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(54) Title: ANTIGEN-BINDING PROTEINS TATRGETING SHARED ANTIGENS

(57) Abstract: Provided herein are HLA-PEPTIDE targets and antigen binding proteins that bind HLA-PEPTIDE targets. Also disclosed are methods for identifying the HLA-PEPTIDE targets as well as identifying one or more antigen binding proteins that bind a give n HLA-PEPTIDE target.

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ANTIGEN-BINDING PROTEINS TARGETING SHARED ANTIGENS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 62/547,146, filed on August 18, 2017, and of U.S. Provisional Application No. 62/581,368, filed on November 3, 2017, which applications are hereby incorporated in entirety by reference for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on August 16, 2018, is named 40698PCT_CRF_sequencelisting.txt and is 1,591,443 bytes in size.

BACKGROUND

[0003] The immune system employs two types of immune responses to provide antigen specific protection from pathogens; humoral immune responses, and cellular immune responses, which involve specific recognition of pathogen antigens via B lymphocytes and T lymphocytes, respectively.

[0004] T lymphocytes, by virtue of being the antigen specific effectors of cellular immunity, play a central role in the body's defense against diseases mediated by intracellular pathogens, such as viruses, intracellular bacteria, mycoplasmas, and intracellular parasites, by directly cytolysing cells infected by such pathogens. The specificity of T lymphocyte responses is conferred by, and activated through T-cell receptors (TCRs). T-cell receptors are antigen specific receptors clonally distributed on individual T lymphocytes whose repertoire of antigenic specificity is generated via somatic gene rearrangement mechanisms analogous to those involved in generating the antibody gene repertoire. T-cell receptors include a heterodimer of transmembrane molecules, the main type being composed of an alpha-beta polypeptide dimer and a smaller subset of a gamma-delta polypeptide dimer. T lymphocyte receptor subunits comprise a variable and constant region similar to immunoglobulins in the extracellular domain, a short hinge region with cysteine that promotes alpha and beta chain pairing, a transmembrane and a short cytoplasmic region. Signal transduction triggered by TCRs is indirectly mediated via CD3-zeta, an associated multi-subunit complex comprising signal transducing subunits.

[0005] T lymphocyte receptors do not generally recognize native antigens but rather recognize cell-surface displayed complexes comprising an intracellularly processed fragment of an antigen in association with a major histocompatibility complex (MHC) for presentation of peptide antigens. Major histocompatibility complex genes are highly polymorphic across species populations, comprising multiple common alleles for each individual gene.

[0006] Major histocompatibility complex class I molecules are expressed on the surface of virtually all nucleated cells in the body and are dimeric molecules comprising a transmembrane heavy chain, comprising the peptide antigen binding cleft, and a smaller extracellular chain termed beta2-microglobulin. MHC class I molecules present peptides derived from the degradation of cytosolic proteins by the proteasome, a multi-unit structure in the cytoplasm, (Niedermann G., 2002. Curr Top Microbiol Immunol. 268:91-136; for processing of bacterial antigens, refer to Wick M J, and Ljunggren H G., 1999. Immunol Rev. 172:153-62). Cleaved peptides are transported into the lumen of the endoplasmic reticulum (ER) by TAP where they are bound to the groove of the assembled class I molecule, and the resultant MHC/peptide complex is transported to the cell membrane to enable antigen presentation to T lymphocytes (Yewdell J W., 2001. Trends Cell Biol. 11:294-7; Yewdell J W. and Bennink J R., 2001. Curr Opin Immunol. 13:13-8). Alternatively, cleaved peptides can be loaded onto MHC class I molecules in TAP-independent manner and can also present extracellularly-derived proteins through a process of cross-presentation. As such, a given MHC/peptide complex presents a novel protein structure on the cell surface that can be targeted by a novel antigen-binding protein (e.g., antibodies or TCRs) once the identity of the complex's structure (peptide sequence and MHC subtype) is determined.

[0007] Tumor cells can express antigens and may display such antigens on the surface of the tumor cell. Such tumor-associated antigens can be used for development of novel immunotherapeutic reagents for the specific targeting of tumor cells. For example, tumor-associated antigens can be used to identify therapeutic antigen binding proteins, e.g., TCRs, antibodies, or antigen-binding fragments. Such tumor-associated antigens may also be utilized in pharmaceutical compositions, e.g., vaccines.

SUMMARY

[0008] In an aspect, provided herein is an isolated antigen binding protein (ABP) that specifically binds to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule,

wherein the HLA-restricted peptide is located in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein: the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA, the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHLY, the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide comprises the sequence GEMSSNSTAL, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence GVYDGEEHSV, the HLA Class I molecule is HLA subtype *01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHVY, or the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY.

[0009] In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide consists of the sequence LLASSILCA, the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide consists of the sequence EVDPIGHLY, the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide consists of the sequence GEMSSNSTAL, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide consists of the sequence GVYDGEEHSV, the HLA Class I molecule is HLA subtype *01:01 and the HLA-restricted peptide consists of the sequence EVDPIGHVY, or the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide consists of the sequence NTDNNLAVY.

[0010] In some embodiments, the HLA-restricted peptide is between about 5-15 amino acids in length. In some embodiments, the HLA-restricted peptide is between about 8-12 amino acids in length.

[0011] In an aspect, the ABP comprises an antibody or antigen-binding fragment thereof.

[0012] In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA. In some embodiments, the ABP comprises a CDR-H3 comprising a sequence set forth in any one of SEQ ID NOS: 3025-3032. In some embodiments, the ABP comprises a CDR-L3 comprising a sequence set forth in any one of SEQ ID NOS: 3043-3050 In some embodiments, the ABP comprises the CDR-H3 and the CDR-L3 from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9). In some embodiments, the ABP comprises all three heavy chain CDRs and all three light chain CDRs from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-

P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9). In some embodiments, the ABP comprises a VH sequence selected from SEQ ID NO: 2994-3001. In some embodiments, the ABP comprises a VL sequence selected from SEQ ID NO: 3002-3009. In some embodiments, the ABP comprises the VH sequence and VL sequence from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9). In some embodiments, the ABP binds to the HLA-PEPTIDE target via any one or more of residues 1-5 of the restricted peptide LLASSILCA .

[0013] In some embodiments, the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY. In some embodiments, the ABP comprises a CDR-H3 comprising a sequence set forth in any one of SEQ ID NOS: 2902-2933. In some embodiments, the ABP comprises a CDR-L3 comprising a sequence set forth in any one of SEQ ID NOS: 2971-2993. In some embodiments, the ABP comprises the CDR-H3 and the CDR-L3 from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 , G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06: In some embodiments, the ABP comprises all three heavy chain CDRs and all three light chain CDRs from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 , G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06: In some embodiments, the ABP comprises a VH sequence selected from SEQ ID NO: 2781-2815. In some embodiments, the ABP comprises a VL sequence selected from SEQ ID NO: 2816-2850. In some embodiments, the ABP comprises the VH sequence and VL sequence from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 , G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06. In some embodiments, the ABP binds to the HLA-PEPTIDE target via residues 6-9 of the restricted peptide NTDNNLAVY and

via residues 157-160 of the HLA subtype allele A*0101. In some embodiments, the ABP binds to the HLA-PEPTIDE target via residues 3-8 of the restricted peptide NTDNNLAVY.

[0014] In another aspect, the ABP comprises a T cell receptor (TCR) or an antigen-binding portion thereof. In some embodiments, the TCR or antigen-binding portion thereof comprises a TCR variable region. In some embodiments, the TCR or antigen-binding portion thereof comprises one or more TCR complementarity determining regions (CDRs). In some embodiments, the TCR comprises an alpha chain and a beta chain. In some embodiments, the TCR comprises a gamma chain and a delta chain. In some embodiments, the antigen binding protein is a portion of a chimeric antigen receptor (CAR) comprising: an extracellular portion comprising the antigen binding protein; and an intracellular signaling domain. In some embodiments, the antigen binding protein comprises an scFv and the intracellular signaling domain comprises an ITAM. In some embodiments, the intracellular signaling domain comprises a signaling domain of a zeta chain of a CD3-zeta (CD3) chain. In some embodiments, the ABP further comprises a transmembrane domain linking the extracellular domain and the intracellular signaling domain. In some embodiments, the transmembrane domain comprises a transmembrane portion of CD28. In some embodiments, the ABP further comprises an intracellular signaling domain of a T cell costimulatory molecule. In some embodiments, the T cell costimulatory molecule is CD28, 4-1BB, OX-40, ICOS, or any combination thereof.

[0015] In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA. In some embodiments, the ABP comprises a TCR alpha CDR3 sequence that is SEQ ID NO: 4277, 4278, 4279, 4280, or 4281. In some embodiments, the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS 4291-4295. In some embodiments, the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, or TCR23. In some embodiments, the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, and TCR23. In some embodiments, the ABP comprises a TCR alpha constant (TRAC) amino acid sequence. In

some embodiments, the ABP comprises a TCR beta constant (TRBC) amino acid sequence. In some embodiments, the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS 4306-4310. In some embodiments, the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS 4321-4325. In some embodiments, the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for any one of the TCR clonotypes selected from TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, and TCR23.

