WHAT IS CLAIMED IS:

1. A polypeptide comprising an antigen binding variable region comprising a CDR3 comprising:

(A) the amino acid sequence of SEQ ID NO:7 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:7; or

(B) the amino acid sequence of SEQ ID NO:14 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:14; or

(C) the amino acid sequence of SEQ ID NO:21 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:21; or

(D) the amino acid sequence of SEQ ID NO:28 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:28; or

(E) the amino acid sequence of SEQ ID NO:35 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:35; or

(F) the amino acid sequence of SEQ ID NO:42 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:42

(a) the variable region comprises a CDR1, CDR2, and/or CDR3; optionally wherein the variable region:

i) of (A) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:5 and 6, respectively, or with an amino acid sequence that is at least 80% sequence identity to SEQ ID NO:5 and SEQ ID NO:6, respectively; or

ii) of (B) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:12 and SEQ ID NO:13, respectively, or with at least 80% sequence identity to SEQ ID NO:12 and SEQ ID NO:13, respectively; or

iii) of (C) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:19 and 20, respectively, or with an amino acid sequence that is at least 80% sequence identity to SEQ ID NO:19 and SEQ ID NO:20, respectively; or

iv) of (D) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:26 and 27, respectively, or with an amino acid sequence that is at least 80% sequence identity to SEQ ID NO:26 and SEQ ID NO:27, respectively; or

v) of (E) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:33 and 34, respectively, or with an amino acid sequence that is at least 80% sequence identity to SEQ ID NO:33 and SEQ ID NO:34, respectively; or

vi) of (F) comprising a CDR1 and/or CDR2 with the amino acid sequence of SEQ ID NO:40 and 41, respectively, or with an amino acid sequence that is at least 80% sequence identity to SEQ ID NO:40 and SEQ ID NO:41, respectively; and/or

(b) the variable region:

i) of (A) comprises an amino acid sequence or SEQ ID NO:3 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:3; or

ii) of (B) comprises an amino acid sequence of SEQ ID NO:10 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:10; or

iii) of (C) comprises an amino acid sequence or SEQ ID NO:17 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:17; or

iv) of (D) comprises an amino acid sequence or SEQ ID NO:24 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:24; or

v) of (E) comprises an amino acid sequence or SEQ ID NO:31 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:31; or

vi) of (F) comprises an amino acid sequence or SEQ ID NO:38 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:38.

(c) The polypeptide:

(i) of (A), (C), or (E) comprises a T cell receptor alpha (TCR-a) variable region and/or a TCR-a variable and constant region; or

(ii) of (B), (D), or (F) comprises a T cell receptor beta (TCR-b) variable region and/or comprises a TCR-b variable and constant region;

(d) the polypeptide is recombinant.

2. The polypeptide of claim 1, wherein the polypeptide further comprises a signal peptide and optionally wherein the signal peptide comprises:

i) the amino acid sequence of SEQ ID NO:4 or an amino acid sequence with at least 80% identity to SEQ ID NO:4; or

ii) the amino acid sequence of SEQ ID NO:11 or an amino acid sequence with at least 80% identity to SEQ ID NO:11; or

iii) the amino acid sequence of SEQ ID NO:18 or an amino acid sequence with at least 80% identity to SEQ ID NO:18; or

iv) the amino acid sequence of SEQ ID NO:25 or an amino acid sequence with at least 80% identity to SEQ ID NO:25; or

v) the amino acid sequence of SEQ ID NO:32 or an amino acid sequence with at least 80% identity to SEQ ID NO:32; or

vi) the amino acid sequence of SEQ ID NO:39 or an amino acid sequence with at least 80% identity to SEQ ID NO:39.

