

Claims:

1. An HA-2 (YIGEVLVSV) peptide-MHC (HLA-A*02) (pMHC) complex binding protein comprising:

a) a T cell receptor (TCR) alpha chain variable domain comprising CDR1 having the amino acid sequence of TSESDYY, CDR2 having the amino acid sequence of QEAYKQQN, and CDR3 having the amino acid sequence of CAYRSERYSTLTF; and

b) a TCR beta chain variable domain comprising CDR1 having the amino acid sequence of GTSNPN, CDR2 having the amino acid sequence of SVGIG, and CDR3 having the amino acid sequence of CAWSVPYLAGGKRPDTQYF.

2. The binding protein of claim 1 comprising:

a) a TCR alpha chain variable (V_α) domain comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the amino acid sequence of

MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL SCTYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPD; and

b) a TCR beta chain variable (V_β) domain comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the amino acid sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNPNLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLS DSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLE.

3. The binding protein of claim 2 comprising:

a) a TCR alpha chain variable (V_α) domain comprising the amino acid sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL SCTYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPD; and

b) a TCR beta chain variable (V_β) domain comprising the amino acid sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLE.

4. The binding protein of claim 1 or 2 comprising:

a) a TCR alpha chain variable (V_α) domain comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the amino acid sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCITYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPD; and

b) a TCR beta chain sequence comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to: i) the amino acid sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsgvstdpqplk
eqpalndsryclssrlrvsatfwqnpnrhfrqcqvfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf; or ii) the amino acid sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsgvstdpqplk
eqpalndsryclssrlrvsatfwqnpnrhfrqcqvfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf, except with the following five substitutions: E153K, S157A, F268I, V271A, and Q274H.

5. The binding protein of claim 4 comprising:

a) a TCR alpha chain variable (V_α) domain comprising the amino acid sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCITYDTSESDYYLFWYK

QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPD; and

b) a TCR beta chain sequence comprising: i) the amino acid sequence of
MLCSLLALLLGTTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSPNPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswvngkevhsqvstdpqplk
eqpalndsryclssrlrvsatfwqnpnrnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf; or ii) the amino acid sequence of
MLCSLLALLLGTTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSPNPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswvngkevhsqvstdpqplk
eqpalndsryclssrlrvsatfwqnpnrnhfrcqvqfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf, except with the following five substitutions: E153K, S157A, F268I,
V271A, and Q274H.

6. The binding protein of claim 1 or 2 comprising:

a) a TCR alpha chain sequence comprising an amino acid sequence having at least 80%,
at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or
100% identity to the amino acid sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCITYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdsksvclftdfdsqtnvsqskdsdvyyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivrilllkvagfnllmtlrlws; and

b) a TCR beta chain variable (V_{β}) domain comprising an amino acid sequence having at
least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at
least 99%, or 100% identity to the amino acid sequence of
MLCSLLALLLGTTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSPNPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLE.

7. The binding protein of claim 6 comprising:

a) a TCR alpha chain sequence comprising the amino acid sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL SCTYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdksvclftdfdsqtnvsqskdsdvyyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivlrilllkvagfnllmtlrlws; and

b) a TCR beta chain variable (V_{β}) domain comprising the amino acid sequence of
MLCSLLALLLGTTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLE.

8. The binding protein of claim 1 or 2 comprising:

a) a TCR alpha chain sequence comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the sequence of

MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL SCTYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdksvclftdfdsqtnvsqskdsdvyyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivlrilllkvagfnllmtlrlws; and

b) a TCR beta chain sequence comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the sequence of

MLCSLLALLLGTTFFGVRSQTIHQWPATLVQPVGSPLSELECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsqvstpdqplk
eqpalndsryclssrlrvsatfwqnpnrhfrqvfqygl sendewtqdrakpvtqivsaeawgradcgftsvsyqqgvl satilyeillgk
atlyavlvsalvlmamvkrkdf.

