CLAIMS:

1. An immunogenic peptide comprising or consisting of a peptide epitope selected from peptide sequences listed in Table 1, optionally wherein the immunogenic peptide:

1) is derived from a MAGEC2 protein, optionally wherein the immunogenic peptide is 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids in length; and/or

2) is capable of eliciting an immune response against MAGEC2 and/or MAGEC2-expressing cells in a subject, 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.

2. An immunogenic composition comprising at least one immunogenic peptide of claim 1, optionally wherein the immunogenic composition:

1) further comprises an adjuvant; and/or

2) is capable of eliciting an immune response against MAGEC2 and/or MAGEC2-expressing cells in a subject, 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.

3. A composition comprising a peptide epitope selected from peptide sequences listed in Table 1, and an MHC molecule, optionally wherein the MHC molecule:

1) is an MHC multimer, optionally wherein the MHC multimer is a tetramer;

2) is an MHC class I molecule; and/or

3) 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.

4. A stable MHC-peptide complex, comprising an immunogenic peptide according of claim 1 in the context of an MHC molecule,
optionally wherein

1) the MHC molecule
    a) is an MHC multimer, optionally wherein the MHC multimer is a tetramer;
    b) is an 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;
2) 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; and/or
3) the stable MHC-peptide complex comprises a detectable label, optionally wherein the detectable label is a fluorophore.

5. An immunogenic composition comprising the stable MHC-peptide complex of claim 4, and an adjuvant.

6. An isolated nucleic acid that encodes the immunogenic peptide of claim 1, or a complement thereof.

7. A vector comprising the isolated nucleic acid of claim 6.

8. A cell that a) comprises the isolated nucleic acid of claim 6, b) comprises the vector of claim 7, and/or c) produces one or more immunogenic peptides claim 1 and/or presents at the cell surface one or more stable MHC-peptide complexes of claim 4, optionally wherein the cell is genetically engineered.

9. A device or kit comprising a) one or more immunogenic peptides of claim 1 and/or b) one or more stable MHC-peptide complexes of claim 4, said device or kit optionally comprising a reagent to detect binding of a) and/or b) to a binding protein, optionally wherein the binding protein is an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain.

10. A method of detecting T cells that bind a stable MHC-peptide complex comprising:

a) contacting a sample comprising T cells with a stable MHC-peptide complex of claim 4; and

b) detecting binding of T cells to the stable MHC-peptide complex, optionally further determining the percentage of stable MHC-peptide-specific T cells that bind to the stable MHC-peptide complex, optionally wherein the sample comprises peripheral blood mononuclear cells (PBMCs) , optionally wherein:

1) the T cells are CD8+ T cells;

2) the detecting and/or determining is performed using fluorescence activated cell sorting (FACS), enzyme linked immunosorbent assay (ELISA), radioimmune assay (RIA), immunochemically, Western blot, or intracellular flow assay;

3) the sample comprises T cells contacted with, or suspected of having been contacted with, one or more MAGEC2 proteins or fragments thereof;

4) 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

5) 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.

11. A method of determining whether a T cell has had exposure to MAGEC2 comprising:

a) incubating a cell population comprising T cells with an immunogenic peptide of claim 1 or a stable MHC-peptide complex of claim 4; and

b) detecting the presence or level of reactivity,

wherein the presence of or a higher level of reactivity compared to a control level indicates that the T cell has had exposure to MAGEC2, optionally wherein the cell population comprising T cells is obtained from a subject;

optionally wherein

1) the level of reactivity is indicated by

a) the presence of binding; and/or

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

2) the method further comprises repeating steps a) and b) at a subsequent point in time, optionally wherein the subject has undergone treatment to ameliorate the disorder characterized by MAGEC2 expression between the first point in time and the subsequent point in time;

3) 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;

4) the control level is

a) a reference number; and/or

b) a level of a subject without the disorder characterized by MAGEC2 expression;

5) 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;

6) 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.

12. 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 T cells obtained from the subject and one or more immunogenic peptides of claim 1 or one or more stable MHC-peptide complexes of claim 4; 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 presence or a higher level of reactivity in the subject sample as compared to the control indicates that the subject has a good clinical outcome;

optionally wherein

1) the level of reactivity is indicated by

a) the presence of binding; and/or

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

2) the method further comprises repeating steps a) and b) at a subsequent point in time, optionally wherein the subject has undergone treatment to ameliorate the disorder characterized by MAGEC2 expression between the first point in time and the subsequent point in time;

3) 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; and/or

4) the control level is

a) a reference number; and/or

b) a level of a subject without the disorder characterized by MAGEC2 expression;

5) 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;

6) 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.