[0016] In some embodiments, the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHLY. In some embodiments, the ABP comprises a TCR alpha CDR3 sequence that is any one of SEQ ID NOS: 4273-4276 or 3052-3350. In some embodiments, the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS: 4287-4290 or 3351-3655. In some embodiments, the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, TCR54, or TCR101-TCR469. In some embodiments, the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, TCR54, or TCR101-TCR469. In some embodiments, the ABP comprises a TCR alpha constant (TRAC) amino acid sequence. In some embodiments, the ABP comprises a TCR beta constant (TRBC) amino acid sequence. In some embodiments, the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 3656-3961 or 4302-4305. In some embodiments, the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 3962-4269 or 4317-4320. In some embodiments, the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%,

or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, and TCR54.

[0017] In some embodiments, the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide comprises the sequence GEMSSNSTAL. In some embodiments, the ABP comprises a TCR alpha CDR3 sequence that is be any one of SEQ ID NOS 4284-4286 or 3138. In some embodiments, the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS 4298-4301 . In some embodiments, the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR ID #s: TCR29, TCR30, TCR32, or TCR33. In some embodiments, the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR29, TCR30, TCR32, or TCR33. In some embodiments, the ABP comprises a TCR alpha constant (TRAC) amino acid sequence. In some embodiments, the ABP comprises a TCR beta constant (TRBC) amino acid sequence. In some embodiments, the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 4313-4316. In some embodiments, the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 4328-4331. In some embodiments, the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR29, TCR30, TCR32, or TCR33.

[0018] In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence GVYDGEEHSV. In some embodiments, the ABP comprises a TCR alpha CDR3 sequence that is SEQ ID NO: 4282 or 4283. In some embodiments, the ABP comprises a TCR beta CDR3 sequence that is SEQ ID NO: 4296 or 4297. In some embodiments, the ABP comprises an alpha CDR3 and a beta CDR3 sequence from TCR clonotype ID #: TCR26 or TCR28. In some embodiments, the ABP comprises a TCR alpha

variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for TCR ID #: TCR26 or TCR28. In some embodiments, the ABP comprises a TCR alpha constant (TRAC) amino acid sequence. In some embodiments, the ABP comprises a TCR beta constant (TRBC) amino acid sequence. In some embodiments, the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4311 or 4312. In some embodiments, the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4326 or 4327. In some embodiments, the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for TCR ID #: TCR26 or TCR28.

[0019] In some embodiments, the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY. In some embodiments, the HLA Class I molecule is HLA subtype HLA-A*03:01 and the HLA-restricted peptide comprises the sequence GVHGGILNK. In some embodiments, the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHVY.

[0020] In another aspect, provided herein is an isolated antigen binding protein (ABP) that specifically binds to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA-restricted peptide is located in in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein the HLA-PEPTIDE target is selected from Table A. In some embodiments, the HLA-restricted peptide is not from a gene selected from WT1 or MART1. In some embodiments, the HLA-restricted peptide is between about 5-15 amino acids in length. In some embodiments, the HLA-restricted peptide is between about 8-12 amino acids in length. In some embodiments, the ABP comprises an antibody or antigen-binding fragment thereof.

[0021] In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein is linked to a scaffold, optionally wherein the scaffold

comprises serum albumin or Fc, optionally wherein Fc is human Fc and is an IgG (IgG1, IgG2, IgG3, IgG4), an IgA (IgA1, IgA2), an IgD, an IgE, or an IgM. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein is linked to a scaffold via a linker, optionally wherein the linker is a peptide linker, optionally wherein the peptide linker is a hinge region of a human antibody. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises an Fv fragment, a Fab fragment, a F(ab')2 fragment, a Fab' fragment, an scFv fragment, an scFv-Fc fragment, and/or a single-domain antibody or antigen binding fragment thereof. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises an scFv fragment. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises one or more antibody complementarity determining regions (CDRs), optionally six antibody CDRs. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises an antibody. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein is a monoclonal antibody. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein is a humanized, human, or chimeric antibody. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein is multispecific, optionally bispecific. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein binds greater than one antigen or greater than one epitope on a single antigen. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises a heavy chain constant region of a class selected from IgG, IgA, IgD, IgE, and IgM. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises a heavy chain constant region of the class human IgG and a subclass selected from IgG1, IgG4, IgG2, and IgG3. In some embodiments of any of the antibodies or antigen binding fragments disclosed herein, the antigen binding protein comprises a modified Fc, optionally wherein the modified Fc comprises one or more mutations that extend half-life, optionally wherein the one or more mutations that extend half-life is YTE.

[0022] In another aspect, provided herein is an isolated HLA-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I

molecule, wherein the HLA-restricted peptide is located in in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein the HLA-PEPTIDE target is selected from Table A, with the proviso that the isolated HLA-PEPTIDE target is not any one of Target nos. 6364-6369, 6386-6389, 6500, 6521-6524, or 6578 and is not an HLA-PEPTIDE target found in Table B or Table C.

[0023] In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA, the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHLY, the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide comprises the sequence GEMSSNSTAL, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-rethe HLA Class I molecule is HLA subtype *01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHVY, orstricted peptide comprises the sequence GVYDGEEHSV, the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY. In some embodiments, the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide consists of or essentially consists of the sequence LLASSILCA In some embodiments, the HLA-restricted peptide is between about 5-15 amino acids in length. In some embodiments, the HLA-restricted peptide is between about 8-12 amino acids in length. In some embodiments, the association of the HLA subtype with the restricted peptide stabilizes non-covalent association of the β2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype. In some embodiments, the stabilized association of the β2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype is demonstrated by conditional peptide exchange. In some embodiments, the isolated HLA-PEPTIDE target further comprises an affinity tag. In some embodiments, the affinity tag is a biotin tag. In some embodiments, the isolated HLA-PEPTIDE target is complexed with a detectable label. In some embodiments, the detectable label comprises a β2-microglobin binding molecule. In some embodiments, the β2-microglobin binding molecule is a labeled antibody. In some embodiments, the labeled antibody is a fluorochrome-labeled antibody.

[0024] Also provided herein is a composition comprising an HLA-PEPTIDE target disclosed herein attached to a solid support. In some embodiments, the solid support comprises a bead, well, membrane, tube, column, plate, sepharose, magnetic bead, or chip. In some embodiments, the the HLA-PEPTIDE target comprises a first member of an affinity binding pair and the solid

support comprises a second member of the affinity binding pair. In some embodiments, the first member is streptavidin and the second member is biotin.

[0025] Also provided herein is a reaction mixture comprising an isolated and purified α-subunit of an HLA subtype as described in Table A; an isolated and purified β2-microglobin subunit of the HLA subtype; an isolated and purified restricted peptide as described in Table A; and a reaction buffer.

[0026] Also provided herein is a an isolated HLA-PEPTIDE target disclosed herein; and a plurality of T-cells isolated from a human subject. In some embodiments, the the T-cells are CD8+ T-cells.

[0027] Also provided herein is an isolated polynucleotide comprising a first nucleic acid sequence encoding an HLA-restricted peptide disclosed herein, operably linked to a promoter, and a second nucleic acid sequence encoding an HLA subtype disclosed herein, wherein the second nucleic acid is operably linked to the same or different promoter as the first nucleic acid sequence, and wherein the encoded peptide and encoded HLA subtype form an HLA/peptide complex disclosed herein.

[0028] Also provided herein is a kit for expressing a stable HLA-PEPTIDE target disclosed herein, comprising a first construct comprising a first nucleic acid sequence encoding an HLA-restricted peptide disclosed herein operably linked to a promoter; and instructions for use in expressing the stable HLA-PEPTIDE complex. In some embodiments, the first construct further comprises a second nucleic acid sequence encoding an HLA subtype disclosed herein. In some embodiments, the second nucleic acid sequence is operably linked to the same or a different promoter. In some embodiments, the kit further comprises a second construct comprising a second nucleic acid sequence encoding an HLA subtype disclosed herein. In some embodiments, one or both of the first and second constructs are lentiviral vector constructs.

[0029] Also provided herein is a host cell comprising a heterologous HLA-PEPTIDE target disclosed herein. Also provided herein is a polynucleotide encoding an HLA-restricted peptide as described in Table A, e.g., a polynucleotide encoding an HLA-restricted peptide disclosed herein. In some embodiments, the does not comprise endogenous MHC. In some embodiments, the comprises an exogenous HLA. In some embodiments, the host cell is a K562 cell.

[0030] Also provided herein is a host cell as described above, and a cell culture medium comprising a restricted peptide as described in Table A. In some embodiments, the host cell is a cultured cell from a tumor cell line. In some embodiments, the tumor cell line is selected from

the group consisting of HCC-1599, NCI-H510A, A375, LN229, NCI-H358, ZR-75-1, MS751, OE19, MOR, BV173, MCF-7, NCI-H82, and NCI-H146.

[0031] In some embodiments, the antigen binding protein binds to the HLA-PEPTIDE target through a contact point with the HLA Class I molecule and through a contact point with the HLA-restricted peptide of the HLA-PEPTIDE target.

[0032] In some embodiments, the ABP is for use as a medicament. In some embodiments, the ABP is for use in treatment of cancer, optionally wherein the cancer expresses or is predicted to express the HLA-PEPTIDE target. In some embodiments, the ABP is for use in treatment of cancer, wherein the cancer is selected from a solid tumor and a hematological tumor.

