CLAIMS:

1. A binding protein that binds a polypeptide comprising an immunogenic peptide comprising a peptide epitope that has the amino acid sequence RAREFMEL (SEQ ID NO: 7), wherein the binding protein comprises:

a) a T cell receptor (TCR) alpha chain variable domain comprising CDR1 having residues 49-54 of SEQ ID NO: 33, CDR2 having residues 72-78 of SEQ ID NO: 33, and CDR3 having residues 113-124 of SEQ ID NO: 33; and

b) a TCR beta chain variable domain comprising CDR1 having residues 46-50 of SEQ ID NO: 35, CDR2 having residues 68-73 of SEQ ID NO: 35, and CDR3 having residues 112-125 of SEQ ID NO: 35.

2. The binding protein of claim 1, comprising:

a) a TCR alpha chain variable (V_α) domain comprising a sequence with at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to residues 1-136 of SEQ ID NO: 33; and

b) a TCR beta chain variable (V_β) domain comprising a sequence with at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to residues 1-136 of SEQ ID NO: 35.

3. The binding protein of claim 2, comprising:

a) a TCR alpha chain variable (V_α) domain comprising residues 1-136 of SEQ ID NO: 33; and

b) a TCR beta chain variable (V_β) domain comprising residues 1-136 of SEQ ID NO: 35.

4. The binding protein of any one of claims 1-3, comprising:

a) a TCR alpha chain comprising a sequence with at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to the sequence of SEQ ID NO: 33; and

b) a TCR beta chain comprising a sequence with at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to the sequence of SEQ ID NO: 35.

5. The binding protein of claim 4, comprising:

a) a TCR alpha chain comprising the sequence of SEQ ID NO: 33; and

b) a TCR beta chain comprising the sequence of SEQ ID NO: 35.

6. The binding protein of any one of claims 1-5, wherein:

1) the TCR alpha chain CDR, TCR V_α domain, and/or TCR alpha chain is encoded by TRAV24*01 F, TRAJ32*02, and MGTM modified TRAC gene;

2) the TCR beta chain CDR, TCR V_β domain, and/or TCR beta chain is encoded by TRBV16*01, TRBJ1-1*01, and MGTM modified TRBC gene;

3) the binding protein is chimeric, humanized, or human;

4) the binding protein comprises a binding domain having a transmembrane domain, and an effector domain that is intracellular;

5) the TCR alpha chain and the TCR beta chain are covalently linked, optionally wherein the TCR alpha chain and the TCR beta chain are covalently linked through a linker peptide;

6) the TCR alpha chain and/or the TCR beta chain are covalently linked to a moiety, optionally wherein the covalently linked moiety:

a) comprises an affinity tag or a label, further optionally wherein the affinity tag is selected from the group consisting of aCD34 enrichment tag, glutathione-S-transferase (GST), calmodulin binding protein (CBP), protein C tag, Myc tag, HaloTag, HA tag, Flag tag, His tag, biotin tag, and V5 tag, and/or wherein the label is a fluorescent protein;

b) is selected from the group consisting of an inflammatory agent, cytokine, toxin, cytotoxic molecule, radioactive isotope, or antibody or antigen-binding fragment thereof;

7) the binding protein binds to the pMHC complex on a cell surface;

8) the MHC or MHC-peptide complex is as follows:

a) the MHC molecule:

i) is a MHC multimer, optionally wherein the MHC multimer is a tetramer;

ii) is a MHC class I molecule; and/or

iii) comprises an MHC alpha chain that is an HLA serotype selected from the group consisting of HLA-A*02, HLA-A*03, HLA-A*01, HLA-A*11, HLA-A*24, and/or HLA-B*07, optionally wherein the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0204,

