What is claimed is:

1. An isolated MAGEA1 (VRFFFPSL) peptide-MHC (HLA-C*07) (pMHC) complex binding protein comprising:

a) a T cell receptor (TCR) alpha chain variable domain comprising CDR1 having the amino acid sequence of NSMFDY, CDR2 having r the amino acid sequence of ISSIKDK, and CDR3 having the amino acid sequence of CAASAQNNDMRF; and

b) a TCR beta chain variable domain comprising CDR1 having the amino acid sequence of KGHSH, CDR2 having the amino acid sequence of LQKENI, and CDR3 having the amino acid sequence of CASSPSYEQYF.

2. The binding protein of claim 1 comprising:

a) a TCR alpha chain variable (V_α) domain comprising a sequence with at least about 80% identity to the amino acid sequence of MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS AQNNDMRFGAGTRLTVKPN; and

b) a TCR beta chain variable (V_β) domain comprising a sequence with at least about 80% identity to the amino acid sequence of MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE QYFGPGTRLTVTE.

3. The binding protein of claim 2 comprising:

a) a TCR alpha chain variable (V_α) domain comprising the amino acid sequence of MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS AQNNDMRFGAGTRLTVKPN; and

b) a TCR beta chain variable (V_β) domain comprising the amino acid sequence of MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL

PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE
QYFGPGTRLTVTE.

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

a) a TCR alpha chain comprising a sequence with at least about 80% identity to the amino acid sequence of
MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY
FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS
AQNNDMRFGAGTRLTVKPNiqnpdpavyqlrdskssdksvclftdfdsqtnvsqskdsdvyitdktvldmrsmdfks
nsavawsnksdfacanafnnsiipedtffpspesscdvklveksfetdtnlnfqnlsvigfrilllkvagfnllmtlrlwss; and

b) a TCR beta chain comprising a sequence with at least about 80% identity to the amino acid sequence of
MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL
PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE
QYFGPGTRLTVTEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwvngkevhsgvstdpqplkeqpaln
dsryclssrlrvsatfwqnprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlsatilyeillgkatlyavl
vsalvlmamvkrkdf.

5. The binding protein of claim 4 comprising:

a) a TCR alpha chain comprising the amino acid sequence of
MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY
FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS
AQNNDMRFGAGTRLTVKPNiqnpdpavyqlrdskssdksvclftdfdsqtnvsqskdsdvyitdktvldmrsmdfks
nsavawsnksdfacanafnnsiipedtffpspesscdvklveksfetdtnlnfqnlsvigfrilllkvagfnllmtlrlwss; and

b) a TCR beta chain comprising the amino acid sequence of
MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL
PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE
QYFGPGTRLTVTEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwvngkevhsgvstdpqplkeqpaln
dsryclssrlrvsatfwqnprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlsatilyeillgkatlyavl
vsalvlmamvkrkdf.

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

a) a TCR alpha chain comprising a sequence with at least about 80% identity to the amino acid sequence of

MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY
FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS
AQNNDMRFGAGTRLTVKPNiqnpdpavyqlrdskssdksvclftdfdsqtnvsqskdsdvyitdktvldmrsmdfks
nsavawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnllvivlrilllkvagfnllmtlrlws; and

b) a TCR beta chain comprising a sequence with at least about 80% identity to the amino acid sequence of

MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL
PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE
QYFGPGTRLTVTEdlnkvfppevavfepskaeiahtqkatlvclatgffpdhvelswwvngkevhsgvstdpqplkeqpal
ndsryclssrlrvsatfwqnprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgitsasyhqgvlsatilyeillgkatlya
vlvsalvlmamvkrkdf.

7. The binding protein of claim 6 comprising:

a) a TCR alpha chain comprising the amino acid sequence of

MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDY
FLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAS
AQNNDMRFGAGTRLTVKPNiqnpdpavyqlrdskssdksvclftdfdsqtnvsqskdsdvyitdktvldmrsmdfks
nsavawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnllvivlrilllkvagfnllmtlrlws; and

b) a TCR beta chain comprising the amino acid sequence of

MDTRLLCCAVICLLGAGLSNAGVMQNPRHLVRRRGQEARLRCSPMKGHSHVYWYRQL
PEEGLKFMVYLQKENIIDESGMPKERFSAEFPKEGPSILRIQQVVRGDSAAYFCASSPSYE
QYFGPGTRLTVTEdlnkvfppevavfepskaeiahtqkatlvclatgffpdhvelswwvngkevhsgvstdpqplkeqpal
ndsryclssrlrvsatfwqnprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgitsasyhqgvlsatilyeillgkatlya
vlvsalvlmamvkrkdf.