[0033] Also provided herein is an ABP which is a conservatively modified variant of an ABP disclosed herein. Also provided herein is an antigen binding protein (ABP) that competes for binding with the antigen binding protein disclosed herein. Also provided herein is an antigen binding protein (ABP) that binds the same HLA-PEPTIDE epitope bound by the antigen binding protein disclosed herein.

[0034] Also provided herein is an engineered cell expressing a receptor comprising the antigen binding protein disclosed herein. In some embodiments, the engineered cell is a T cell, optionally a cytotoxic T cell (CTL). In some embodiments, the antigen binding protein is expressed from a heterologous promoter.

[0035] Also provided herein is an isolated polynucleotide or set of polynucleotides encoding an antigen binding protein described herein or an antigen-binding portion thereof. Also provided herein is an isolated polynucleotide or set of polynucleotides encoding the HLA/peptide targets described herein. Also provided herein is an vector or set of vectors comprising the polynucleotide or set of polynucleotides as disclosed herein. Also provided herein is a host cell comprising the polynucleotide or set of polynucleotides disclosed herein, optionally wherein the host cell is CHO or HEK293, or optionally wherein the host cell is a T cell.

[0036] Also provided herein is a method of producing an antigen binding protein comprising expressing the antigen binding protein with the host cell as described above and isolating the expressed antigen binding protein.

[0037] Also provided herein is a pharmaceutical composition comprising the antigen binding protein disclosed herein and a pharmaceutically acceptable excipient. Also provided herein is a method of treating cancer in a subject, comprising administering to the subject an effective amount of the antigen binding protein disclosed herein or a pharmaceutical composition

disclosed herein, optionally wherein the cancer is selected from a solid tumor and a hematological tumor. In some embodiments, the cancer expresses or is predicted to express the HLA-PEPTIDE target.

[0038] Also provided herein is a comprising the antigen binding protein disclosed herein or a pharmaceutical composition disclosed herein and instructions for use. Also provided herein is a composition comprising at least one HLA-PEPTIDE target disclosed herein and an adjuvant. Also provided herein is a least one HLA-PEPTIDE target disclosed herein and a pharmaceutically acceptable excipient. Also provided herein is a composition comprising an amino acid sequence comprising a polypeptide of at least one HLA-PEPTIDE target disclosed in Table A, optionally the amino acid sequence consisting essentially of or consisting of the polypeptide. Also provided herein is a virus comprising the isolated polynucleotide or set of polynucleotides disclosed herein In some embodiments, the virus is a filamentous phage. Also provided herein is a yeast cell comprising the isolated polynucleotide or set of polynucleotides disclosed herein.

[0039] Also provided herein is a method of identifying an antigen binding protein disclosed herein, comprising providing at least one HLA-PEPTIDE target listed in Table A; and binding the at least one target with the antigen binding protein, thereby identifying the antigen binding protein. In some embodiments, the antigen binding protein is present in a phage display library comprising a plurality of distinct antigen binding proteins. In some embodiments, the phage display library is substantially free of antigen binding proteins that non-specifically bind the HLA of the HLA-PEPTIDE target. In some embodiments, the antigen binding protein is present in a TCR library comprising a plurality of distinct TCRs or antigen binding fragments thereof. In some embodiments, the binding step is performed more than once, optionally at least three times. In some embodiments, the method further comprises contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target to determine if the antigen binding protein selectively binds the HLA-PEPTIDE target, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to soluble target HLA-PEPTIDE complexes versus soluble HLA-PEPTIDE complexes that are distinct from target complexes, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to target HLA-PEPTIDE complexes expressed on the surface of one or more cells versus HLA-PEPTIDE complexes that are distinct from target complexes expressed on the surface of one or more cells.

[0040] Also provided herein is a method of identifying an antigen binding protein disclosed herein, comprising obtaining at least one HLA-PEPTIDE target listed in Table A; administering the HLA-PEPTIDE target to a subject, optionally in combination with an adjuvant; and isolating the antigen binding protein from the subject. In some embodiments, the isolating the antigen binding protein comprises screening the serum of the subject to identify the antigen binding protein. In some embodiments, the method further comprises contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target to determine if the antigen binding protein selectively binds to the HLA-PEPTIDE target, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to soluble target HLA-PEPTIDE complexes versus soluble HLA-PEPTIDE complexes that are distinct from target complexes, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to target HLA-PEPTIDE complexes expressed on the surface of one or more cells versus HLA-PEPTIDE complexes that are distinct from target complexes expressed on the surface of one or more cells. In some embodiments, the subject is a mouse, a rabbit, or a llama. In some embodiments, the isolating the antigen binding protein comprises isolating a B cell from the subject that expresses the antigen binding protein and optionally directly cloning sequences encoding the antigen binding protein from the isolated B cell. In some embodiments, the method further comprises creating a hybridoma using the B cell. In some embodiments, the method further comprises cloning CDRs from the B cell. In some embodiments, the method further comprises immortalizing the B cell, optionally via EBV transformation. In some embodiments, the method further comprises creating a library that comprises the antigen binding protein of the B cell, optionally wherein the library is phage display or yeast display. In some embodiments, the method further comprises humanizing the antigen binding protein. Also provided herein is a method of identifying an antigen binding protein disclosed herein, comprising obtaining a cell comprising the antigen binding protein; contacting the cell with an HLA-multimer comprising at least one HLA-PEPTIDE target listed in Table A; and identifying the antigen binding protein via binding between the HLA-multimer and the antigen binding protein. Also provided herein is a method of identifying an antigen binding protein disclosed herein, comprising obtaining one or more cells comprising the antigen binding protein; activating the one or more cells with at least one HLA-PEPTIDE target listed in Table A presented on a natural or an artificial antigen presenting cell (APC); and identifying the antigen binding protein via selection of one or more cells activated by interaction with at least one HLA-

PEPTIDE target listed in Table A. In some embodiments, the the cell is a T cell, optionally a CTL. In some embodiments, the method further comprises isolating the cell, optionally using flow cytometry, magnetic separation, or single cell separation. In some embodiments, the method further comprises sequencing the antigen binding protein.

[0041] Also provided herein is a method of identifying an antigen binding protein disclosed herein, comprising providing at least one HLA-PEPTIDE target listed in Table A; and identifying the antigen binding protein using the target.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0042] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0043] FIG. 1 shows the general structure of a Human Leukocyte Antigen (HLA) Class I molecule. By User atropos235 on en.wikipedia - Own work, CC BY 2.5, https://commons.wikimedia.org/w/index.php?curid=1805424

[0044] FIG. 2 depicts exemplary construct elements for cloning TCRs into expression systems for therapy development.

[0045] FIG. 3 depicts an exemplary construct backbone sequence for cloning TCRs into expression systems for therapy development. FIG. 3 discloses SEQ ID NO: 4332.

[0046] FIG. 4 depicts an exemplary construct sequence for cloning a TCR specific for A*0201_LLASSILCA- (SEQ ID NO: 2737) into expression systems for therapy development. FIG. 4 discloses SEQ ID NO: 4333.

[0047] FIG. 5 depicts an exemplary exemplary construct sequence for cloning a TCR specific for A*0101_EVDPIGHLY (SEQ ID NO: 1) into expression systems for therapy development. FIG. 5 discloses SEQ ID NO: 4334.

[0048] FIG. 6 shows spectra data for peptide EVDPIGHLY (SEQ ID NO: 1). The figure contains the peptide fragmentation information as well as information related to the patient sample, including HLA types.

[0049] FIG. 7 shows spectra data for peptide GVHGGILNK (SEQ ID NO: 1424). The figure contains the peptide fragmentation information as well as information related to the patient sample, including HLA types.

[0050] FIG. 7A shows spectra data for peptide GVYDGEEHSV.

[0051] FIG. 7B shows spectra data for peptide NTDNNLAVY.

[0052] FIGS. 7C-7K show spectra data for additional peptides disclosed in Table A.

[0053] FIG. 8 shows the design of target screen 1 for the G2 target HLA-A*01:01_NTDNNLAVY (SEQ ID NO: 23).

[0054] FIG. 9A shows the target and minipool negative control design for the G2 target. FIG. 9A discloses SEQ ID NOS 23 and 4335-4337, respectively, in order of appearance.

[0055] FIG. 9B shows stability ELISA results for the G2 counterscreen "minipool" and G2 targets. FIG. 9B discloses SEQ ID NOS 23, 4335-4337 and 4363, respectively, in order of appearance.

[0056] FIG. 10 shows stability ELISA results for the additional G2 "complete" pool counterscreen peptides. FIG. 10 discloses SEQ ID NOS 4338-4352, respectively, in order of appearance.

[0057] FIG. 11 shows shows the design of target screen 2 for the G7 target HLA-A*02:01_ LLASSILCA (SEQ ID NO: 2737).

[0058] FIG. 12 shows stability ELISA results for the additional G7 "complete pool" counterscreen peptides. FIG. 12 discloses SEQ ID NOS 4341-4343, 4350-4358 and 4335-4337, respectively, in order of appearance.

[0059] FIG. 13A shows the target and minipool negative control design for the G7 target. FIG. 13A discloses SEQ ID NOS 2737 and 4338-4340, respectively, in order of appearance.