3. An engineered T-cell Receptor (TCR) comprising a TCR-a polypeptide and a TCR-b polypeptide, wherein:

(A) the TCR-a polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:7 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:7; and the TCR-b polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:14 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:14;

(B) the TCR-a polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:21 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:21; and the TCR-b polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:28 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:28; or

(C) the TCR-a polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:35 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:35; and the TCR-b polypeptide comprises a CDR3 with the amino acid sequence of SEQ ID NO:42 or an amino acid sequence with at least 80% sequence identity to SEQ ID NO:42

Optionally wherein:

(a) the TCR-a polypeptide comprising a variable region comprising CDR1, CDR2, and CDR3 and a TCR-b polypeptide comprising a variable region comprising CDR1, CDR2, and CDR3;

(i) the TCR-a region:

(I) of (A) comprises a CDR1 having the amino acid sequence of SEQ ID NO:5 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:5; and/or the TCR-b polypeptide comprises a CDR1 having the amino acid sequence of SEQ ID NO:12 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:12; or

(II) of (B) comprises a CDR1 having the amino acid sequence of SEQ ID NO:19 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:19; and/or the TCR-b polypeptide comprises a CDR1 having the amino acid sequence of SEQ ID NO:26 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:26; or

(III) of (C) comprises a CDR1 having the amino acid sequence of SEQ ID NO:33 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:33; and/or the TCR-b polypeptide comprises a CDR1 having the amino acid sequence of SEQ ID NO:40 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:40

(ii)The TCR-a region:

(I) of (A) comprises a CDR2 having the amino acid sequence of SEQ ID NO:6 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:6; and/or the TCR-b polypeptide comprises a CDR2 having the amino acid sequence of SEQ ID NO:13 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:13; or

(II) of (B) comprises a CDR2 having the amino acid sequence of SEQ ID NO:20 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:20; and/or the TCR-b polypeptide comprises a CDR2 having the amino acid sequence of SEQ ID NO:27 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:27; or

(III) of (C) comprises a CDR2 having the amino acid sequence of SEQ ID NO:34 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:34; and/or the TCR-b polypeptide comprises a CDR2 having the amino acid sequence of SEQ ID NO:41 or having an amino acid sequence with at least 80% sequence identity to SEQ ID NO:41.

(b) the CDR1, CDR2, and CDR3 of the TCR-a region:

(i) of (A) comprise the amino acid sequence of SEQ ID NOS:5, 6, and 7, respectively; and wherein the CDR1, CDR3, and CDR3 of the TCR-b polypeptide comprise the amino acid sequence of SEQ ID NO:12, 13, and 14, respectively; or

(ii) of (B) comprise the amino acid sequence of SEQ ID NOS:19, 20, and 21, respectively; and wherein the CDR1, CDR3, and CDR3 of the TCR-b polypeptide comprise the amino acid sequence of SEQ ID NO:26, 27, and 28, respectively; or

(iii) of (C) comprise the amino acid sequence of SEQ ID NOS:33, 34, and 35, respectively; and wherein the CDR1, CDR3, and CDR3 of the TCR-b polypeptide comprise the amino acid sequence of SEQ ID NO:40, 41, and 42, respectively.

(c) The TCR-a region:

(i) of (A) comprises the amino acid sequence of SEQ ID NO:3 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:3; and the TCR-b polypeptide comprises the amino acid sequence of SEQ ID NO:10 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:10; or

(ii) of (B) comprises the amino acid sequence of SEQ ID NO:17 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:17; and the TCR-b polypeptide comprises the amino acid sequence of SEQ ID NO:24 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:24; or

(iii) of (C) comprises the amino acid sequence of SEQ ID NO:31 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:31; and the TCR-b polypeptide comprises the amino acid sequence of SEQ ID NO:38 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:38

(d) The TCR-a region:

(i) of (A) comprises the amino acid sequence of SEQ ID NO:2 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:2 and/or the TCR-b polypeptide comprises the amino acid sequence of SEQ ID NO:9 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:9; or

(ii) of (B) comprises the amino acid sequence of SEQ ID NO:16 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:16 and/or the TCR-b

polypeptide comprises the amino acid sequence of SEQ ID NO:23 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:23; or

(iii) of (C) comprises the amino acid sequence of SEQ ID NO:30 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:30 and/or the TCR-b polypeptide comprises the amino acid sequence of SEQ ID NO:37 or an amino acid sequence with at least 70% sequence identity to SEQ ID NO:37.

4. The TCR of claim 3, wherein the TCR-b polypeptide and TCR-a polypeptide are operably linked and optionally wherein the TCR-b polypeptide and TCR-a polypeptide are operably linked through a peptide bond.