9. The binding protein of claim 8 comprising:

a) a TCR alpha chain sequence comprising the sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTL SCTYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE

RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdksvclftdfdsqtnvsqskdsdvyyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivlrilllkvagfnllmtlrllws; and

b) a TCR beta chain sequence comprising the sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPSLECTVEGTSPNPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsgvstdpqplk
eqpalndsryclssrlrvsatfwqnprnhfrcqvfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf.

10. The binding protein of claim 1 or 2 comprising:

a) a TCR alpha chain sequence comprising an amino acid sequence having at least 80%,
at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or
100% identity to the sequence of

MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCITYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE
RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdksvclftdfdsqtnvsqskdsdvyyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivlrilllkvagfnllmtlrllws; and

b) a TCR beta chain sequence comprising an amino acid sequence having at least 80%, at
least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or
100% identity to the sequence of

MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPSLECTVEGTSPNPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsgvstdpqplk
eqpalndsryclssrlrvsatfwqnprnhfrcqvfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf, except with the following five substitutions: E153K, S157A, F268I,
V271A, and Q274H.

11. The binding protein of claim 10 comprising:

a) a TCR alpha chain sequence comprising the sequence of
MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCITYDTSESDYYLFWYK
QPPSRQMILVIRQEAYKQQNATENRFSVNFQKAAKSFSCLKISDSQLGDAAMYFCAYRSE

RYSTLTFGKGTMLLVSPDiqnpdpavyqlrdsksdksvclftdfdsqtnvsqskdsdvyitdktvldmrsmdfksnsa
vawsnksdfacanafnnsiipedtffpssdvpcdvklveksfetdtnlnfqnlvivlrilllkvagfnllmtlrws; and

b) a TCR beta chain sequence comprising the sequence of
MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPSLECTVEGTSNPPLYWYRQAAGR
GLQLLFYSVGIGQISSEVPQNLSASRPQDRQFILSSKLLLSDSGFYLCAWSVPYLAGGK
RPDTQYFGPGTRLTVLEdlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswwwngkevhsgvstdpqplk
eqpalndsryclssrlrsvatfwqnprnhfrcqvfyglsendewtqdrakpvtqivsaeawgradcgftsvsyqqgvlstilyeillgk
atlyavlvsalvlmamvkrkdf, except with the following five substitutions: E153K, S157A, F268I,
V271A, and Q274H.

12. The binding protein of any one of claims 1-11, wherein the TCR alpha chain or TCR V α domain is encoded by a TRAV38-2DV8 and TRAJ11 gene.

13. The binding protein of any one of claims 1-12, wherein the TCR beta chain or TCR V β domain is encoded by a TRBV30 and TRBJ2-3 gene.

14. The binding protein of any one of claims 1-13, wherein the binding protein is chimeric, humanized, or human.

15. The binding protein of any one of claims 1-14, wherein the binding protein is 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.

16. The binding protein of claim 15, wherein the binding protein comprises a transmembrane domain and an effector domain that is intracellular.

17. The binding protein of any one of claims 1-16, wherein the TCR alpha chain and the TCR beta chain are covalently linked.

18. The binding protein of claim 17, wherein the TCR alpha chain and the TCR beta chain are covalently linked through a linker peptide.

19. The binding protein of any one of claims 1-18, wherein the TCR alpha chain and/or the TCR beta chain are covalently linked to a moiety.
20. The binding protein of claim 19, wherein the moiety is an affinity tag or a label.
21. The binding protein of claim 20, wherein the affinity tag is selected from the group consisting of 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.
22. The binding protein of claim 19, wherein the moiety is selected from the group consisting of an inflammatory agent, cytokine, toxin, cytotoxic molecule, radioactive isotope, and antibody or antigen-binding fragment thereof.
23. The binding protein of any one of claims 1-22, wherein the binding protein binds to the pMHC complex on a cell surface.
24. The binding protein of any one of claims 1-23, wherein the MHC is an MHC multimer.
25. The binding protein of claim 24, wherein the MHC multimer is a tetramer.
26. The binding protein of any one of claims 1-25, wherein the MHC is an MHC class I molecule.
27. The binding protein of any one of claims 1-26, wherein the MHC comprises an MHC alpha chain that is an HLA serotype HLA-A*02.
28. The binding protein of any one of claims 1-27, wherein the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0205, HLA-A*0206, and HLA-A*0207 allele.