HLA-A*0205, HLA-A*0206, HLA-A*0207, HLA-A*0210, HLA-A*0211, HLA-A*0212, HLA-A*0213, HLA-A*0214, HLA-A*0216, HLA-A*0217, HLA-A*0219, HLA-A*0220, HLA-A*0222, HLA-A*0224, HLA-A*0230, HLA-A*0242, HLA-A*0253, HLA-A*0260, HLA-A*0274 allele, HLA-A*0301, HLA-A*0302, HLA-A*0305, HLA-A*0307, HLA-A*0101, HLA-A*0102, HLA-A*0103, HLA-A*0116 allele, HLA-A*1101, HLA-A*1102, HLA-A*1103, HLA-A*1104, HLA-A*1105, HLA-A*1119 allele, HLA-A*2402, HLA-A*2403, HLA-A*2405, HLA-A*2407, HLA-A*2408, HLA-A*2410, HLA-A*2414, HLA-A*2417, HLA-A*2420, HLA-A*2422, HLA-A*2425, HLA-A*2426, HLA-A*2458 allele, HLA-B*0702, HLA-B*0704, HLA-B*0705, HLA-B*0709, HLA-B*0710, HLA-B*0715, and HLA-B*0721 allele;

b) the peptide epitope and the MHC molecule are covalently linked and/or wherein the alpha and beta chains of the MHC molecule are covalently linked;

c) the stable MHC-peptide complex comprises a detectable label, optionally wherein the detectable label is a fluorophore;

9) binding of the binding protein to the MAGEC2 peptide-MHC (pMHC) complex elicits an immune response, optionally wherein the immune response is i) a T cell response and/or a CD8+ T cell response and/or ii) selected from the group consisting of T cell expansion, cytokine release, and/or cytotoxic killing;

10) the binding protein is capable of specifically and/or selectively binding to the MAGEC2 immunogenic peptide-MHC (pMHC) complex with a K_d less than or equal to $1x10^{-4}$ M, less than or equal to $5x10^{-5}$ M, less than or equal to $1x10^{-5}$ M, less than or equal to $5x10^{-6}$ M, less than or equal to $1x10^{-6}$ M, less than or equal to $5x10^{-7}$ M, less than or equal to $1x10^{-7}$ M, less than or equal to $5x10^{-8}$ M, less than or equal to $1x10^{-8}$ M, less than or equal to $5x10^{-9}$ M, less than or equal to $1x10^{-9}$ M, less than or equal to $5x10^{-10}$ M, less than or equal to $1x10^{-10}$ M, less than or equal to $5x10^{-11}$ M, less than or equal to $1x10^{-11}$ M, less than or equal to $5x10^{-12}$ M, or less than or equal to $1x10^{-12}$ M; and/or

11) the binding protein does not bind to a peptide-MHC (pMHC) complex selected from the group consisting of ALKDVEERV/HLA-A*02, LLFGLALIEV/HLA-A*02, SESIKKKVL/HLA-B*44, and ASSTLYLVF/HLA-B*57.

7. An isolated nucleic acid molecule encodes a binding protein of any one of claims 1-6, optionally wherein the nucleic acid is codon optimized for expression in a host cell.

8. A vector comprising the isolated nucleic acid of claim 7, optionally wherein i) the vector is a cloning vector, expression vector, or viral vector; and/or ii) the vector further comprises a nucleic acid sequence encoding CD8α and/or CD8β, optionally wherein:

1) the nucleic acid sequence encoding CD8α or CD8β is operably linked to a nucleic acid encoding a tag, optionally wherein the nucleic acid encoding a tag is at the 5' upstream of the nucleic acid sequence encoding CD8α or CD8β such that the tag is fused to the N-terminus of CD8α or CD8β, optionally wherein the tag is a CD34 enrichment tag; and/or

2) the isolated nucleic acid of claim 7, and the nucleic acid sequence encoding CD8α and/or CD8β are interconnected with an internal ribosome entry site or a nucleic acid sequence encoding a self-cleaving peptide, optionally wherein the self-cleaving peptide is P2A, E2A, F2A or T2A.

9. A host cell or a population of host cells, wherein the host cell comprises the isolated nucleic acid of claim 7, comprises the vector of claim 8, and/or expresses the binding protein according to any one of claims 1-6, optionally wherein the cell is genetically engineered.