[0060] FIG. 13B shows stability ELISA results for the G7 counterscreen "minipool" and G7 targets. FIG. 13B discloses SEQ ID NOS 2737, 4338-4340 and 4344, respectively, in order of appearance.

[0061] FIGS. 14A and 14B show phage panning results for the G2 and G7 targets, respectively.

[0062] FIGS. 15A and 15B show biolayer interferometry (BLI) results for G2 target Fab clone G-2P1H11 and G7 target G7R4-B5-P2E9, respectively.

[0063] FIG. 16 shows a map of the amino acid substitutions for the positional scanning experiment described herein. FIG. 16 discloses SEQ ID NOS 23 and 2737, respectively, in order of appearance.

[0064] FIG. 17A shows a stability heat map for the G2 positional variant-HLAs. FIG. 17A discloses SEQ ID NO: 23.

[0065] FIG. 17B shows an affinity heat map for Fab clone G2-P1H11. FIG. 17B discloses SEQ ID NO: 23.

[0066] FIG. 18A shows a stability heat map for the G7 positional variants. FIG. 18A discloses SEQ ID NO: 2737.

[0067] FIG. 18B shows an affinity heat map for Fab clone G7R4-B5-P2E9. FIG. 18B discloses SEQ ID NO: 2737.

[0068] FIG. 19 shows cell binding results for Fab clones G2-P1H11 and G7R4-B5-P2E9 to HLA-transduced K562 cells pulsed with target or negative control peptides.

[0069] FIG. 20 shows cell binding results for Fab clones G2-P1H11 and G7R4-B5-P2E9 to HLA-transduced K562 cells pulsed with target or negative control peptides.

[0070]

[0071] FIG. 21 shows an example of hydrogen-deuterium exchange (HDX) data plotted on a crystal structure PDB 5bs0.

[0072] FIG. 22 shows an exemplary HDX heatmap for scFv clone G2-P1G07 visualized in its entirety using a consolidated perturbation view. FIG. 22 discloses SEQ ID NO: 4359.

[0073] FIG. 23 shows HDX heat maps across the HLA α1 and α2 helices for the tested G2 scFv and Fab clones. FIG. 23 discloses SEQ ID NOS 4360-4361, respectively, in order of appearance.

[0074] FIG. 24 shows an HDX heat map across the restricted peptide NTDNNLAVY (SEQ ID NO: 23) for the tested G2 scFv and Fab clones.

[0075] FIG. 25 depicts an experimental workflow by which TCRs which specifically bind HLA-PEPTIDE targets were isolated.

[0076] FIG. 26 shows a flow cytometry sorting procedure for sorting MHC-target-specific CD8+ T cells.

[0077] FIG. 27 shows flow cytometry results for exemplary HLA-PEPTIDE targets B*44:02_GEMSSNSTAL (SEQ ID NO: 2721) and A*01:01_EVDPIGHLY (SEQ ID NO: 1).

[0078] FIG. 28 shows flow cytometry results for the HLA-PETPIDE target A*03:01_GVHGGILNK (SEQ ID NO: 1424). FIG. 28 also discloses "EVDPIGHVY" as SEQ ID NO: 6.

[0079] FIG. 29A shows total number of isolated CD8+ T cells per HLA-PEPTIDE target summed across all donors tested. FIG. 29A discloses SEQ ID NOS 23, 302, 2737, 96, 1424, 2721, 6 and 1, respectively, in order of appearance.

[0080] FIG. 29B shows frequency of isolated CD8+ T cells per HLA-PEPTIDE target summed across all donors tested. FIG. 29B discloses SEQ ID NOS 1, 2737, 302, 1424, 6, 2721, 96 and 23, respectively, in order of appearance.

[0081] FIG. 30A depicts the number of unique TCR clonotypes per HLA-PEPTIDE target for each tested donor. FIG. 30A discloses SEQ ID NOS 23, 2737, 96, 1424, 2721, 6 and 1, respectively, in order of appearance.

[0082] FIG. 30B depicts the total number of unique clonotypes per HLA-PEPTIDE target, summed across all donors tested. FIG. 30B discloses SEQ ID NOS 23, 2737, 96, 1424, 2721, 6 and 1, respectively, in order of appearance.

[0083] FIG. 31 shows examples of Jurkat cells expressing A*0201_LLASSILCA- (SEQ ID NO: 2737), A*0201_GVYDGEEHSV- (SEQ ID NO: 96), B*4402_GEMSSNSTAL- (SEQ ID NO: 2721), and A*0101_EVDPIGHLY (SEQ ID NO: 1)-specific TCRs binding to their respective HLA-PEPTIDE targets but not to the control peptide tetramer.

[0084] FIG 32 shows the gating strategy and flow data demonstrating that human CD8+ cells transduced with TCRs identified herein bind to their specific HLA-PEPTIDE target. FIG. 32 discloses SEQ ID NOS 2737 and 2737, respectively, in order of appearance.

[0085] FIG. 33 shows an exemplary lentiviral vector useful for transducing recipient cells with a TCR disclosed herein.

DETAILED DESCRIPTION

[0086] Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodologies by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 4th ed. (2012) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer-defined protocols and conditions unless otherwise noted.

[0087] As used herein, the singular forms "a," "an," and "the" include the plural referents unless the context clearly indicates otherwise. The terms "include," "such as," and the like are intended to convey inclusion without limitation, unless otherwise specifically indicated.

[0088] As used herein, the term "comprising" also specifically includes embodiments "consisting of" and "consisting essentially of" the recited elements, unless specifically indicated otherwise. For example, a multispecific ABP "comprising a diabody" includes a multispecific ABP "consisting of a diabody" and a multispecific ABP "consisting essentially of a diabody."

[0089] The term "about" indicates and encompasses an indicated value and a range above and below that value. In certain embodiments, the term "about" indicates the designated value ± 10%, ± 5%, or ± 1%. In certain embodiments, where applicable, the term "about" indicates the designated value(s) ± one standard deviation of that value(s).

[0090] The term "immunoglobulin" refers to a class of structurally related proteins generally comprising two pairs of polypeptide chains: one pair of light (L) chains and one pair of heavy (H) chains. In an "intact immunoglobulin," all four of these chains are interconnected by disulfide bonds. The structure of immunoglobulins has been well characterized. *See, e.g.,* Paul, *Fundamental Immunology* 7th ed., Ch. 5 (2013) Lippincott Williams & Wilkins, Philadelphia, PA. Briefly, each heavy chain typically comprises a heavy chain variable region (V_H) and a heavy chain constant region (C_H). The heavy chain constant region typically comprises three domains, abbreviated C_{H1}, C_{H2}, and C_{H3}. Each light chain typically comprises a light chain variable region (V_L) and a light chain constant region. The light chain constant region typically comprises one domain, abbreviated C_L.

[0091] The term "antigen binding protein" or "ABP" is used herein in its broadest sense and includes certain types of molecules comprising one or more antigen-binding domains that specifically bind to an antigen or epitope.

[0092] In some embodiments, the ABP comprises an antibody. In some embodiments, the ABP consists of an antibody. In some embodiments, the ABP consists essentially of an antibody. An ABP specifically includes intact antibodies (e.g., intact immunoglobulins), antibody fragments, ABP fragments, and multi-specific antibodies. In some embodiments, the ABP comprises an alternative scaffold. In some embodiments, the ABP consists of an alternative scaffold. In some embodiments, the ABP consists essentially of an alternative scaffold. In some embodiments, the ABP comprises an antibody fragment. In some embodiments, the ABP consists of an antibody fragment. In some embodiments, the ABP consists essentially of an antibody fragment. In some

embodiments, the ABP comprises a TCR or antigen binding portion thereof. In some embodiments, the ABP consists of a TCR or antigen binding portion thereof. In some embodiments, the ABP consists essentially of a TCR or antigen binding portion thereof. In some embodiments, a CAR comprises an ABP. An "HLA-PEPTIDE ABP," "anti-HLA-PEPTIDE ABP," or "HLA-PEPTIDE-specific ABP" is an ABP, as provided herein, which specifically binds to the antigen HLA-PEPTIDE. An ABP includes proteins comprising one or more antigen-binding domains that specifically bind to an antigen or epitope via a variable region, such as a variable region derived from a B cell (e.g., antibody) or T cell (e.g., TCR).

[0093] The term "antibody" herein is used in the broadest sense and includes polyclonal and monoclonal antibodies, including intact antibodies and functional (antigen-binding) antibody fragments, including fragment antigen binding (Fab) fragments, F(ab')2 fragments, Fab' fragments, Fv fragments, recombinant IgG (rIgG) fragments, variable heavy chain (VH) regions capable of specifically binding the antigen, single chain antibody fragments, including single chain variable fragments (scFv), and single domain antibodies (e.g., sdAb, sdFv, nanobody) fragments. The term encompasses genetically engineered and/or otherwise modified forms of immunoglobulins, such as intrabodies, peptibodies, chimeric antibodies, fully human antibodies, humanized antibodies, and heteroconjugate antibodies, multispecific, e.g., bispecific, antibodies, diabodies, triabodies, and tetrabodies, tandem di-scFv, tandem tri-scFv. Unless otherwise stated, the term "antibody" should be understood to encompass functional antibody fragments thereof. The term also encompasses intact or full-length antibodies, including antibodies of any class or sub-class, including IgG and sub-classes thereof, IgM, IgE, IgA, and IgD.