29. The binding protein of claim 28, wherein the HLA allele is HLA-A*0201.
30. The binding protein of any one of claims 1-29, wherein binding of the binding protein to the HA-2 peptide-MHC (pMHC) complex elicits an immune response.
31. The binding protein of claim 30, wherein the immune response is a T cell response.
32. The binding protein of claim 31, wherein the T cell response is selected from the group consisting of T cell expansion, cytokine release, and cytotoxic killing.
33. The binding protein of any one of claims 1-32, wherein the binding protein is capable of specifically binding to the HA-2 (YIGEVLVSV)peptide-MHC (HLA-A*02) (pMHC) complex with a dissociation constant (K_d) less than or equal to 1×10^{-4} M.
34. An isolated nucleic acid molecule that encodes a binding protein of any one of claims 1-33.
35. The isolated nucleic acid of claim 34, wherein the isolated nucleic acid is codon optimized for expression in a host cell.
36. A vector comprising the isolated nucleic acid of claim 34 or 35.
37. The vector of claim 36, wherein the vector is a cloning vector, expression vector, or viral vector.
38. The vector of claim 36 or 37, wherein the vector further comprises a nucleic acid sequence encoding CD8 α and/or CD8 β .
39. The vector of claim 38, wherein the nucleic acid sequence encoding CD8 α or CD8 β is operably linked to a nucleic acid encoding a tag.

40. The vector of claim 39, wherein the nucleic acid encoding a tag is at the 5' upstream of the nucleic acid sequence encoding CD8 α or CD8 β such that the tag is fused to the N-terminus of CD8 α or CD8 β .
41. The vector of claim 39 or 40, wherein the tag is a CD34 enrichment tag.
42. The vector of any one of claims 36-41, wherein the isolated nucleic acid of claim 34 or 35, and the nucleic acid sequence encoding CD8 α and/or CD8 β are interconnected with an internal ribosome entry site or a nucleic acid sequence encoding a self-cleaving peptide.
43. The vector of claim 42, wherein the self-cleaving peptide is P2A, E2A, F2A or T2A.
44. The vector of any one of claims 36-43, comprising the sequence of
AATTAATTGCTTGCAATTAACCCTTTAACGGTTATAAGGATCTAGATGAGATAGAAA
GATTTGGTTTTTCGGATTTGTGTTACATAAGATGCCTAAAATAAAAATTGAGATTCAA
TTTTTTTTTAAACTTTTTTTTTTAATTGGTGGTAAGAATATTCCTCTACCTGTTTGAGAGT
AATGAAATTGTAGTATGATTTTTCAACAACTAAAAAACAACATAAATCTCACATA
ATAACTTTATTTCAATCACACAATTGAATACCAATATTAATTAATGGTTGACAGTAC
TTACCAGCCTGCAGGTGAAAGACCCACCTGTAGGTTTGGCAAGTTAGCTTAAGTAA
CGCCATTTTGCAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTCAGATCAA
GGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
GTTCCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTC
AGCAGTTTCTAGCGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGAC
CCTGTGCCTTATTTGAACTAACCAATCAGTTTGCTTCTTGCTTCTGTTTGTGTGCTTCT
GCTCCCTGAGCTCAATAAAAGAGCCCACAACCCCTCACTTGGTGGGCCAGTCCTCTG
ATAGACTGTGTCCCCTGGATACCCGTACGGTACCGCTAGCGCCACCATGCTGTGTAG
CCTGCTGGCCCTGCTCCTGGGCACATTTTTTTGGCGTCAGATCCCAGACCATCCATCA
GTGGCCTGCCACACTGGTGCAGCCTGTTGGATCTCCCCTGTCTCTGGAATGTACCGT
GGAAGGCACAAGCAACCCCAACCTCTACTGGTATAGGCAGGCCGCTGGAAGAGGAC
TGCAGCTGCTGTTTTACAGCGTCGGCATCGGCCAGATCAGCAGCGAGGTTCCACAGA