10. The host cell or a population of host cells of claim 9, wherein the host cell:

1) comprises a chromosomal gene knockout of a TCR gene, an HLA gene, or both;

2) comprises a knockout of an HLA gene selected from an αl macroglobulin gene, α2 macroglobulin gene, α3 macroglobulin gene, β1 microglobulin gene, β2 microglobulin gene, and combinations thereof;

3) a knockout of a TCR gene selected from a TCR α variable region gene, TCR β variable region gene, TCR constant region gene, and combinations thereof;

4) expresses CD8α and/or CD8β, optionally wherein the CD8α and/or CD8β is fused to a CD34 enrichment tag, further optionally wherein host cells are enriched using the CD34 enrichment tag;

5) is a hematopoietic progenitor cell, peripheral blood mononuclear cell (PBMC), cord blood cell, or immune cell,

optionally wherein the immune cell is a cytotoxic lymphocyte, cytotoxic lymphocyte precursor cell, cytotoxic lymphocyte progenitor cell, cytotoxic lymphocyte stem cell, $CD4^+$ T cell, $CD8^+$ T cell, CD4/CD8 double negative T cell, gamma delta (γδ) T cell, natural killer (NK) cell, NK-T cell, dendritic cell, or combination thereof,

further optionally wherein the T cell:

a) is a naive T cell, central memory T cell, effector memory T cell, or a combination thereof;

b) is a primary T cell or a cell of a T cell line; and/or

c) does not express or has a lower surface expression of an endogenous TCR; and/or

6) is capable of producing a cytokine or a cytotoxic molecule when contacted with a target cell that comprises a peptide-MHC (pMHC) complex comprising a MAGEC2 peptide epitope in the context of an MHC molecule, optionally wherein:

a) the host cell is contacted with the target cell *in vitro* or *ex vivo*;

b) the cytokine is TNF-α, IL-2, and/or IFN-γ;

c) the cytotoxic molecule is perforins and/or granzymes, optionally wherein the cytotoxic molecule is granzyme B;

d) the host cell is capable of producing a higher level of cytokine or a cytotoxic molecule when contacted *in vitro* or *ex vivo* with a target cell with a heterozygous expression of MAGEC2, optionally wherein the host cell is capable of producing an at least 1.05-fold higher level of cytokine or a cytotoxic molecule;

e) the host cell is capable of killing a target cell that comprises a peptide-MHC (pMHC) complex comprising the MAGEC2 peptide epitope in the context of an MHC molecule, optionally wherein:

i) the killing is determined by a killing assay;

ii) the ratio of the host cell and the target cell in the killing assay is from 20:1 to 1:4;

iii) the target cell is a target cell pulsed with 1 μg/mL to 50 pg/mL of MAGEC2 peptide, optionally wherein the target cell is a cell monoallelic for an MHC matched to the MAGEC2 peptide;

iv) the host cell is capable of killing a higher number of target cells when contacted *in vitro* or *ex vivo* with target cells with a heterozygous expression of MAGEC2, optionally wherein the cell killing is at least 1.05-fold higher; and/or

v) the host cell is capable of killing a higher number of target cells when contacted *in vitro* or *ex vivo* with target cells with a heterozygous expression of MAGEC 2, optionally wherein the cell killing is at least 1.05-fold higher;

f) the MHC or MHC-peptide complex is as follows:

i) the MHC molecule:

A) is a MHC multimer, optionally wherein the MHC multimer is a tetramer;

B) is a MHC class I molecule; and/or

C) comprises an MHC alpha chain that is an HLA serotype selected from the group consisting of HLA-A*02, HLA-A*03, HLA-A*01, HLA-A*11, HLA-A*24, and/or HLA-B*07, optionally wherein the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0204, HLA-A*0205, HLA-A*0206, HLA-A*0207, HLA-A*0210, HLA-A*0211, HLA-A*0212, HLA-A*0213, HLA-A*0214, HLA-A*0216, HLA-A*0217, HLA-A*0219, HLA-A*0220, HLA-A*0222, HLA-A*0224, HLA-A*0230, HLA-A*0242, HLA-A*0253, HLA-A*0260, HLA-A*0274 allele, HLA-A*0301, HLA-A*0302, HLA-A*0305, HLA-A*0307, HLA-A*0101, HLA-A*0102, HLA-A*0103, HLA-A*0116 allele, HLA-A*1101, HLA-A*1102, HLA-A*1103, HLA-A*1104, HLA-A*1105, HLA-A*1119 allele, HLA-A*2402, HLA-A*2403, HLA-A*2405, HLA-A*2407, HLA-A*2408, HLA-A*2410, HLA-A*2414, HLA-A*2417, HLA-A*2420, HLA-A*2422, HLA-A*2425, HLA-A*2426, HLA-A*2458 allele, HLA-B*0702, HLA-B*0704, HLA-B*0705, HLA-B*0709, HLA-B*0710, HLA-B*0715, and HLA-B*0721 allele;