8. The binding protein of any one of claims 1-7, wherein 1) the TCR V_α domain or TCR alpha chain is encoded by a TRAV29-DV5 and TRAJ43 gene, and 2) the TCR V_β domain or TCR beta chain is encoded by a TRBV18 and TRBJ2-7 gene.

9. The binding protein of any one of claims 1-8, wherein the binding protein is chimeric, humanized, or human.

10. The binding protein of any one of claims 1-9, wherein the binding protein comprises a binding domain having a transmembrane domain, and an effector domain that is intracellular.

11. The binding protein of any one of claims 1-10, wherein 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.

12. The binding protein of any one of claims 1-11, wherein the TCR alpha chain and/or the TCR beta chain are covalently linked to a moiety, optionally wherein the covalently linked moiety comprises an affinity tag or a label.

13. The binding protein of claim 12, wherein the affinity tag is selected from the group consisting of a CD34 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.

14. The binding protein of either one of claims 12 or 13, wherein the covalently linked moiety is selected from the group consisting of an inflammatory agent, cytokine, toxin, cytotoxic molecule, radioactive isotope, or antibody or antigen-binding fragment thereof.

15. The binding protein of any one of claims 1-14, wherein the binding protein binds to the pMHC complex on a cell surface.

16. The binding protein of any one of claims 1-15, wherein the MHC is a MHC multimer, optionally wherein the MHC multimer is a tetramer.

17. The binding protein of any one of claims 1-16, wherein the MHC is a MHC class I molecule.

18. The binding protein of any one of claims 1-17, wherein the MHC comprises an MHC alpha chain that is an HLA serotype HLA-C*07, optionally wherein the HLA allele is selected from the group consisting of HLA-C*0702, HLA-C*0701, and HLA-C*0704 allele.

19. The binding protein of any one of claims 1-18, wherein binding of the binding protein to a MAGEA1 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.

20. The binding protein of any one of claims 1-19, wherein the binding protein is capable of specifically and/or selectively binding to a MAGEA1 immunogenic peptide-MHC (pMHC) complex with a K_d less than or equal to $1x10^{-4}$ M.

21. The binding protein of any one of claims 1-20, wherein 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, ASSTLYLVF/HLA-B*57, and a pMHC complex comprising a LAMB4-IR, TLE3, SLC16A2, SLC6A13, BTBD2, RXFP1, and/or PIGO peptide epitope.

22. An isolated nucleic acid molecule that encodes a binding protein of any one of claims 1-21, wherein the nucleic acid is codon optimized for expression in a host cell.

23. A vector comprising the isolated nucleic acid of claim 22, optionally wherein i) the vector is a cloning vector, expression vector, or viral vector and/or ii) the vector comprises the sequence of SEQ ID NO: 51 or the sequence of SEQ ID NO: 52.

24. The vector of claim 23, wherein the vector further comprises a nucleic acid sequence encoding CD8α, CD8β, a dominant negative TGFβ receptor II (DN-TGFβRII), selectable protein marker, optionally wherein the selectable protein marker is dihydrofolate reductase (DHFR).

25. The vector of claim 24, wherein the nucleic acid sequence encoding CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker is operably linked to a nucleic acid encoding a tag.

26. The vector of claim 24 or 25, wherein the nucleic acid encoding a tag is at the 5' upstream of the nucleic acid sequence encoding CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker such that the tag is fused to the N-terminus of CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker.

27. The vector of claim 25 or 26, wherein the tag is a CD34 enrichment tag.

28. The vector of any one of claims 23-27, wherein the nucleic acid encoding the binding protein, the nucleic acid sequence encoding TCRα, TCRβ, CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker are interconnected with an internal ribosome entry site or a nucleic acid sequence encoding a self-cleaving peptide.

29. The vector of claim 28, wherein the self-cleaving peptide is P2A, E2A, F2A or T2A.

30. A host cell which comprises the vector according to any one of claims 23-29, and/or expresses the binding protein according to any one of claims 1-21, optionally wherein the cell is genetically engineered.

31. The host cell of claim 30, wherein the host cell comprises a chromosomal gene knockout of a TCR gene, an HLA gene, or both.

32. The host cell of claim 30 or 31, wherein the host cell 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.

33. The host cell of any one of claims 30-32, wherein the host cell comprises 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.

34. The host cell of any one of claims 30-33, wherein the host cell expresses CD8α, CD8β, a DN-TGFβRII, and/or a selectable protein marker, optionally wherein the selectable protein marker is DHFR, further optionally wherein the CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker is fused to a CD34 enrichment tag.