ATCTGAGCGCCTCCAGGCCTCAGGACAGACAGTTTATCCTGAGCAGCAAGAAGCTG
CTGCTGAGCGACTCCGGCTTTTACCTCTGTGCTTGGAGCGTTCCATACCTGGCCGGTG
GCAAACGCCCTGACACTCAATATTTTCGGCCCAGGCACCCGGCTGACAGTGCTCGAA
GATCTGAACAAGGTGTTCCCTCCAGAGGTGGCCGTGTTTCGAGCCTTCTAAGGCCGAG
ATCGCCACACACAAAAAGCCACCCTCGTGTGCCTGGCCACCGGCTTTTTCCCGAC
CACGTGGAAGTGTCTTGGTGGGTCAACGGCAAAGAGGTGCACTCCGGCGTGTCAAC
GGATCCCCAGCCTCTGAAAGAACAGCCTGCCCTGAACGACAGCCGGTACTGCCTGA
GCTCCAGACTGAGAGTGTCCGCCACCTTCTGGCAGAACCCCCGGAACCACTTCAGAT
GCCAGGTGCAGTTTTACGGCCTGAGCGAGAACGACGAGTGGACCCAGGACAGAGCC
AAGCCCGTGACACAAATCGTGTCTGCCGAAGCCTGGGGAAGAGCCGATTGCGGCAT
CACCAGCGCCTCCTATCACCAGGGCGTGCTGAGCGCCACAATCCTGTACGAAATCCT
GCTGGGCAAGGCCACCCTGTACGCCGTGCTGGTGTCTGCTCTGGTGTGATGGCCAT
GGTCAAGCGGAAGGACTTTGGCAGCGGCAGAGCCAAAAGGTCCGGGAGCGGTGCG
ACAAACTTTAGCCTGTTGAAACAAGCCGGCGACGTTGAAGAGAACCCCGGACCTAT
GGCCTGTCCTGGCTTCCTGTGGGCCCTTGTGATCAGCACTTGCCTGGAATTCAGCAT
GGCTCAGACAGTCACCCAGTCTCAGCCCGAAATGAGCGTCCAAGAGGCTGAAACCG
TGAATCTGTCTTGTACCTACGACACCTCCGAGAGCGATTACTACCTCTTTTGGTATAA
GCAACCGCCGTCCAGGCAAATGATCCTCGTGATCCGGCAAGAAGCTTACAAACAGC
AGAATGCTACCGAAAACCGGTTCTCCGTCAATTTTCAGAAAGCCGCTAAGAGCTTTA
GCCTGAAAATCTCCGACTCTCAGCTCGGCGACGCTGCTATGTATTTCTGTGCCTACC
GCAGTGAGCGCTACAGCACTTTGACTTTTCGGGAAGGGGACTATGCTTCTAGTCTCTC
CAGACATCCAGAACCCCGACCCCGCCGTGTACCAGCTGAGGGACTCCAAGTCCAGC
GACAAGAGCGTGTGTCTGTTTACGGACTTCGACAGCCAGACCAACGTGAGTCAAAG
CAAGGACAGCGACGTCTACATAACGGATAAGACCGTGCTGGACATGCGGAGCATGG
ACTTCAAGAGCAACAGCGCCGTGGCCTGGTCCAACAAGAGCGACTTCGCCTGCGCC
AACGCCTTCAACAACAGCATCATCCCCGAGGACACCTTCTTCCCCAGCAGCGACGTG
CCCTGCGACGTGAAACTGGTGGAGAAGTCCTTCGAGACAGACACCAATCTGAACTTT
CAGAACCTGCTGGTGATCGTGCTGCGGATTCTGCTGCTGAAAGTGGCCGGCTTCAAT
CTGCTGATGACCCTGCGGCTGTGGAGCAGCAGGGCTAAGAGGTCCGGCAGCGGAGC
CACCAATTTTTCCCTGCTGAAACAGGCTGGTGACGTGGAAGAAAACCCTGGCCCCAT
GGCGCTGCCCGTCACCGCGCTGCTGCTGCCCCTGGCGCTGCTGTTACACGCCGCTCG