13. 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 T cells obtained from the subject and one or more immunogenic peptides of claim 1 or one or more stable MHC-peptide complexes of claim 4, in a first sample obtained from the subject prior to providing at least a portion of the therapy to the subject, and

b) determining the presence or level of reactivity between the one more immunogenic peptides of claim 1, or the one or more stable MHC-peptide complexes of claim 4, and T cells obtained from the subject present in a second sample obtained from the subject following provision of the therapy to the subject,

wherein the presence or a higher 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;

optionally wherein

1) the level of reactivity is indicated by

a) the presence of binding; and/or

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

2) the method further comprises repeating steps a) and b) at a subsequent point in time, optionally wherein the subject has undergone treatment to ameliorate the disorder characterized by MAGEC2 expression between the first point in time and the subsequent point in time;

3) 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;

4) the control level is

a) a reference number; and/or

b) a level of a subject without the disorder characterized by MAGEC2 expression;

5) 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;

6) 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.

14. A composition of any one of claims 1-9 for use as a medicament.

15. Use of a composition of any one of claims 1-9 in the manufacture of a medicament for preventing and/or treating a disorder characterized by MAGEC2 expression in a subject.

16. A method of identifying a peptide-binding molecule, or antigen-binding fragment thereof, that binds to a peptide epitope selected from the peptide sequences listed in Table 1 comprising:

a) providing a cell presenting a peptide epitope selected from the peptide sequences listed in Table 1 in the context of an MHC molecule on the surface of the cell;

b) determining binding of a plurality of candidate peptide-binding molecules or antigen-binding fragments thereof to the peptide epitope in the context of the MHC molecule on the cell; and

c) identifying one or more peptide-binding molecules or antigen-binding fragments thereof that bind to the peptide epitope in the context of the MHC molecule;

optionally wherein:

1) the step a) comprises contacting the MHC molecule on the surface of the cell with a peptide epitope selected from the peptide sequences listed in Table 1;

2) the step a) comprises expressing the peptide epitope selected from the peptide sequences listed in Table 1 in the cell using a vector comprising a heterologous sequence encoding the peptide epitope;

3) 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

4) 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.

17. A method of identifying a peptide-binding molecule or antigen-binding fragment thereof that binds to a peptide epitope selected from the peptide sequences listed in Table 1 comprising:

a) providing a peptide epitope either alone or in a stable MHC-peptide complex, comprising a peptide epitope selected from the peptide sequences listed in Table 1, either alone or in the context of an MHC molecule;

b) determining binding of a plurality of candidate peptide-binding molecules or antigen-binding fragments thereof to the peptide or stable MHC-peptide complex; and

c) identifying one or more peptide-binding molecules or antigen-binding fragments thereof that bind to the peptide epitope or the stable MHC-peptide complex, optionally wherein:

1) 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;

2) 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;

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

4) the plurality of candidate peptide binding molecules comprises

a) an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain;

b) at least 2, 5, 10, 100, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, or more, different candidate peptide binding molecules; and/or

c) one or more candidate peptide binding molecules that are obtained from a sample from a subject or a population of subjects; or the plurality of candidate peptide binding molecules comprises one or more candidate peptide binding molecules that comprise mutations in a parent scaffold peptide binding molecule obtained from a sample from a subject, optionally wherein:

i) the subject or population of subjects are a) not afflicted with a disorder characterized by MAGEC2 expression and/or have recovered from a disorder characterized by MAGEC2 expression, or b) are afllicted with a disorder characterized by MAGEC2 expression;

ii) the subject or population of subjects has been administered a composition according to any one of claims 1-9;

iii) 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;

iv) the subject is an animal model of a disorder characterized by MAGEC2 expression, an HLA-transgenic mouse, and/or a human TCR transgenic mouse; and/or

v) the sample comprises peripheral blood mononuclear cells (PBMCs), T cells, and/or CD8+ memory T cells;

5) the peptide-binding molecule or antigen-binding fragment thereof is an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single

chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain;

6) 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

7) 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.