[0094] As used herein, "variable region" refers to a variable nucleotide sequence that arises from a recombination event, for example, it can include a V, J, and/or D region of an immunoglobulin or T cell receptor (TCR) sequence from a B cell or T cell, such as an activated T cell or an activated B cell.

[0095] The term "antigen-binding domain" means the portion of an ABP that is capable of specifically binding to an antigen or epitope. One example of an antigen-binding domain is an antigen-binding domain formed by an antibody V_H -V_L dimer of an ABP. Another example of an antigen-binding domain is an antigen-binding domain formed by diversification of certain loops from the tenth fibronectin type III domain of an Adnectin. An antigen-binding domain can include antibody CDRs 1, 2, and 3 from a heavy chain in that order; and antibody CDRs 1, 2,

and 3 from a light chain in that order. An antigen-binding domain can include TCR CDRs, e.g., αCDR1., αCDR2, αCDR3, βCDR1, βCDR2, and βCDR3. TCR CDRs are described herein.

[0096] The antibody V_H and V_L regions may be further subdivided into regions of hypervariability ("hypervariable regions (HVRs);" also called "complementarity determining regions" (CDRs)) interspersed with regions that are more conserved. The more conserved regions are called framework regions (FRs). Each V_H and V_L generally comprises three antibody CDRs and four FRs, arranged in the following order (from N-terminus to C-terminus): FR1 - CDR1 - FR2 - CDR2 - FR3 - CDR3 - FR4. The antibody CDRs are involved in antigen binding, and influence antigen specificity and binding affinity of the ABP. See Kabat et al., *Sequences of Proteins of Immunological Interest* 5th ed. (1991) Public Health Service, National Institutes of Health, Bethesda, MD, incorporated by reference in its entirety.

[0097] The light chain from any vertebrate species can be assigned to one of two types, called kappa (κ) and lambda (λ), based on the sequence of its constant domain.

[0098] The heavy chain from any vertebrate species can be assigned to one of five different classes (or isotypes): IgA, IgD, IgE, IgG, and IgM. These classes are also designated α, δ, ε, γ, and μ, respectively. The IgG and IgA classes are further divided into subclasses on the basis of differences in sequence and function. Humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0099] The amino acid sequence boundaries of an antibody CDR can be determined by one of skill in the art using any of a number of known numbering schemes, including those described by Kabat et al., *supra* ("Kabat" numbering scheme); Al-Lazikani et al., 1997, *J. Mol. Biol.*, 273:927-948 ("Chothia" numbering scheme); MacCallum et al., 1996, *J. Mol. Biol.* 262:732-745 ("Contact" numbering scheme); Lefranc et al., *Dev. Comp. Immunol.*, 2003, 27:55-77 ("IMGT" numbering scheme); and Honegge and Plückthun, *J. Mol. Biol.*, 2001, 309:657-70 ("AHo" numbering scheme); each of which is incorporated by reference in its entirety.

[00100] Table 14 provides the positions of antibody CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3 as identified by the Kabat and Chothia schemes. For CDR-H1, residue numbering is provided using both the Kabat and Chothia numbering schemes.

[00101] Antibody CDRs may be assigned, for example, using ABP numbering software, such as Abnum, available at www.bioinf.org.uk/abs/abnum/, and described in Abhinandan and Martin, *Immunology*, 2008, 45:3832-3839, incorporated by reference in its entirety.

Table 14. Residues in CDRs according to Kabat and Chothia numbering schemes.

CDR	Kabat	Chothia
L1	L24-L34	L24-L34
L2	L50-L56	L50-L56
L3	L89-L97	L89-L97
H1 (Kabat Numbering)	H31-H35B	H26-H32 or H34*
H1 (Chothia Numbering)	H31-H35	H26-H32
H2	H50-H65	H52-H56
H3	H95-H102	H95-H102

* The C-terminus of CDR-H1, when numbered using the Kabat numbering convention, varies between H32 and H34, depending on the length of the CDR.

[00102] The "EU numbering scheme" is generally used when referring to a residue in an ABP heavy chain constant region (e.g., as reported in Kabat et al., *supra*). Unless stated otherwise, the EU numbering scheme is used to refer to residues in ABP heavy chain constant regions described herein.

[00103] The terms "full length antibody," "intact antibody," and "whole antibody" are used herein interchangeably to refer to an antibody having a structure substantially similar to a naturally occurring antibody structure and having heavy chains that comprise an Fc region. For example, when used to refer to an IgG molecule, a "full length antibody" is an antibody that comprises two heavy chains and two light chains.

[00104] The amino acid sequence boundaries of a TCR CDR can be determined by one of skill in the art using any of a number of known numbering schemes, including but not limited to the IMGT unique numbering, as described by LeFranc, M.-P, Immunol Today. 1997 Nov;18(11):509; Lefranc, M.-P., "IMGT Locus on Focus: A new section of Experimental and Clinical Immunogenetics", Exp. Clin. Immunogenet., 15, 1-7 (1998); Lefranc and Lefranc, The T Cell Receptor FactsBook, ; and M.-P. Lefranc/ Developmental and Comparative Immunology 27 (2003) 55–77, all of which are incorporated by reference.

[00105] An "ABP fragment" comprises a portion of an intact ABP, such as the antigen-binding or variable region of an intact ABP. ABP fragments include, for example, Fv fragments, Fab fragments, $F(ab')_2$ fragments, Fab' fragments, scFv (sFv) fragments, and scFv-Fc fragments. ABP fragments include antibody fragments. Antibody fragments can include Fv fragments, Fab fragments, $F(ab')_2$ fragments, Fab' fragments, scFv (sFv) fragments, scFv-Fc fragments, and TCR fragments.

[00106] "Fv" fragments comprise a non-covalently-linked dimer of one heavy chain variable domain and one light chain variable domain.

[00107] "Fab" fragments comprise, in addition to the heavy and light chain variable domains, the constant domain of the light chain and the first constant domain (C_{H1}) of the heavy chain. Fab fragments may be generated, for example, by recombinant methods or by papain digestion of a full-length ABP.

[00108] "$F(ab')_2$" fragments contain two Fab' fragments joined, near the hinge region, by disulfide bonds. $F(ab')_2$ fragments may be generated, for example, by recombinant methods or by pepsin digestion of an intact ABP. The F(ab') fragments can be dissociated, for example, by treatment with ß-mercaptoethanol.

[00109] "Single-chain Fv" or "sFv" or "scFv" fragments comprise a V_H domain and a V_L domain in a single polypeptide chain. The V_H and V_L are generally linked by a peptide linker. *See* Plückthun A. (1994). Any suitable linker may be used. In some embodiments, the linker is a $(GGGGS)_n$. In some embodiments, n = 1, 2, 3, 4, 5, or 6. *See* ABPs from *Escherichia coli*. In Rosenberg M. & Moore G.P. (Eds.), *The Pharmacology of Monoclonal ABPs* vol. 113 (pp. 269-315). Springer-Verlag, New York, incorporated by reference in its entirety.

[00110] "scFv-Fc" fragments comprise an scFv attached to an Fc domain. For example, an Fc domain may be attached to the C-terminal of the scFv. The Fc domain may follow the V_H or V_L, depending on the orientation of the variable domains in the scFv (i.e., V_H -V_L or V_L -V_H). Any suitable Fc domain known in the art or described herein may be used. In some cases, the Fc domain comprises an IgG4 Fc domain.

[00111] The term "single domain antibody" refers to a molecule in which one variable domain of an ABP specifically binds to an antigen without the presence of the other variable domain. Single domain ABPs, and fragments thereof, are described in Arabi Ghahroudi et al., *FEBS Letters*, 1998, 414:521-526 and Muyldermans et al., *Trends in Biochem. Sci.*, 2001, 26:230-245, each of which is incorporated by reference in its entirety. Single domain ABPs are also known as sdAbs or nanobodies.

[00112] The term "Fc region" or "Fc" means the C-terminal region of an immunoglobulin heavy chain that, in naturally occurring antibodies, interacts with Fc receptors and certain proteins of the complement system. The structures of the Fc regions of various immunoglobulins, and the glycosylation sites contained therein, are known in the art. *See* Schroeder and Cavacini, *J. Allergy Clin. Immunol.*, 2010, 125:S41-52, incorporated by reference in its entirety. The Fc region may be a naturally occurring Fc region, or an Fc region modified as described in the art or elsewhere in this disclosure.

[00113] The term "alternative scaffold" refers to a molecule in which one or more regions may be diversified to produce one or more antigen-binding domains that specifically bind to an antigen or epitope. In some embodiments, the antigen-binding domain binds the antigen or epitope with specificity and affinity similar to that of an ABP. Exemplary alternative scaffolds include those derived from fibronectin (e.g., Adnectins™), the β-sandwich (e.g., iMab), lipocalin (e.g., Anticalins®), EETI-II/AGRP, BPTI/LACI-D1/ITI-D2 (e.g., Kunitz domains), thioredoxin peptide aptamers, protein A (e.g., Affibody®), ankyrin repeats (e.g., DARPins), gamma-B-crystallin/ubiquitin (e.g., Affilins), $CTLD_3$ (e.g., Tetranectins), Fynomers, and (LDLR-A module) (e.g., Avimers). Additional information on alternative scaffolds is provided in Binz et al., *Nat. Biotechnol.*, 2005 23:1257-1268; Skerra, *Current Opin. in Biotech.*, 2007 18:295-304; and Silacci et al., *J. Biol. Chem.*, 2014, 289:14392-14398; each of which is incorporated by reference in its entirety. An alternative scaffold is one type of ABP.