ii) the peptide epitope and the MHC molecule are covalently linked and/or wherein the alpha and beta chains of the MHC molecule are covalently linked;

iii) the stable MHC-peptide complex comprises a detectable label, optionally wherein the detectable label is a fluorophore; and/or

g) i) the host cell does not induce T cell expansion, cytokine release, or cytotoxic killing when contact *in vitro* or *ex vivo* with a target cell that comprises a peptide-MHC (pMHC) complex selected from the group consisting of ALKDVEERV/HLA-A*02, LLFGLALIEV/HLA-A*02, SESIKKKVL/HLA-B*44, and ASSTLYLVF/HLA-B*57 and/or ii) the host cell does not express MAGEC2 antigen, is not recognized by a binding protein of any one of claims 1-6, is not of serotype HLA-B*07, does not express an HLA-B*07 allele, is not of serotype HLA-A*24, and/or does not express an HLA-A*24 allele.

11. A composition comprising a) a binding protein according to any one of claims 1-6, b) an isolated nucleic acid according to claim 7, c) a vector according to claim 8, and/or d) a host cell or a population of host cells according to claim 9 or 10, and a carrier.

12. A device or kit comprising a) a binding protein according to any one of claims 1-6, b) an isolated nucleic acid according to claim 7, c) a vector according to claim 8, and/or d) a host cell or a population of host cells according to claim 9 or 10, said device or kit optionally comprising a reagent to detect binding of a), and/or d) to a pMHC complex.

13. A method of producing a binding protein according to any one of claims 1-6, wherein the method comprises the steps of: (i) culturing a transformed host cell which has been transformed by a nucleic acid comprising a sequence encoding a binding protein according to any one of claims 1-6 under conditions suitable to allow expression of said binding protein; and (ii) recovering the expressed binding protein.

14. A method of producing a host cell expressing a binding protein according to any one of claims 1-6, wherein the method comprises the steps of: (i) introducing a nucleic acid comprising a sequence encoding a binding protein according to any one of claims 1-6 into the host cell; and (ii) culturing the transformed host cell under conditions suitable to allow expression of said binding protein.

15. A method of detecting the presence or absence of a MAGEC2 antigen and/or a cell expressing MAGEC2, optionally wherein the cell is a hyperproliferative cell, comprising

detecting the presence or absence of said MAGEC2 antigen in a sample by use of at least one binding protein according to any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10, wherein detection of the MAGEC2 antigen is indicative of the presence of a MAGEC2 antigen and/or cell expressing MAGEC2, optionally wherein:

1) the at least one binding protein, or the at least one host cell, forms a complex with the MAGEC2 peptide in the context of an MHC molecule, and the complex is detected in the form of fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay;

2) the method further comprises obtaining the sample from a subject.

16. A method of detecting the level of a disorder characterized by MAGEC2 expression in a subject, comprising:

a) contacting a sample obtained from the subject with at least one binding protein according to any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10; and

b) detecting the level of reactivity,

wherein the presence or a higher level of reactivity compared to a control level indicates the level of the disorder characterized by MAGEC2 expression in the subject;

optionally wherein:

i) the control level is:

A) a reference number, or

B) a level from a subject without the disorder characterized by MAGEC2 expression; and/or

ii) the level of reactivity is indicated by

A) the presence of binding; and/or

B) T cell activation and/or effector function, optionally wherein

1) the T cell activation or effector function is T cell proliferation, killing, or cytokine release; and/or

2) the T cell binding, activation, and/or effector function is detected using fluorescence activated cell sorting (FACS), enzyme linked immunosorbent

assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay.