18. Genetically engineered T cells that express a peptide-binding molecule or antigen-binding fragment thereof for use as a medicament, wherein the peptide-binding molecule or antigen-binding fragment thereof i) binds to a peptide epitope selected from the sequences listed in Table 1, ii) is identified according to the method of claim 17, and/or iii) binds to a stable MHC-peptide complex comprising a peptide epitopes selected from the sequences listed in Table 1 in the context of an MHC molecule, optionally wherein the peptide-binding molecule or antigen-binding fragment thereof is an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain, further optionally wherein:

1) 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;

2) 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;

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

4) the T cells are isolated from a) the subject, b) a donor not afflicted with the disorder characterized by MAGEC2 expression, or c) a donor recovered from a disorder characterized by MAGEC2 expression;

5) 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

6) 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.

19. Use of a genetically engineered T cells that express a peptide-binding molecule or antigen-binding fragment thereof in the manufacture of a medicament for treating a disorder characterized by MAGEC2 expression in a subject, wherein the peptide-binding molecule or antigen-binding fragment thereof i) binds to a peptide epitope selected from the sequences listed in Table 1, ii) is identified according to the method of claim 17, and/or iii) binds to a stable MHC-peptide complex comprising a peptide epitopes selected from the sequences listed in Table 1 in the context of an MHC molecule, optionally wherein the peptide-binding molecule or antigen-binding fragment thereof is an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain, further optionally wherein:

1) 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;

2) 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;

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

4) the T cells are isolated from a) the subject, b) a donor not afflicted with the disorder characterized by MAGEC2 expression, or c) a donor recovered from a disorder characterized by MAGEC2 expression;

5) the cell is an allogeneic cell, syngeneic cell, or autologous cell;

6) the cell is a host cell or a population of host cells according to claim 26 or 27;

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

8) the composition further comprises a pharmaceutically acceptable carrier;

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

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

11) 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;

12) the use further comprises administering at least one additional treatment for the disorder characterized by MAGEC2 expression, optionally wherein the at least one additional treatment for the disorder characterized by MAGEC2 expression is administered concurrently or sequentially with the composition;

13) 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

14) 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 .

20. Antigen-specific T cells for use as a medicament, wherein the antigen-specific T cells are generated by:

a) stimulating immune cells from a subject with a composition according to any one of claims 1-9; and

b) expanding antigen-specific T cells *in vitro* or *ex vivo*, optionally i) isolating immune cells from the subject before stimulating the immune cells and/or ii) wherein the immune cells comprise PBMCs, T cells, CD8+ T cells, naive T cells, central memory T cells, and/or effector memory T cells.

21. Use of antigen-specific T cells in the manufacture of a medicament for treating a disorder characterized by MAGEC2 expression in a subject, wherein the antigen-specific T cells are generated by:

a) stimulating immune cells from a subject with a composition according to any one of claims 1-9; and

b) expanding antigen-specific T cells *in vitro* or *ex vivo*, optionally i) isolating immune cells from the subject before stimulating the immune cells and/or ii) wherein the immune cells comprise PBMCs, T cells, CD8+ T cells, naive T cells, central memory T cells, and/or effector memory T cells;

optionally wherein:

1) the agents are placed in contact under conditions and for a time suitable for the formation of at least one immune complex between the peptide epitope, immunogenic peptide, stable MHC-peptide complex, T cell receptor, and/or immune cells;

2) the peptide epitope, immunogenic peptide, stable MHC-peptide complex, and/or T cell receptor are expressed by cells and the cells are expanded and/or isolated during one or more steps;

3) the cell is an allogeneic cell, syngeneic cell, or autologous cell;

4) the cell is a host cell or a population of host cells according to claim 26 or 27;

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

6) the composition further comprises a pharmaceutically acceptable carrier;

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

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

9) 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;

10) the use further comprises administering at least one additional treatment for the disorder characterized by MAGEC2 expression, optionally wherein the at least one additional treatment for the disorder characterized by MAGEC2 expression is administered concurrently or sequentially with the composition;

11) 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

12) 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.

