Methods allowed visualization and isolation of memory B cells months to years after antigen had been cleared.

Proof of principle for the methods disclosed herein was established using tetramers of tetanus toxin C-fragment (TTCF), as reported in detail in Franz et al. (Blood, 118(2):348-357 (2011)), ~~which reference is hereby incorporated by reference in its entirety~~.

TTCF (i.e., the 52 kDa, non-toxic, C-terminal fragment of TTCF) was selected as a model antigen because the majority of individuals have been vaccinated with tetanus toxoid and persistent IgG antibody titers are induced by the vaccine (Amanna et al., N. Engl. J. Med., 357:1903-1915, 2007). Accordingly, use of TTCF afforded a large pool of subjects in which the methods disclosed herein could be verified. One of skill in the art will appreciate, however, that the present methods can be adapted to include any disease-related antigen using routine skill. As demonstrated in the examples below, such adaption has been shown through the acquisition of antibodies directed against MICA and angiopoietin-2, which are cancer-related antigens.

Example 1: Antigen Expression and Tetramer Formation

As described in further detail below, TTCF was expressed in *Eschericia coli* and a BirA site was attached to the N-terminus for site-specific mono-biotinylation by BirA

WHAT IS CLAIMED IS:

1. A composition comprising a peptide that immunospecifically binds to MHC class I polypeptide-related sequence A (MICA), wherein the peptide comprises complementarity determining region (CDR) 3 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions, and CDR3 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions.

2. The composition of claim 1, wherein the peptide comprises complementarity determining region (CDR) 3 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1, and CDR3 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1.

3. The compositions of any one of claims 1-2, wherein the peptide comprises CDR2 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or CDR2 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or both.

4. The composition of claim 3, wherein the peptide comprises complementarity determining region CDR2 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1, or CDR2 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1, or both.

5. The compositions of any one of claims 1-4, wherein the peptide comprises CDR1 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or CDR1 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or both.

6. The composition of claim 5, wherein the peptide comprises complementarity determining region CDR1 of the V_H of antibody ID 1, 6, 7, 8 or 9 shown in Table 1, or CDR1 of the V_L of antibody ID 1, 6, 7, 8 or 9 shown in Table 1, or both.

7. The composition of any one of claims 1-6, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:2, 149, 168, 186, or 204, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID-1, 6, 7, 8 or 9 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:2, 149, 168, 186, or 204 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID-1, 6, 7, 8 or 9 shown in table 1; and

a V_L chain with identity to SEQ ID NO:11, 151, 170, 189, or 206 wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody 1 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:11 151, 170, 189, or 206 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody 1 shown in table 1.

8. The composition of claim 7, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:2, 149, 168, 186, or 204 and a V_L chain comprising SEQ ID NO:11, 151, 170, 189, or 206.

9. The composition of any one of claims 1-8 further comprising an anti-cancer therapeutic.

10. The composition of any one of claims 1-9, formulated as a pharmaceutical composition.

11. A composition comprising a peptide that immunospecifically binds to angiopoietin, wherein the peptide comprises complementarity determining region (CDR)

3 of the V_H of antibody ID 2, 3, 4, 5 or 10 shown in Table 1 having 5 or fewer conservative amino acid substitutions, and CDR3 of the V_L of antibody ID 2, 3, 4 or 5 shown in Table 1 having 5 or fewer conservative amino acid substitutions.

12. The composition of claim 11, wherein the peptide comprises complementarity determining region (CDR) 3 of the V_H of antibody ID 2, 3, 4, 5 or 10 shown in Table 1, and CDR3 of the V_L of antibody ID 2, 3, 4, 5 or 10 shown in Table 1.

13. The compositions of any one of claims 11-12, wherein the peptide comprises CDR2 of the V_H of antibody ID 2, 3, 4, or 10 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or CDR2 of the V_L of antibody ID 2, 3, 4, 5 or 10 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or both.

14. The composition of claim 13, wherein the peptide comprises complementarity determining region CDR2 of the V_H of antibody ID 2, 3, 4, 5 or 10 shown in Table 1, or CDR2 of the V_L of antibody ID 2, 3, 4, 5 or 10 shown in Table 1, or both.

15. The compositions of any one of claims 11-14, wherein the peptide comprises CDR1 of the V_H of antibody ID 2, 3, 4, 5 or 10 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or CDR1 of the V_L of antibody ID 2, 3, 4, 5 or 10 shown in Table 1 having 5 or fewer conservative amino acid substitutions, or both.

16. The composition of claim 15, wherein the peptide comprises complementarity determining region CDR1 of the V_H of antibody ID 2, 3, 4, 5 or 10 shown in Table 1, or CDR1 of the V_L of antibody ID 2, 3, 4, 5 or 10 shown in Table 1, or both.

17. The composition of any one of claims 11-16, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:20, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID 2

shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:20 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID 2 shown in table 1; and

a V_L chain with identity to SEQ ID NO:29, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody ID 2 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:29 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody ID 2 shown in table 1.