[00114] A "multispecific ABP" is an ABP that comprises two or more different antigen-binding domains that collectively specifically bind two or more different epitopes. The two or more different epitopes may be epitopes on the same antigen (e.g., a single HLA-PEPTIDE molecule expressed by a cell) or on different antigens (e.g., different HLA-PEPTIDE molecules expressed by the same cell, or a HLA-PEPTIDE molecule and a non-HLA-PEPTIDE molecule). In some aspects, a multi-specific ABP binds two different epitopes (i.e., a "bispecific ABP"). In some aspects, a multi-specific ABP binds three different epitopes (i.e., a "trispecific ABP").

[00115] A "monospecific ABP" is an ABP that comprises one or more binding sites that specifically bind to a single epitope. An example of a monospecific ABP is a naturally occurring IgG molecule which, while divalent (i.e., having two antigen-binding domains), recognizes the same epitope at each of the two antigen-binding domains. The binding specificity may be present in any suitable valency.

[00116] The term "monoclonal antibody" refers to an antibody from a population of substantially homogeneous antibodies. A population of substantially homogeneous antibodies comprises antibodies that are substantially similar and that bind the same epitope(s), except for variants that may normally arise during production of the monoclonal antibody. Such variants are generally present in only minor amounts. A monoclonal antibody is typically obtained by a process that includes the selection of a single antibody from a plurality of antibodies. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, yeast clones, bacterial clones, or other

recombinant DNA clones. The selected antibody can be further altered, for example, to improve affinity for the target ("affinity maturation"), to humanize the antibody, to improve its production in cell culture, and/or to reduce its immunogenicity in a subject.

[00117] The term "chimeric antibody" refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[00118] "Humanized" forms of non-human antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human antibody (recipient antibody) in which residues from one or more CDRs are replaced by residues from one or more CDRs of a non-human antibody (donor antibody). The donor antibody can be any suitable non-human antibody, such as a mouse, rat, rabbit, chicken, or non-human primate antibody having a desired specificity, affinity, or biological effect. In some instances, selected framework region residues of the recipient antibody are replaced by the corresponding framework region residues from the donor antibody. Humanized antibodies may also comprise residues that are not found in either the recipient antibody or the donor antibody. Such modifications may be made to further refine antibody function. For further details, *see* Jones et al., *Nature*, 1986, 321:522-525; Riechmann et al., *Nature*, 1988, 332:323-329; and Presta, *Curr. Op. Struct. Biol.*, 1992, 2:593-596, each of which is incorporated by reference in its entirety.

[00119] A "human antibody" is one which possesses an amino acid sequence corresponding to that of an antibody produced by a human or a human cell, or derived from a non-human source that utilizes a human antibody repertoire or human antibody -encoding sequences (e.g., obtained from human sources or designed *de novo*). Human antibodies specifically exclude humanized antibodies.

[00120] "Affinity" refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g., an ABP) and its binding partner (e.g., an antigen or epitope). Unless indicated otherwise, as used herein, "affinity" refers to intrinsic binding affinity, which reflects a 1:1 interaction between members of a binding pair (e.g., ABP and antigen or epitope). The affinity of a molecule X for its partner Y can be represented by the dissociation equilibrium constant (K_D). The kinetic components that contribute to the dissociation equilibrium constant are described in more detail below. Affinity can be measured by common methods known in the art, including those described herein, such as surface plasmon resonance (SPR) technology (e.g., BIACORE®) or biolayer interferometry (e.g., FORTEBIO®).

[00121] With regard to the binding of an ABP to a target molecule, the terms "bind," "specific binding," "specifically binds to," "specific for," "selectively binds," and "selective for" a particular antigen (e.g., a polypeptide target) or an epitope on a particular antigen mean binding that is measurably different from a non-specific or non-selective interaction (e.g., with a non-target molecule). Specific binding can be measured, for example, by measuring binding to a target molecule and comparing it to binding to a non-target molecule. Specific binding can also be determined by competition with a control molecule that mimics the epitope recognized on the target molecule. In that case, specific binding is indicated if the binding of the ABP to the target molecule is competitively inhibited by the control molecule. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 50% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 40% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 30% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 20% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 10% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 1% of the affinity for HLA-PEPTIDE. In some aspects, the affinity of a HLA-PEPTIDE ABP for a non-target molecule is less than about 0.1% of the affinity for HLA-PEPTIDE.

[00122] The term "k_d" (sec^{-1}), as used herein, refers to the dissociation rate constant of a particular ABP - antigen interaction. This value is also referred to as the k_{off} value.

[00123] The term "k_a" ($M^{-1} \times sec^{-1}$), as used herein, refers to the association rate constant of a particular ABP -antigen interaction. This value is also referred to as the k_{on} value.

[00124] The term "K_D" (M), as used herein, refers to the dissociation equilibrium constant of a particular ABP -antigen interaction. $K_D = k_d/k_a$. In some embodiments, the affinity of an ABP is described in terms of the K_D for an interaction between such ABP and its antigen. For clarity, as known in the art, a smaller K_D value indicates a higher affinity interaction, while a larger K_D value indicates a lower affinity interaction.

[00125] The term "K_A" (M^{-1}), as used herein, refers to the association equilibrium constant of a particular ABP-antigen interaction. $K_A = k_a/k_d$.

[00126] An "immunoconjugate" is an ABP conjugated to one or more heterologous molecule(s), such as a therapeutic (cytokine, for example) or diagnostic agent.

[00127] "Fc effector functions" refer to those biological activities mediated by the Fc region of an ABP having an Fc region, which activities may vary depending on isotype. Examples of ABP effector functions include C1q binding to activate complement dependent cytotoxicity (CDC), Fc receptor binding to activate ABP-dependent cellular cytotoxicity (ADCC), and ABP dependent cellular phagocytosis (ADCP).

[00128] When used herein in the context of two or more ABPs, the term "competes with" or "cross-competes with" indicates that the two or more ABPs compete for binding to an antigen (e.g., HLA-PEPTIDE). In one exemplary assay, HLA-PEPTIDE is coated on a surface and contacted with a first HLA-PEPTIDE ABP, after which a second HLA-PEPTIDE ABP is added. In another exemplary assay, a first HLA-PEPTIDE ABP is coated on a surface and contacted with HLA-PEPTIDE, and then a second HLA-PEPTIDE ABP is added. If the presence of the first HLA-PEPTIDE ABP reduces binding of the second HLA-PEPTIDE ABP, in either assay, then the ABPs compete with each other. The term "competes with" also includes combinations of ABPs where one ABP reduces binding of another ABP, but where no competition is observed when the ABPs are added in the reverse order. However, in some embodiments, the first and second ABPs inhibit binding of each other, regardless of the order in which they are added. In some embodiments, one ABP reduces binding of another ABP to its antigen by at least 25%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, or at least 95%. A skilled artisan can select the concentrations of the ABPs used in the competition assays based on the affinities of the ABPs for HLA-PEPTIDE and the valency of the ABPs. The assays described in this definition are illustrative, and a skilled artisan can utilize any suitable assay to determine if ABPs compete with each other. Suitable assays are described, for example, in Cox et al., "Immunoassay Methods," in *Assay Guidance Manual [Internet]*, Updated December 24, 2014 (www.ncbi.nlm.nih.gov/books/NBK92434/; accessed September 29, 2015); Silman et al., *Cytometry*, 2001, 44:30-37; and Finco et al., *J. Pharm. Biomed. Anal.*, 2011, 54:351-358; each of which is incorporated by reference in its entirety.

[00129] The term "epitope" means a portion of an antigen that specifically binds to an ABP. Epitopes frequently consist of surface-accessible amino acid residues and/or sugar side chains and may have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that the

binding to the former but not the latter may be lost in the presence of denaturing solvents. An epitope may comprise amino acid residues that are directly involved in the binding, and other amino acid residues, which are not directly involved in the binding. The epitope to which an ABP binds can be determined using known techniques for epitope determination such as, for example, testing for ABP binding to HLA-PEPTIDE variants with different point-mutations, or to chimeric HLA-PEPTIDE variants.

[00130] Percent "identity" between a polypeptide sequence and a reference sequence, is defined as the percentage of amino acid residues in the polypeptide sequence that are identical to the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, MEGALIGN (DNASTAR), CLUSTALW, CLUSTAL OMEGA, or MUSCLE software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[00131] A "conservative substitution" or a "conservative amino acid substitution," refers to the substitution an amino acid with a chemically or functionally similar amino acid. Conservative substitution tables providing similar amino acids are well known in the art. By way of example, the groups of amino acids provided in Tables 15-17 are, in some embodiments, considered conservative substitutions for one another.

[00132] **Table 15.** Selected groups of amino acids that are considered conservative substitutions for one another, in certain embodiments.

Acidic Residues	D and E
Basic Residues	K, R, and H
Hydrophilic Uncharged Residues	S, T, N, and Q
Aliphatic Uncharged Residues	G, A, V, L, and I
Non-polar Uncharged Residues	C, M, and P
Aromatic Residues	F, Y, and W

[00133] **Table 16.** Additional selected groups of amino acids that are considered conservative substitutions for one another, in certain embodiments.