17. A method for monitoring the progression of a disorder characterized by MAGEC2 expression in a subject, the method comprising:

a) detecting in a subject sample the presence or level of reactivity between a sample obtained from the subject and at least one binding protein of any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10;

b) repeating step a) at a subsequent point in time; and

c) comparing the level of MAGEC2 or the cell of interest expressing MAGEC2 detected in steps a) and b) to monitor the progression of the disorder characterized by MAGEC2 expression in the subject, wherein an absent or reduced MAGEC2 level or the cell of interest expressing MAGEC2 detected in step b) compared to step a) indicates an inhibited progression of the disorder characterized by MAGEC2 expression in the subject and a presence or increased MAGEC2 level or the cell of interest expressing MAGEC2 detected in step b) compared to step a) indicates a progression of the disorder characterized by MAGEC2 expression in the subject, optionally wherein:

i) between the first point in time and the subsequent point in time, the subject has undergone treatment to treat the disorder characterized by MAGEC2 expression; and/or

ii) the level of reactivity is indicated by

A) the presence of binding; and/or

B) T cell activation and/or effector function, optionally wherein

1) the T cell activation or effector function is T cell proliferation, killing, or cytokine release; and/or

2) the T cell binding, activation, and/or effector function is detected using fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay.

18. A method for predicting the clinical outcome of a subject afflicted with a disorder characterized by MAGEC2 expression comprising:

a) determining the presence or level of reactivity between a sample obtained from the subject and at least one binding protein according to any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10; and

b) comparing the presence or level of reactivity to that from a control, wherein the control is obtained from a subject having a good clinical outcome;

wherein the absence or a reduced level of reactivity in the subject sample as compared to the control indicates that the subject has a good clinical outcome, optionally wherein the level of reactivity is indicated by

A) the presence of binding; and/or

B) T cell activation and/or effector function, optionally wherein

1) the T cell activation or effector function is T cell proliferation, killing, or cytokine release; and/or

2) the T cell binding, activation, and/or effector function is detected using fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay.

19. A method of assessing the efficacy of a therapy for a disorder characterized by MAGEC2 expression comprising:

a) determining the presence or level of reactivity between a sample obtained from the subject and at least one binding protein according to any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10, in a first sample obtained from the subject prior to providing at least a portion of the therapy for the disorder characterized by MAGEC2 expression to the subject, and

b) determining the presence or level of reactivity between a sample obtained from the subject and at least one binding protein according to any one of claims 1-6, at least one host cell or a population of host cells according to claim 9 or 10, in a second sample obtained from the subject following provision of the therapy for the disorder characterized by MAGEC2 expression,

wherein the absence or a reduced level of reactivity in the second sample, relative to the first sample, is an indication that the therapy is efficacious for treating the disorder characterized

by MAGEC2 expression in the subject, and wherein the presence or an increased level of reactivity in the second sample, relative to the first sample, is an indication that the therapy is not efficacious for treating the disorder characterized by MAGEC2 expression in the subject,

optionally wherein the level of reactivity is indicated by

A) the presence of binding; and/or

B) T cell activation and/or effector function, optionally wherein

1) the T cell activation or effector function is T cell proliferation, killing, or cytokine release; and/or

2) the T cell binding, activation, and/or effector function is detected using fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay.

20. A composition comprising cells expressing at least one binding protein according to any one of claims 1-6 for use as a medicament.

21. Use of a composition comprising cells expressing at least one binding protein according to any one of claims 1-6 in the manufacture of a medicament for preventing and/or treating a disorder characterized by MAGEC2 expression in a subject, wherein the medicament binds target cells expressing MAGEC2, optionally wherein:

1) the cell expressing the at least one binding protein is an allogeneic cell, syngeneic cell, or autologous cell;

2) the cell expressing the at least one binding protein is a host cell or a population of host cells according to claim 9 or 10;

3) the target cell is a cancer cell expressing MAGEC2;

4) the composition further comprises a pharmaceutically acceptable carrier;

5) the composition induces an immune response against the target cell expressing MAGEC2 in the subject;

6) the composition induces an antigen-specific T cell immune response against the target cell expressing MAGEC2 in the subject;

7) the antigen-specific T cell immune response comprises at least one of a $CD4^+$ helper T lymphocyte (Th) response and a CD8+ cytotoxic T lymphocyte (CTL) response;

8) the medicament further comprises at least one additional treatment for the disorder characterized by MAGEC2 expression;

9) the disorder characterized by MAGEC2 expression is a cancer or relapse thereof, optionally wherein the cancer is selected from the group consisting of melanoma, head & neck cancer, lung cancer, cervical cancer, prostate cancer, multiple myeloma, hepatocellular carcinoma, breast invasive carcinoma, and bladder urothelial carcinoma; and/or

10) the subject is an animal model of a disorder characterized by MAGEC2 expression and/or a mammal, optionally wherein the mammal is a human, a primate, or a rodent.