5. The TCR of claim 3, wherein the TCR comprises a modification, is chimeric, is a single chain TCR, wherein the TCR-b polypeptide and TCR-a polypeptide are on the same polypeptide and wherein the TCR-b is amino-proximal to the TCR-a; wherein the TCR-b polypeptide and TCR-a polypeptide are on the same polypeptide and wherein the TCR-a is amino-proximal to the TCR-b; wherein the TCR comprises a linker between the TCR-a and TCR-b polypeptide; and/or wherein the linker comprises glycine and serine residues.

6. A peptide comprising at least 55% sequence identity to a peptide of one of SEQ ID NOS:43-45

(a) the peptide:

(i) comprises at least 6 contiguous amino acids of one of SEQ ID NO:43-45; or

(ii) consists of 9 or 10 amino acids, or

(iii) consist of a peptide of one of SEQ ID NOS:43-45.

(b) the peptide is immunogenic; and/or

(c) the peptide modified, optionally wherein:

(i) the modification comprises conjugation to a molecule; and/or

ii) the molecule comprises an antibody, a lipid, an adjuvant, or a detection moiety; and/or

iii) the peptide comprises 1, 2 or 3 substitutions relative to a peptide of one of SEQ ID NOS:43-45.

7. A polypeptide comprising the peptide of claim 6 and at least one MHC polypeptide, optionally wherein:

(i) the MHC polypeptide and peptide are operatively linked through a peptide bond or van der Waals forces; or

(ii) the MHC polypeptide is conjugated to a detection tag; or

(iii) the peptide is bound to a peptide specific binding molecule.

8. A method of producing peptide-specific immune effector cells comprising:

(a) contacting a starting population of immune effector cells with a peptide or polypeptide of claims 6 or 7, thereby generating peptide-specific immune effector cells,

(b) purifying immune effector cells specific to the peptide,

(c) isolating a TCR sequence from the purified immune effector cells,

optionally wherein:

(i) contacting comprises co-culturing the starting population of immune effector cells with antigen presenting cells (APCs), artificial antigen presenting cells (aAPCs), or an artificial antigen presenting surface (aAPSs); wherein the APCs, aAPCs, or the aAPSs present the peptide on their surface; and/or

(ii) purifying comprises a population of CD8-positive and peptide MHC tetramer-positive T cells from the immune effector cells following the co-culturing, wherein the population of CD8-positive and peptide MHC tetramer-positive T cells are purified by fluorescence activated cell sorting (FACS), wherein purifying further comprises generation of a clonal population of peptide-specific immune effector cells by limiting or serial dilution of sorted cells followed by expansion of individual clones by a rapid expansion protocol, and/or wherein the method further comprises cloning of a T cell receptor (TCR) from the clonal population of peptide-specific immune effector cells.

9. The method of claim 8, wherein the immune effector cells are T cells, peripheral blood lymphocytes, NK cells, invariant NK cells, NKT cells, have been differentiated from mesenchymal

stem cell (MSC) or induced pluripotent stem (iPS) cells, or are T cells selected from $CD8^+$ T cells, $CD4^+$ T cells, γδ T cells or cytotoxic T lymphocytes (CTLs)

optionally wherein:

(A) producing cancer specific immune effector cells comprises:

(i) isolating a starting population of immune effector cells from peripheral blood mononuclear cells (PBMCs); or

(ii) the starting population of immune effector cells is obtained from a subject; or

(iii) the subject is a human; or

(iv) the subject has cancer and wherein the cancer comprises and/or wherein the subject has been determined to have:

(a) a FANCI antigen positive cancer or cancer cells that are positive for a peptide of SEQ ID NO:43; or

(b) a RAD51 antigen positive cancer or cancer cells that are positive for a peptide of SEQ ID NO:44; or

(c) a PBK antigen positive cancer or cancer cells that are positive for a peptide of SEQ ID NO:45.

(B) the method further comprises introducing the peptide or a nucleic acid encoding the peptide into the dendritic cells prior to the co-culturing and optionally wherein the peptide or nucleic acids encoding the peptide are introduced by electroporation or by adding the peptide or nucleic acid encoding the peptide to the dendritic cell culture media; or

(C) a population of CD8 or CD4-positive and peptide MHC tetramer-positive T cells are purified from the immune effector cells following the co-culturing and optionally wherein a clonal population of peptide-specific immune effector cells are generated by limiting or serial dilution followed by expansion of individual clones by a rapid expansion protocol.