22. A binding protein that binds a polypeptide comprising an immunogenic peptide according to any one of claims 1-3, and/or the stable MHC-peptide complex of claim 4, optionally wherein the binding protein is an antibody, an antigen-binding fragment of an antibody, a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a

chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain, optionally wherein the binding protein comprises:

1) a) a T cell receptor (TCR) alpha chain CDR sequence with at least about 80% identity to a TCR alpha chain CDR sequence selected from the group consisting of TCR alpha chain CDR sequences listed in Table 2; and/or

b) a TCR beta chain CDR sequence with at least about 80% identity to a TCR beta chain CDR sequence selected from the group consisting of TCR beta chain CDR sequences listed in Table 2, wherein the binding protein is capable of binding to a MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M;

2) a) a TCR alpha chain variable (V_α) domain sequence with at least about 80% identity to a TCR V_α domain sequence selected from the group consisting of TCR V_α domain sequences listed in Table 2; and/or

b) a TCR beta chain variable (V_β) domain sequence with at least about 80% identity to a TCR V_β domain sequence selected from the group consisting of TCR V_β domain sequences listed in Table 2, wherein the binding protein is capable of binding to a MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M;

3) a) a TCR alpha chain sequence with at least about 80% identity to a TCR alpha chain sequence selected from the group consisting of TCR alpha chain sequences listed in Table 2; and/or

b) a TCR beta chain sequence with at least about 80% identity to a TCR beta chain sequence selected from the group consisting of TCR beta chain sequences listed in Table 2, wherein the binding protein is capable of binding to a MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M;

4) a) a TCR alpha chain CDR sequence selected from the group consisting of TCR alpha chain CDR sequences listed in Table 2; and/or

b) a TCR beta chain CDR sequence selected from the group consisting of TCR beta chain CDR sequences listed in Table 2, wherein the binding protein is capable of binding to a

MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M;

5) a) a TCR alpha chain variable (V_α) domain sequence selected from the group consisting of TCR V_α domain sequences listed in Table 2; and/or

b) a TCR beta chain variable (V_β) domain sequence selected from the group consisting of TCR V_β domain sequences listed in Table 2, wherein the binding protein is capable of binding to a MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M; or

6) a) a TCR alpha chain sequence selected from the group consisting of TCR alpha chain sequences listed in Table 2; and/or

b) a TCR beta chain sequence selected from the group consisting of TCR beta chain sequences listed in Table 2, wherein the binding protein is capable of binding to a MAGEC2 immunogenic peptide-MHC (pMHC) complex, optionally wherein the binding affinity has a K_d less than or equal to about $5x10^{-4}$ M.

23. The binding protein of claim 22, wherein:

1) the TCR alpha chain CDR, TCR V_α domain, and/or TCR alpha chain is encoded by a TRAV, TRAJ, and/or TRAC gene or fragment thereof selected from the group of TRAV, TRAJ, and TRAC genes listed in Table 2;

2) the TCR beta chain CDR, TCR V_β domain, and/or TCR beta chain is encoded by a TRBV, TRBJ, and/or TRBC gene or fragment thereof selected from the group of TRBV, TRBJ, and TRBC genes listed in Table 2;

3) each CDR of the binding protein has up to five amino acid substitutions, insertions, deletions, or a combination thereof as compared to the cognate reference CDR sequence listed in Table 2;

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

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

6) 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;

7) 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;

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

9) 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;

10) 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;

11) 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 about $1x10^{-4}$ M, less than or equal to about $5x10^{-5}$ M, less than or equal to about $1x10^{-5}$ M, less than or equal to about $5x10^{-6}$ M, less than or equal to about $1x10^{-6}$ M, less than or equal to about $5x10^{-7}$ M, less than or equal to about $1x10^{-7}$ M, less than or equal to about $5x10^{-8}$ M, less than or equal to about $1x10^{-8}$ M, less than or equal to about $5x10^{-9}$ M, less than or equal to about $1x10^{-9}$ M, less than or equal to about $5x10^{-10}$ M, less than or equal to about $1x10^{-10}$ M, less than or equal to about $5x10^{-11}$ M, less than or equal to about $1x10^{-11}$ M, less than or equal to about $5x10^{-12}$ M, or less than or equal to about $1x10^{-12}$ M;

12) the binding protein has a higher binding affinity to the peptide-MHC (pMHC) than does a known T-cell receptor, optionally wherein the higher binding affinity is at least 1.05-fold higher;

13) the binding protein induces higher T cell expansion, cytokine release, and/or cytotoxic killing than does a known T-cell receptor when contacted with target cells with a heterozygous expression of MAGEC2, optionally wherein the induction is at least 1.05-fold higher, optionally wherein the cytotoxic killing is a target cancer cell, further 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;

14) 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.