18. The composition of claim 17, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:20 and a V_L chain comprising SEQ ID NO:29.

19. The composition of any one of claims 11-16, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:38, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID 3 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:38 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID 3 shown in table 1; and

a V_L chain with identity to SEQ ID NO:47, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody ID 3 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:47 corresponding to

FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody ID 3 shown in table 1.

20. The composition of claim 19, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:38 and a V_L chain comprising SEQ ID NO:47.

21. The composition of any one of claims 11-16, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:56, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID 4 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:56 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID 4 shown in table 1; and

a V_L chain with identity to SEQ ID NO:65, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody ID 4 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:65 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody ID 4 shown in table 1.

22. The composition of claim 21, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:56 and a V_L chain comprising SEQ ID NO:65.

23. The composition of any one of claims 11-16, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:74, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID-5 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:74 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID-5 shown in table 1; and

a V_L chain with identity to SEQ ID NO:83, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody ID-5 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:83 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody ID-5 shown in table 1.

24. The composition of claim 23, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:74 and a V_L chain comprising SEQ ID NO:83.

25. The composition of any one of claims 11-24, wherein the peptide immunospecifically binds to angiopoietin-2.

26. The composition of any one of claims 11-25 further comprising an anti-cancer therapeutic.

27. The composition of any one of claims 11-26, formulated as a pharmaceutical composition.

28. Use of a composition of any one of claims 1-27 in the manufacture of a medicament for treating cancer in a subject.

29. The composition of any one of claims 11-16, wherein the peptide is an antibody or antibody fragment comprising:

a V_H chain with identity to SEQ ID NO:222, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_H of antibody ID-10 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:74 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_H of antibody ID-10 shown in table 1; and

a V_L chain with identity to SEQ ID NO:224, wherein regions corresponding to CDR1, CDR2, and CDR3 comprise CDR1, CDR2, and CDR3 of the V_L of antibody ID-10 shown in table 1 having 5 or fewer conservative amino acid substitutions within the CDR1, CDR2, and CDR3 regions, and regions within SEQ ID NO:224 corresponding to FR1, FR2, FR3, FR4, comprise amino acid sequences with at least 80%, 85%, 90%, 95%, 96%, 97%, 98, 99%, or 100% identity to FR1, FR2, FR3, FR4 of the V_L of antibody ID-10 shown in table 1.

30. The composition of claim 23, wherein the peptide is an antibody or antibody fragment comprising a V_H chain comprising SEQ ID NO:222 and a V_L chain comprising SEQ ID NO:224.

31. The composition of any one of claims 1-8 and 11-16 further comprising an histone deacetylase inhibitor (HDAC) selected from the group consisting of hydroxamic acid, vorinostat, suberoylanilide hydroxamic acid (SAHA, trichostatin A (TSA), LAQ824, panobinostat (LBH589), belinostat (PXD101), ITF2357 italfarmaco SpA, cyclic tetrapeptide, depsipeptide (romidepsin, FK228), benzamide; entinostat (SNDX-

275/MS-275), MGCD0103, short-chain aliphatic acids, valproic acid, phenyl butyrate, AN-9, pivanex, CHR-3996, and CHR-2845.

32. The composition of any one of claims 1-8 and 11-16 further comprising a proteasome inhibitor selected from the group consisting of bortezomib, NPI-0052, carfilzomib (PR-171), CEP 18770, and MLN9708.

33. A method of obtaining immune cells directed against a self antigen from a subject, the method comprising

identifying a subject exhibiting a positive immune response towards the self antigen;

providing a multimeric form of the self antigen ;

contacting the multimeric form of the self antigen with a sample from the subject exhibiting a positive immune response towards the self antigen; and

obtaining immune cells bound to the multimeric form of the self antigen.

34. A method of obtaining immune cells from a cancer patient directed against a self antigen, the method comprising

identifying a subject exhibiting a positive immune response towards the self antigen;

providing a multimeric form of the self antigen ;

contacting the multimeric form of the self antigen with a sample from the subject exhibiting a positive immune response towards the self antigen; and

obtaining immune cells bound to the multimeric form of the self antigen.

35. The method of any one of claims 33- 34, wherein the multimeric form of the self antigen is a tetrameric form of the self antigen.

36. The method of claim 35, wherein the multimeric form of the self antigen comprises a detectable moiety.

37. The method of claim 33, wherein the subject is a mammal.

38. The method of claim 37, wherein the subject is a human.

39. The method of claim 33, wherein the sample if from a human subject.

40. The method of claim 33, wherein the self antigen relates to condition or disease.

41. The method of claim 33, wherein the self antigen relates to cancer.

42. The method of claim 40, wherein the condition or disease is a cancer selected from the group consisting of melanoma, lung, breast, kidney, ovarian, prostate, pancreatic, gastric, and colon carcinoma, lymphoma or leukemia.