GCCAGAGCTTCCCACCCAGGGCACATTCTCCAACGTGTCCACCAATGTGTCTGGGAGG
CGGCGGATCGTCCCAGTTCAGAGTGTCCCCTCTGGACCGCACCTGGAACCTGGGCGA
GACCGTGGAGCTGAAATGTCAGGTCCTGCTGAGCAACCCGACCTCCGGGTGCAGTT
GGCTGTTCCAGCCGCGTGGTGCTGCCGCAAGCCCTACGTTCTTGCTTTACCTGAGCC
AGAACAAGCCCAAGGCGGGCCGAGGGCCTGGACACCCAGAGATTCTCCGGCAAGCGC
CTGGGGGACACATTCGTGCTTACTTTGAGCGATTTCGCGAGAGAGAACGAGGGGCTAC
TATTTCTGTTCGGCGCTGAGCAATTCCATCATGTATTTAGCCACTTTGTGCCAGTGT
TCCTGCCTGCCAAGCCTACCACAACACCAGCTCCCCGTCCCCCGACTCCGGCGCCTA
CCATCGCGAGTCAACCGTTGAGCCTGAGGCCTGAGGCTTGTCGGCCCCGCTGCGGGG
GGTGCCGTCCACACCAGGGGCCTCGACTTTGCGTGCGACATCTATATTTGGGCGCCT
CTGGCGGGTACCTGCGGGGTGCTGCTGCTGTCATTGGTGATTACCCTGTACTGCAAT
CACCGCAACCGCCGGCGGGTCTGTAAGTGCCACGGCCTGTGGTCAAGTCCGGTGTA
CAAACCGTCGCTCTCGGCTCGCTACGTGCGCGCTAAGCGCAGCGGTTCCGGGGCCAC
CAACTTTTCATTGCTGAAGCAGGCCGGTGATGTGGAGGAGAATCCAGGGCCCCATGC
GCCCCAGGCTTTGGCTCCTTCTTGCTGCTCAGCTCACTGTCTTGCATGGCAACTCCGT
TCTGCAGCAGACTCCCGCCTACATCAAGGTGCAGACGAACAAGATGGTGATGCTGT
CATGCGAGGCCAAGATCTCTCTTTCAAATATGAGAATTTATTGGCTACGACAGCGCC
AGGCCCCCTCCAGCGACAGCCACCACGAGTTCCTGGCGCTTTGGGATTCTGCTAAAG
GCACCATCCATGGAGAGGAGGTGGAACAGGAGAAGATAGCTGTCTTCCGCGACGCA
TCCCGCTTCATCCTGAACCTGACCAGCGTGAAGCCGGAGGACAGCGGCATCTACTTC
TGTATGATCGTTGGCTCCCCCGAGCTGACCTTCGGCAAAGGCACCCAGCTGTCCGTG
GTGGACTTCCTGCCCACCACAGCCCAGCCAACCAAGAAATCCACCCTCAAGAAGCG
CGTGTGCCGACTGCCCCGCCCTGAAACCCAGAAGGGCCCTCTGTGCTCCCCCATCAC
CCTTGGACTGCTGGTGGCGGGAGTCCTGGTGCTGCTCGTATCTCTGGGTGTGCGCCAT
CCACCTGTGCTGCCGCCGCCGCCGCCGCCCTGAGGTTTATGAAACAGTTTTACAA
GTGATAAATCGATAGATCCTAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGA
CTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCC
TTTGTATCATGCTATTGCTTCCCGTATGGCTTTTCATTTTCTCCTCCTTGATAAATCCT
GGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGT
GCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGC
TCCTTTCCGGGACTTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGGAACCTCATCGCCG

CTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGT
GTTGTGCGGGGAAATCATCGTCCTTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATT
CTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTT
CCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGAC
GAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCCTGAGATCCTTTAAGACCAATGCTG
GAGTTCTTCGCCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGC
AATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTT
TGTCCAAACATCATCAATGTATCTTATCATGTCTGTATACAGGTTACCTCAGTCTCCTA
GGTACGTCTTATATCTATGAAAAAACATTCAAAAGCACAACATCTAGAAGAAGCTTAC
CTTTTTTCACTACTCTATTGCAAAGATATGTACCGATTTCTCTCGAAGTACAAAAAAC
CGCTAGTTTTCAAATTCACCTCAAGACTTTGAAAAAAAATTGAATCTGTCAATGTCA
AATAAAATCAGAAACAAATGTCATAATGTTACGTTAATGTTGTCAGGTCGAAAAAT
AAAATTGCAAATAGAAATTTTGTTCCTTTTTTTATTGGTTTTTTATTGGTGGGAAAAATA
TTCCCTCTAACTGCAAAAGGGTTAATTATGTTAGAGGTAGAGTCGACGCTAGCTGGC
TTGTTGTCCACAACCATTAACCTTAAAAGCTTTAAAAGCCTTATATATTCTTTTTTT
TCTTATAAACTTAAAACCTTAGAGGCTATTTAAGTTGCTGATTTATATTAATTTTAT
TGTTCAAACATGAGAGCTTAGTACGTGAAACATGAGAGCTTAGTACATTAGCCATGA
GAGCTTAGTACATTAGCCATGAGGGTTTAGTTCATTAAACATGAGAGCTTAGTACAT
TAAACATGAGAGCTTAGTACATACTATCAACAGGTTGAACTGCTGATCTGTACAGTA
GAATTGGTAAAGAGAGTTGTGTAAAATATTGAGTTCGCACATCTTGTTGTCTGATTA
TTGATTTTTTGGCGAAACCATTTGATCATATGACAAGATGTGTATCTACCTTAACCTAA
TGATTTTGATAAAAATCATTAGGTACC.

45. A host cell which comprises the isolated nucleic acid of claim 34 or 35, comprises the vector of any one of claims 36-44, and/or expresses the binding protein of any one of claims 1-33.

46. The host cell of claim 45, wherein the cell is genetically engineered.

47. The host cell of claim 45 or 46, wherein the host cell comprises a chromosomal gene knockout of a TCR gene, an HLA gene, or both.

48. The host cell of any one of claims 45-47, wherein the host cell comprises a knockout of an HLA gene selected from an $\alpha 1$ macroglobulin gene, $\alpha 2$ macroglobulin gene, $\alpha 3$ macroglobulin gene, $\beta 1$ microglobulin gene, $\beta 2$ microglobulin gene, or a combination thereof.
49. The host cell of any one of claims 45-48, 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, or a combination thereof.
50. The host cell of any one of claims 45-49, wherein the host cell expresses CD8 α and/or CD8 β .
51. The host cell of claim 50, wherein the CD8 α and/or CD8 β is fused to a CD34 enrichment tag.
52. The host cell of any one of claims 45-51, wherein the host cell is a hematopoietic progenitor cell, peripheral blood mononuclear cell (PBMC), cord blood cell, or immune cell.
53. The host cell of claim 52, 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 ($\gamma\delta$) T cell, natural killer (NK) cell, NK-T cell, dendritic cell, or a combination thereof.
54. The host cell of any one of claims 45-53, wherein the host cell is a naive T cell, central memory T cell, effector memory T cell, or a combination thereof.
55. The host cell of any one of claims 45-54, wherein the host cell is a primary T cell or a cell of a T cell line.
56. The host cell of any one of claims 45-55, wherein the host cell does not express or has a lower surface expression of an endogenous TCR.