35. The host cell of any one of claims 30-34, wherein the host cell is a hematopoietic progenitor cell, peripheral blood mononuclear cell (PBMC), cord blood cell, or immune cell.

36. The host cell of claim 35, wherein the immune cell is a T cell, 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 a combination thereof.

37. The host cell of claim 36, wherein the T cell is a naive T cell, central memory T cell, effector memory T cell, or a combination thereof.

38. The host cell of claim 36 or 37, wherein the T cell is a primary T cell or a cell of a T cell line.

39. The host cell of any one of claims 36-38, wherein the T cell does not express or has a lower surface expression of an endogenous TCR.

40. The host cell of any one of claims 36-39, wherein the host cell 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 MAGEA1 peptide epitope in the context of an MHC molecule.

41. The host cell of claim 40, wherein the cytokine is TNF-α, IL-2, and/or IFN-γ.

42. The host cell of claim 40 or 41, wherein the cytotoxic molecule is perforins and/or granzymes, optionally wherein the cytotoxic molecule is granzyme B.

43. The host cell of any one of claims 40-42, wherein 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 MAGEA1.

44. The host cell of claim 43, wherein the host cell is capable of producing an at least 1.05-fold higher level of cytokine or a cytotoxic molecule.

45. The host cell of any one of claims 36-42 wherein the host cell is capable of killing a target cell that comprises a peptide-MHC (pMHC) complex comprising the MAGEA1 peptide epitope in the context of an MHC molecule.

46. The host cell of claim 45, wherein the killing is determined by a killing assay.

47. The host cell of claim 45 or 46, wherein the ratio of the host cell and the target cell in the killing assay is from 20:1 to 1:4.

48. The host cell of any one of claims 45-47, wherein the target cell is a target cell pulsed with 1 μg/mL to 50 pg/mL of MAGEA1 peptide, optionally wherein the target cell is a cell monoallelic for an MHC matched to the MAGEA1 peptide.

49. The host cell of any one of claims 45-48, wherein the host cell is capable of killing a higher number of target cells when contacted with target cells with a heterozygous expression of MAGEA1, optionally wherein the cell killing is at least 1.05-fold higher.

50. The host cell of any one of claims 30-49, wherein the target cell is a cell line or a primary cell, optionally wherein the target cell is selected from the group consisting of a HEK293 derived cell line, a cancer cell line, a primary cancer cell, a transformed cell line, and an immortalized cell line.

51. The host cell of any one of claims 30-50, wherein the MAGEA1 immunogenic peptide comprises the amino acid sequence VRFFFPSL.

52. The host cell of any one of claims 30-51, wherein the MHC is an MHC class I molecule.

53. The host cell of any one of claims 30-52, wherein the MHC comprises an MHC alpha chain that is an HLA serotype HLA-C*07, optionally wherein the HLA allele is selected from the group consisting of HLA-C*0702, HLA-C*0701, and HLA-C*0704 allele.

54. The host cell of any one of claims 30-53, wherein a) the host cell does not induce T cell expansion, cytokine release, or cytotoxic killing when contacted with a target cell that comprises a peptide-MHC (pMHC) complex comprising a LAMB4-IR, TLE3, SLC16A2, SLC6A13, BTBD2, RXFP1, and/or PIGO peptide epitope; and/or b) the host cell does not express MAGEA1 antigen, is not recognized by a binding protein of any one of claims 1-21, is not of serotype HLA-C*07, and/or does not express an HLA-C*07 allele.

55. A population of host cells according to any one of claims 30-54.

56. A composition comprising a) a binding protein according to any one of claims 1-21, b) an isolated nucleic acid according to claim 22, c) a vector according to any one of claims 23-29, d) a host cell according to any one of claims 30-54, and/or e) a population of host cells according to claim 55, and a carrier.

57. A device or kit comprising a) a binding protein according to any one of claims 1-21, b) an isolated nucleic acid according to claim 22, c) a vector according to any one of claims 23-29, d) a host cell according to any one of claims 30-54, and/or e) a population of host cells according to claim 55, said device or kit optionally comprising a reagent to detect binding of a), d) and/or e) to a pMHC complex.

58. A method of producing a binding protein according to any one of claims 1-21, 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 1-21 under conditions suitable to allow expression of said binding protein; and (ii) recovering the expressed binding protein.

59. A method of producing a host cell expressing a binding protein according to any one of claims 1-21, 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 1-21 into the host cell; and (ii) culturing the transformed host cell under conditions suitable to allow expression of said binding protein.