Group 1	A, S, and T
Group 2	D and E
Group 3	N and Q
Group 4	R and K

Group 5	I, L, and M
Group 6	F, Y, and W

[00134] **Table 17.** Further selected groups of amino acids that are considered conservative substitutions for one another, in certain embodiments.

Group A	A and G
Group B	D and E
Group C	N and Q
Group D	R, K, and H
Group E	I, L, M, V
Group F	F, Y, and W
Group G	S and T
Group H	C and M

[00135] Additional conservative substitutions may be found, for example, in Creighton, *Proteins: Structures and Molecular Properties* 2nd ed. (1993) W. H. Freeman & Co., New York, NY. An ABP generated by making one or more conservative substitutions of amino acid residues in a parent ABP is referred to as a "conservatively modified variant."

[00136] The term "amino acid" refers to the twenty common naturally occurring amino acids. Naturally occurring amino acids include alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C); glutamic acid (Glu; E), glutamine (Gln; Q), Glycine (Gly; G); histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

[00137] The term "vector," as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Certain vectors are capable of directing the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as "expression vectors."

[00138] The terms "host cell," "host cell line," and "host cell culture" are used interchangeably and refer to cells into which an exogenous nucleic acid has been introduced, and the progeny of such cells. Host cells include "transformants" (or "transformed cells") and "transfectants" (or "transfected cells"), which each include the primary transformed or transfected cell and progeny derived therefrom. Such progeny may not be completely identical in nucleic acid content to a parent cell, and may contain mutations.

[00139] The term "treating" (and variations thereof such as "treat" or "treatment") refers to clinical intervention in an attempt to alter the natural course of a disease or condition in a subject in need thereof. Treatment can be performed both for prophylaxis and during the course of clinical pathology. Desirable effects of treatment include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis.

[00140] As used herein, the term "therapeutically effective amount" or "effective amount" refers to an amount of an ABP or pharmaceutical composition provided herein that, when administered to a subject, is effective to treat a disease or disorder.

[00141] As used herein, the term "subject" means a mammalian subject. Exemplary subjects include humans, monkeys, dogs, cats, mice, rats, cows, horses, camels, goats, rabbits, and sheep. In certain embodiments, the subject is a human. In some embodiments the subject has a disease or condition that can be treated with an ABP provided herein. In some aspects, the disease or condition is a cancer. In some aspects, the disease or condition is a viral infection.

[00142] The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic or diagnostic products (e.g., kits) that contain information about the indications, usage, dosage, administration, combination therapy, contraindications and/or warnings concerning the use of such therapeutic or diagnostic products.

[00143] The term "tumor" refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder" and "tumor" are not mutually exclusive as referred to herein. The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In some embodiments, the cell proliferative disorder is a cancer. In some aspects, the tumor is a solid tumor. In some aspects, the tumor is a hematologic malignancy.

[00144] The term "pharmaceutical composition" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective in treating a subject, and which contains no additional components which are unacceptably toxic to the subject in the amounts provided in the pharmaceutical composition.

[00145] The terms "modulate" and "modulation" refer to reducing or inhibiting or, alternatively, activating or increasing, a recited variable.

[00146] The terms "increase" and "activate" refer to an increase of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

[00147] The terms "reduce" and "inhibit" refer to a decrease of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

[00148] The term "agonize" refers to the activation of receptor signaling to induce a biological response associated with activation of the receptor. An "agonist" is an entity that binds to and agonizes a receptor.

[00149] The term "antagonize" refers to the inhibition of receptor signaling to inhibit a biological response associated with activation of the receptor. An "antagonist" is an entity that binds to and antagonizes a receptor.

[00150] The terms "nucleic acids" and "polynucleotides" may be used interchangeably herein to refer to polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides can include, but are not limited to coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA, isolated RNA, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. Exemplary modified nucleotides include, e.g., 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-substituted adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthioN6- isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2- thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine.

ISOLATED HLA-PEPTIDE TARGETS

[00151] The major histocompatibility complex (MHC) is a complex of antigens encoded by a group of linked loci, which are collectively termed H-2 in the mouse and HLA in humans. The two principal classes of the MHC antigens, class I and class II, each comprise a set of cell surface glycoproteins which play a role in determining tissue type and transplant compatibility. In transplantation reactions, cytotoxic T-cells (CTLs) respond mainly against class I glycoproteins, while helper T-cells respond mainly against class II glycoproteins.

[00152] Human major histocompatibility complex (MHC) class I molecules, referred to interchangeably herein as HLA Class I molecules, are expressed on the surface of nearly all cells. These molecules function in presenting peptides which are mainly derived from endogenously synthesized proteins to CD8+ T cells via an interaction with the alpha-beta T-cell receptor. The class I MHC molecule comprises a heterodimer composed of a 46-kDa α chain which is non-covalently associated with the 12-kDa light chain beta-2 microglobulin. The α chain generally comprises α1 and α2 domains which form a groove for presenting an HLA-restricted peptide, and an α3 plasma membrane-spanning domain which interacts with the CD8 co-receptor of T-cells. FIG. 1 (prior art) depicts the general structure of a Class I HLA molecule.

[00153] Class I MHC-restricted peptides (also referred to interchangeably herein as HLA-restricted antigens, HLA-restricted peptides, MHC-restricted antigens, restricted peptides, or peptides) generally bind to the heavy chain alpha1-alpha2 groove via about two or three anchor residues that interact with corresponding binding pockets in the MHC molecule. The beta-2 microglobulin chain plays an important role in MHC class I intracellular transport, peptide binding, and conformational stability. For most class I molecules, the formation of a heterotrimeric complex of the MHC class I heavy chain, peptide (self, non-self, and/or antigenic) and beta-2 microglobulin leads to protein maturation and export to the cell-surface.

[00154] Binding of a given HLA subtype to an HLA-restricted peptide forms a complex with a unique and novel surface that can be specifically recognized by an ABP such as, e.g., a TCR on a T cell or an antibody or antigen-binding fragment thereof. HLA complexed with an HLA-restricted peptide is referred to herein as an HLA-PEPTIDE or HLA-PEPTIDE target. In some cases the restricted peptide is located in the α1/α2 groove of the HLA molecule. In some cases the restricted peptide is bound to the α1/α2 groove of the HLA

molecule via about two or three anchor residues that interact with corresponding binding pockets in the HLA molecule.

[00155] Accordingly, provided herein are antigens comprising HLA-PEPTIDE targets. The HLA-PEPTIDE targets may comprise a specific HLA-restricted peptide having a defined amino acid sequence complexed with a specific HLA subtype.

[00156] HLA-PEPTIDE targets identified herein may be useful for cancer immunotherapy. In some embodiments, the HLA-PEPTIDE targets identified herein are presented on the surface of a tumor cell. The HLA-PEPTIDE targets identified herein may be expressed by tumor cells in a human subject. The HLA-PEPTIDE targets identified herein may be expressed by tumor cells in a population of human subjects. For example, the HLA-PEPTIDE targets identified herein may be shared antigens which are commonly expressed in a population of human subjects with cancer.

[00157] The HLA-PEPTIDE targets identified herein may have a prevalence with an individual tumor type The prevalence with an individual tumor type may be about 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%. The prevalence with an individual tumor type may be about 0.1%-100%, 0.2-50%, 0.5-25%, or 1-10%.

[00158] Preferably, HLA-PEPTIDE targets are not generally expressed in most normal tissues. For example, the HLA-PEPTIDE targets may in some cases not be expressed in tissues in the Genotype-Tissue Expression (GTEx) Project, or may in some cases be expressed only in immune privileged or non-essential tissues. Exemplary immune privileged or non-essential tissues include testis, minor salivary glands, the endocervix, and the thyroid. In some cases, an HLA-PEPTIDE target may be deemed to not be expressed on essential tissues or non-immune privileged tissues if the median expression of a gene from which the restricted peptide is derived is less than 0.5 RPKM (Reads Per Kilobase of transcript per Million napped reads) across GTEx samples, if the gene is not expressed with greater than 10

RPKM across GTEX samples, if the gene was expressed at >=5 RPKM in no more two samples across all essential tissue samples, or any combination thereof.

Exemplary HLA Class I subtypes of the HLA-PEPTIDE targets

[00159] In humans, there are many MHC haplotypes (referred to interchangeably herein as MHC subtypes, HLA subtypes, MHC types, and HLA types). Exemplary HLA subtypes include, by way of example only, HLA-A2, HLA-A1, HLA-A3, HLA-A11, HLA-A23, HLA-A24, HLA-A25, HLA-A26, HLA-A28, HLA-A29, HLA-A30, HLA-A31, HLA-A32, HLA-A33, HLA-A34, HLA-68, HLA-B7, HLA-B8, HLA-B40, HLA-B44, HLA-B13, HLA-B15, HLA-B-18, HLA-B27, HLA-B35, HLA-B37, HLA-B38, HLA-B39, HLA-B45, HLA-B46, HLA-B49, HLA-B51, HLA-B54, HLA-B55, HLA-B56, HLA-B57, HLA-B58, HLA-C*01, HLA-C*02, HLA-C*03, HLA-C*04, HLA-C*05, HLA-C*06, HLA-C*07, HLA-C*12, HLA-C*14, HLA-C*16, HLA-Cw8, and all 4 digit and 6 digit subtypes thereof. As is known to those skilled in the art there are allelic variants of the above HLA types, all of which are encompassed by the present invention. A full list of HLA Class Alleles can be found on http://hla.alleles.org/alleles/. For example, a full list of HLA Class I Alleles can be found on http://hla.alleles.org/alleles/class1.html.