57. The host cell of any one of claims 53-56, 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 an HA-2 peptide epitope in the context of an MHC molecule.
58. The host cell of claim 57, wherein the cytokine is TNF- α , IL-2, and/or IFN- γ .
59. The host cell of claim 57 or 58, wherein the cytotoxic molecule is perforins and/or granzymes.
60. The host cell of claim 59, wherein the cytotoxic molecule is granzyme B.
61. The host cell of any one of claims 57-60, wherein the host cell is capable of killing a target cell that comprises a peptide-MHC (pMHC) complex comprising the HA-2 peptide epitope in the context of an MHC molecule.
62. The host cell of claim 61, wherein the killing is determined by a killing assay.
63. The host cell of claim 61 or 62, wherein the ratio of the host cell and the target cell in the killing assay is from 20:1 to 0.625:1.
64. The host cell of any one of claims 61-63, wherein the target cell is a T2 cell pulsed with 1 $\mu\text{g/mL}$ to 50 pg/mL of HA-2 peptide.
65. The host cell of any one of claims 61 and 62, wherein the target cell is a DEL, THP-1, or TF-1 cell line.
66. The host cell of any one of claims 57-65, wherein the HA-2 peptide epitope comprises the amino acid sequence YIGEVLVSV.

67. The host cell of any one of claims 57-65, wherein the HA-2 peptide epitope comprises the amino acid sequence YIGEVLVSM.
68. The host cell of any one of claims 57-67, wherein the MHC molecule is an MHC class I molecule.
69. The host cell of any one of claims 57-68, wherein the MHC molecule comprises an MHC alpha chain that is an HLA serotype HLA-A*02.
70. The host cell of any one of claims 57-69, wherein the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0205, HLA-A*0206, and HLA-A*0207 allele.
71. The host cell of claim 70, wherein the HLA allele is HLA-A*0201.
72. The host cell of any one of claims 57-71, wherein the target cell is a cell line selected from the group consisting of Del, THP-1, and TF-1 cell lines, is a hematopoietic cancer cell expressing HA-2, or is not NB4.
73. The host cell of claim 72, wherein the cancer cell is of a hematological malignancy selected from the group consisting of a leukemia, a lymphoma, a myelodysplastic disorder, a myeloproliferative neoplasm, and myeloma.
74. The host cell of any one of claims 57-73, wherein the host cell does not express HA-2 antigen, is not recognized by a binding protein of any one of claims 1-33, is not of serotype HLA-A*02, and/or does not express an HLA-A*02 allele.
75. A population of host cells of any one of claims 45-74.
76. A composition comprising: a carrier and a) a binding protein according to any one of claims 1-33, b) an isolated nucleic acid according to claim 34 or 35, c) a vector according to any

one of claims 36-44, d) a host cell according to any one of claims 45-74, and/or e) a population of host cells according to claim 75.

77. A device or kit comprising: a) a binding protein according to any one of claims 1-33, b) an isolated nucleic acid according to claim 34 or 35, c) a vector according to any one of claims 36-44, d) a host cell according to any one of claims 45-74, and/or e) a population of host cells according to claim 75.

78. The device or kit of claim 77, wherein said device or kit further comprises a reagent to detect binding of a), d) and/or e) to a pMHC complex.

79. A method of producing a binding protein according to any one of claims 1-33, 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 1-33 under conditions suitable to allow expression of said binding protein; and (ii) recovering the expressed binding protein.

80. A method of producing a host cell expressing a binding protein according to any one of claims 1-33, 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 1-33 into the host cell; (ii) culturing the transformed host cell under conditions suitable to allow expression of said binding protein.