43. The method of any one of claims 33-34, wherein the self antigen is MHC class I chain-related protein A (MICA).

44. The method of any one of claims 33-34, wherein the self antigen is an angiopoietin.

45. The method of any one of claims 33-34, wherein the immune cell is a memory B-cell.

46. The method of any one of claims 33-34, wherein the self antigen is a cancer specific self antigen.

47. The method of claim 33, wherein the subject is a cancer patient.

WHAT IS CLAIMED IS:

1. A composition comprising an antibody or antibody fragment that immunospecifically binds to MHC class I polypeptide-related sequence A (MICA), wherein the antibody or antibody fragment comprises a heavy chain variable region (V_H) and a light chain variable region (V_L), and wherein

(a) the V_H complementarity determining region (CDR) 1 comprises the amino acid sequence set forth in SEQ ID NO: 153, the V_H CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 156, the V_H CDR3 comprises the amino acid sequence set forth in SEQ ID NO:158, he V_L CDR1 comprises the amino acid sequence set forth in SEQ ID NO: 160, the V_L CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 162 and the V_L CDR3 comprises the amino acid sequence set forth in SEQ ID NO:164;

(b) the V_H complementarity determining region (CDR) 1 comprises the amino acid sequence set forth in SEQ ID NO: 190, the V_H CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 192, the V_H CDR3 comprises the amino acid sequence set forth in SEQ ID NO: 194, the V_L CDR1 comprises the amino acid sequence set forth in SEQ ID NO: 197, the V_L CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 199 and the V_L CDR3 comprises the amino acid sequence set forth in SEQ ID NO:201.

(c) the V_H complementarity determining region (CDR) 1 comprises the amino acid sequence set forth in SEQ ID NO: 208, the V_H CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 210, the V_H CDR3 comprises the amino acid sequence set forth in SEQ ID NO:212, the V_L CDR1 comprises the amino acid sequence set forth in SEQ ID NO: 215, the V_L CDR2 comprises the amino acid sequence set forth in SEQ ID NO: 217 and the V_L CDR3 comprises the amino acid sequence set forth in SEQ ID NO:219.

2. The composition of claim 1, wherein the antibody or antibody fragment comprises:

(a) a V_H comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 149, and a V_L comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 151;

(b) a V_H comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 186, and a V_L comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 188; or

(c) a V_H comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 204, and a V_L comprising an amino acid sequence with at least 95% identity to the amino acid sequence set forth in SEQ ID NO: 206.

3. The composition of claim 1, wherein:

(i) the amino acid sequence of the V_H is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 149, and the amino acid sequence of the V_L is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 151;

(ii) the amino acid sequence of the V_H is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 186, and the amino acid sequence of the V_L is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 188; or

(iii) the amino acid sequence of the V_H is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 204, and the amino acid sequence of the V_L is at least 98% identical to the amino acid sequence set forth in SEQ ID NO: 206.

4. The composition of claim 1, wherein:

(i) the amino acid sequence of the V_H is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 149, and the amino acid sequence of the V_L is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 151;

(ii) the amino acid sequence of the V_H is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 186, and the amino acid sequence of the V_L is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 188; or

(iii) the amino acid sequence of the V_H is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 204, and the amino acid sequence of the V_L is at least 99% identical to the amino acid sequence set forth in SEQ ID NO: 206.

5. A composition comprising an antibody or antibody fragment that immunospecifically binds to MHC class I polypeptide-related sequence A (MICA), wherein the antibody or antibody fragment comprises:

(i) a V_H comprising the amino acid sequence set forth in SEQ ID NO: 149, and a V_L comprising the amino acid sequence set forth in SEQ ID NO: 151;

(ii) a V_H comprising the amino acid sequence set forth in SEQ ID NO: 186, and a V_L comprising the amino acid sequence set forth in SEQ ID NO: 188; or

(iii) a V_H comprising the amino acid sequence set forth in SEQ ID NO: 204, and a V_L comprising the amino acid sequence set forth in SEQ ID NO: 206.

6. The composition of any one of claims 1-5, further comprising an anti-cancer therapeutic.

7. The composition of any one of claims 1-6, formulated as a pharmaceutical composition.

8. The composition of any one of claims 1-7, further comprising an histone deacetylase inhibitor (HDAC) selected from the group consisting of suberoylanilide hydroxamic acid (SAHA), trichostatin A (TSA), LAQ824, panobinostat (LBH589), belinostat (PXD101), ITF2357, romidepsin (FK228), entinostat (SNDX-275/MS-275), MGCD0103, valproic acid, phenyl butyrate, AN-9, CHR-3996, and CHR-2845.

9. The composition of any of claims 1-8, further comprising a proteasome inhibitor selected from the group consisting of bortezomib, NPI-0052, carfilzomib (PR-171), CEP 18770, and MLN9708.

10. Use of a composition of any one of claims 1-9 in the manufacture of a medicament for treating cancer in a subject.