10. The method of claim 9, wherein the method further comprises cloning of a T cell receptor (TCR) from the clonal population of peptide-specific immune effector cells and optionally wherein cloning of the TCR is cloning of a TCR alpha and a beta chain, the TCR is cloned using a 5'-Rapid amplification of cDNA ends (RACE) method, and/or the cloned TCR is subcloned into an expression vector.

11. The method of claim 10, where the method further comprises transducing a host cell with the expression vector to generate an engineered cell that expresses the TCR and optionally wherein the host cell is an immune cell, wherein the immune cell is a T cell and optionally wherein the T cell is a $CD8^+$ T cell, CD4+ T cell, or γδ T cell and the engineered cell is an engineered T cell.

12. A peptide-specific engineered T cell or TCR produced according to the method of claim 8.

13. A fusion protein comprising the TCR of any one of claims 3-5 and a CD3 binding region and optionally wherein the CD3 binding region comprises a CD3-specific fragment antigen binding (Fab), single chain variable fragment (scFv), single domain antibody, or single chain antibody.

14. A nucleic acid or expression vector encoding the polypeptide of any one of claims 1-5 or 18, the TCR of any one of claims 3 or 5 or the peptide of any one of claims 6 or 7.

15. The nucleic acid or expression vector of claim 14, wherein the nucleic acid is RNA, DNA, a cDNA encoding the peptide or polypeptide or a complement of the peptide or polypeptide, or has at least 70% sequence identity to one of SEQ ID NOS:1, 8, 15, 22, 29, 36 or a fragment thereof.

16. A cell comprising the polypeptide of any one of claims 1 or 7, the TCR of any one of claims 3-5, or the nucleic acid(s) or expression vector of claim 15.

17. The cell of claim 16, wherein the cell comprises a stem cell, a progenitor cell, an immune cell, a natural killer (NK) cell, a hematopoietic stem or progenitor cell, a T cell, a cell differentiated from mesenchymal stem cells (MSCs), an induced pluripotent stem cell (iPSC), a cell isolated or derived from peripheral blood mononuclear cell (PBMCs) a cell isolated from a cancer patient, and/or a T cell selected from a cytotoxic T lymphocyte (CTL), a $CD8^+$ T cell, a $CD4^+$ T cell, an invariant NK T (iNKT) cell, a gamma-delta T cell, a NKT cell, or a regulatory T cell.

18. An *in vitro* isolated dendritic cell comprising the nucleic acid or expression vector of claim 14; and optionally wherein the dendritic cell is a mature dendritic cell and/or wherein the cell is a cell with an HLA-A, HLA-B, or HLA-C type.

19. A composition comprising the cell of claim 17.

20. A method of making an engineered cell comprising transferring the nucleic acid(s) of claim 15 into a cell and optionally wherein the method further comprises culturing the cell in media, incubating the cell at conditions that allow for the division of the cell, screening the cell, and/or freezing the cell.

21. Use of the composition of claim 19 in the manufacture of a medicament for treating or preventing cancer or for stimulating an immune response in a subject.

22. The use of claim 21, wherein the subject is a human subject, has previously been treated for the cancer, has been determined to be resistant to the previous treatment, and/or has been determined to be HLA-A2 or HLA-A24 positive.

23. The use of claim 21, wherein the cancer comprises and/or wherein the subject has been determined to have:

i) stage I, II, III, or IV cancer;

ii) metastatic and/or recurrent cancer;

iii) a FANCI antigen positive cancer;

iv) cancer cells that are positive for a peptide of SEQ ID NO:43;

v) a RAD51 antigen positive cancer;

vi) cancer cells that are positive for a peptide of SEQ ID NO:44;

vii) a PBK antigen positive cancer;

viii) cancer cells that are positive for a peptide of SEQ ID NO:45.

24. A method for prognosing a patient or for detecting T cell responses in a patient, the method comprising: contacting a biological sample obtained from the patient with the peptide, polypeptide, composition, or molecular complex of claims 6 or 7.

25. The method of claim 24, wherein the biological sample comprises a blood sample or a fraction thereof, lymphocytes, or a fractionated sample comprising lymphocytes.

26. A kit comprising the peptide or polypeptide of claims 6 or 7 in a container.

27. The composition of claim 19 for use in therapy.