24. An isolated nucleic acid molecule i) that hybridizes, under stringent conditions, with the complement of a nucleic acid encoding a polypeptide selected from the group consisting of

polypeptide sequences listed in Table 2, ii) a sequence with at least about 80% homology to a nucleic acid encoding a polypeptide selected from the group consisting of the polypeptide sequences listed in Table 2, and/or iii) ii) a sequence with at least about 80% homology to a nucleic acid encoding listed in Table 2, optionally wherein the isolated nucleic acid molecule comprises 1) a TRAV, TRAJ, and/or TRAC gene or fragment thereof selected from the group of TRAV, TRAJ, and TRAC genes listed in Table 2 and/or 2) a TRBV, TRBJ, and/or TRBC gene or fragment thereof selected from the group of TRBV, TRBJ, and TRBC genes listed in Table 2, further optionally wherein the nucleic acid is codon optimized for expression in a host cell.

25. A vector comprising the isolated nucleic acid of claim 24, optionally wherein i) the vector is a cloning vector, expression vector, or viral vector; ii) the vector comprises a vector sequence listed in Table 3; and/or iii) 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 24, 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.

26. A host cell or a population of host cells, wherein the host cell comprises the isolated nucleic acid of claim 24, comprises the vector of claim 25, and/or expresses the binding protein according to claim 22 or 23, optionally wherein the cell is genetically engineered.

27. The host cell or a population of host cells of claim 26, 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*, *ex vivo*, or *in 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 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 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 with target cells with a heterozygous expression of MAGEC2, optionally wherein the cell killing is at least 1.05-fold higher;

f) the MAGEC2 immunogenic peptide is as according to claim 1 and/or wherein 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

k) i) the host cell does not induce T cell expansion, cytokine release, or cytotoxic killing when contact 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 claim 22 or 23, 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.

28. A composition comprising a) a binding protein according to claim 22 or 23, b) an isolated nucleic acid according to claim 24, c) a vector according to claim 25, and/or d) a host cell or a population of host cells according to claim 26 or 27, and a carrier.

29. A device or kit comprising a) a binding protein according to claim 22 or 23, b) an isolated nucleic acid according to claim 24, c) a vector according to claim 25, and/or d) a host cell or a population of host cells according to claim 26 or 27, said device or kit optionally comprising a reagent to detect binding of a), d) and/or e) to a pMHC complex.

30. A method of producing a binding protein according to claim 22 or 23, 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 claim 22 or 23 under conditions suitable to allow expression of said binding protein; and (ii) recovering the expressed binding protein.

31. A method of producing a host cell expressing a binding protein according to claim 22 or 23, wherein the method comprises the steps of: (i) introducing a nucleic acid comprising a sequence encoding a binding protein according to claim 22 or 23 into the host cell; and (ii) culturing the transformed host cell under conditions suitable to allow expression of said binding protein.

32. 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27, 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.

33. 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27; 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.

34. 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27;

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.

35. 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27; 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.

36. 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27, 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 claim 22 or 23, at least one host cell or a population of host cells according to claim 26 or 27, 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.

37. A composition comprising cells expressing at least one binding protein according to claim 22 or 23 for use as a medicament.

38. Use of a composition comprising cells expressing at least one binding protein according to claim 22 or 23 in the manufacture of a medicament for preventing and/or treating a disorder characterized by MAGEC2 expression, wherein the use comprises contacting target cells expressing MAGEC2 with a therapeutically effective amount of the medicament, optionally wherein the medicament is administered to a subject, optionally wherein:

11) the cell is an allogeneic cell, syngeneic cell, or autologous cell;

12) the cell is a host cell or a population of host cells according to claim 26 or 27;

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

14) the composition further comprises a pharmaceutically acceptable carrier;

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

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

17) 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;

18) the use further comprises administering at least one additional treatment for the disorder characterized by MAGEC2 expression, optionally wherein the at least one additional treatment for the disorder characterized by MAGEC2 expression is administered concurrently or sequentially with the composition;

19) 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

20) 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.