HLA-restricted peptides

[00160] The HLA-restricted peptides (referred to interchangeably herein) as "restricted peptides" can be peptide fragments of tumor-specific genes, e.g., cancer-specific genes. Preferably, the cancer-specific genes are expressed in cancer samples. Genes which are aberrantly expressed in cancer samples can be identified through a database. Exemplary databases include, by way of example only, The Cancer Genome Atlas (TCGA) Research Network: http://cancergenome.nih.gov/; the International Cancer Genome Consortium: https://dcc.icgc.org/. In some embodiments, the cancer-specific gene has an observed expression of at least 10 RPKM in at least 5 samples from the TCGA database. The cancer-specific gene may have an observable bimodal distribution

[00161] The cancer-specific gene may have an observed expression of greater than 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 TPM in at least one TCGA tumor tissue. In preferred embodiments, the cancer-specific gene has an observed expression of greater than 100 TPM in at least one TCGA tumor tissue. In some cases, the cancer specific gene has an observed bimodal distribution of expression across TCGA samples. Without wishing to be bound by theory, such bimodal expression pattern is consistent with a biological model in which there

is minimal expression at baseline in all tumor samples and higher expression in a subset of tumors experiencing epigenetic dysregulation.

[00162] Preferably, the cancer-specific gene is not generally expressed in most normal tissues. For example, the cancer-specific gene may in some cases not be expressed in tissues in the Genotype-Tissue Expression (GTEx) Project, or may in some cases be expressed in immune privileged or non-essential tissues. Exemplary immune privileged or non-essential tissues include testis, minor salivary glands, the endocervix, and thyroid. In some cases, an cancer-specific gene may be deemed to not be expressed an essential tissues or non-immune privileged tissue if the median expression of the cancer-specific gene is less than 0.5 RPKM (Reads Per Kilobase of transcript per Million napped reads) across GTEx samples, if the gene is not expressed with greater than 10 RPKM across GTEX samples, if the gene was expressed at >=5 RPKM in no more two samples across all essential tissue samples, or any combination thereof.

[00163] In some embodiments, the cancer-specific gene meets the following criteria by assessment of the GTEx: (1) median GTEx expression in brain, heart, or lung is less than 0.1 transcripts per million (TPM), with no one sample exceeding 5 TPM, (2) median GTEx expression in other essential organs (excluding testis, thyroid, minor salivary gland) is less than 2 TPM with no one sample exceeding 10 TPM.

[00164] In some embodiments, the cancer-specific gene is not likely expressed in immune cells generally, e.g., is not an interferon family gene, is not an eye-related gene, not an olfactory or taste receptor gene, and is not a gene related to the circadian cycle (e.g., not a CLOCK, PERIOD, CRY gene)

[00165] The restricted peptide preferably may be presented on the surface of a tumor.

[00166] The restricted peptides may have a size of about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, or about 15 amino molecule residues, and any range derivable therein. In particular embodiments, the restricted peptide has a size of about 8, about 9, about 10, about 11, or about 12 amino molecule residues. The restricted peptide may be about 5-15 amino acids in length, preferably may be about 7-12 amino acids in length, or more preferably may be about 8-11 amino acids in length.

Exemplary HLA-PEPTIDE targets

[00167] Exemplary HLA-PEPTIDE targets are shown in Table A. In each row of Table A the HLA allele and corresponding HLA-restricted peptide sequence of each complex is shown. The

peptide sequence can consist of the respective sequence shown in each row of Table A. Alternatively the peptide sequence can comprise the respective sequence shown in each row of Table A. Alternatively the peptide sequence can consist essentially of the respective sequence shown in each row of Table A.

[00168] In some embodiments, the HLA-PEPTIDE target is a target as shown in Table A.

[00169] In some embodiments, the HLA-PEPTIDE target is a target shown in Table A, with the proviso that the isolated HLA-PEPTIDE target is not any one of Target nos. 6364-6369, 6386-6389, 6500, 6521-6524, or 6578 and is not an HLA-PEPTIDE target found in Table B or Table C.

[00170] In some embodiments, the HLA-restricted peptide is not from a gene selected from WT1 or MART1.

[00171] HLA Class I molecules which do not associate with a restricted peptide ligand are generally unstable. Accordingly, the association of the restricted peptide with the α1/α2 groove of the HLA molecule may stabilize the non-covalent association of the β2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype.

[00172] Stability of the non-covalent association of the β2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype can be determined using any suitable means. For example, such stability may be assessed by dissolving insoluble aggregates of HLA molecules in high concentrations of urea (e.g., about 8M urea), and determining the ability of the HLA molecule to refold in the presence of the restricted peptide during urea removal, e.g., urea removal by dialysis. Such refolding approaches are described in, e.g., Proc. Natl. Acad. Sci. USA Vol. 89, pp. 3429-3433, April 1992, hereby incorporated by reference.

[00173] For other example, such stability may be assessed using conditional HLA Class I ligands. Conditional HLA Class I ligands are generally designed as short restricted peptides which stabilize the association of the β2 and α subunits of the HLA Class I molecule by binding to the α1/α2 groove of the HLA molecule, and which contain one or more amino acid modifications allowing cleavage of the restricted peptide upon exposure to a conditional stimulus. Upon cleavage of the conditional ligand, the β2 and α-subunits of the HLA molecule dissociate, unless such conditional ligand is exchanged for a restricted peptide which binds to the α1/α2 groove and stabilizes the HLA molecule. Conditional ligands can be designed by introducing amino acid modifications in either known HLA peptide ligands or

in predicted high-affinity HLA peptide ligands. For HLA alleles for which structural information is available, water-accessibility of side chains may also be used to select positions for introduction of the amino acid modifications. Use of conditional HLA ligands may be advantageous by allowing the batch preparation of stable HLA-peptide complexes which may be used to interrogate test restricted peptides in a high throughput manner. Conditional HLA Class I ligands, and methods of production, are described in, e.g., Proc Natl Acad Sci U S A. 2008 Mar 11; 105(10): 3831–3836; Proc Natl Acad Sci U S A. 2008 Mar 11; 105(10): 3825–3830; J Exp Med. 2018 May 7; 215(5): 1493–1504; Choo, J. A. L. et al. Bioorthogonal cleavage and exchange of major histocompatibility complex ligands by employing azobenzene-containing peptides. Angew Chem Int Ed Engl 53, 13390–13394 (2014); Amore, A. et al. Development of a Hypersensitive Periodate-Cleavable Amino Acid that is Methionine- and Disulfide-Compatible and its Application in MHC Exchange Reagents for T Cell Characterisation. ChemBioChem 14, 123–131 (2012); Rodenko, B. et al. Class I Major Histocompatibility Complexes Loaded by a Periodate Trigger. J Am Chem Soc 131, 12305–12313 (2009); and Chang, C. X. L. et al. Conditional ligands for Asian HLA variants facilitate the definition of CD8+ T-cell responses in acute and chronic viral diseases. Eur J Immunol 43, 1109–1120 (2013). These references are incorporated by reference in their entirety.

[00174] Accordingly, in some embodiments, the ability of an HLA-restricted peptide described herein, e.g., described in Table A, to stabilize the association of the β2- and α-subunits of the HLA molecule, is assessed by performing a conditional ligand mediated-exchange reaction and assay for HLA stability. HLA stability can be assayed using any suitable method, including, e.g., mass spectrometry analysis, immunoassays (e.g., ELISA), size exclusion chromatography, and HLA multimer staining followed by flow cytometry assessment of T cells.

[00175] Other exemplary methods for assessing stability of the non- covalent association of the β2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype include peptide exchange using dipeptides. Peptide exchange using dipeptides has been described in, e.g., Proc Natl Acad Sci U S A. 2013 Sep 17, 110(38):15383-8; Proc Natl Acad Sci U S A. 2015 Jan 6, 112(1):202-7, which is hereby incorporated by reference.

[00176] Provided herein are useful antigens comprising an HLA-PEPTIDE target. The HLA-PEPTIDE targets may comprise a specific HLA-restricted peptide having a defined amino acid sequence complexed with a specific HLA subtype allele.

[00177] The HLA-PEPTIDE target may be isolated and/or in substantially pure form. For example, the HLA-PEPTIDE targets may be isolated from their natural environment, or may be produced by means of a technical process. In some cases, the HLA-PEPTIDE target is provided in a form which is substantially free of other peptides or proteins.

[00178] THE HLA-PEPTIDE targets may be presented in soluble form, and optionally may be a recombinant HLA-PEPTIDE target complex. The skilled artisan may use any suitable method for producing and purifying recombinant HLA-PEPTIDE targets. Suitable methods include, e.g., use of E. coli expression systems, insect cells, and the like. Other methods include synthetic production, e.g., using cell free systems. An exemplary suitable cell free system is described in WO2017089756, which is hereby incorporated by reference in its entirety.

[00179] Also provided herein are compositions comprising an HLA-PEPTIDE target.

[00180] In some cases, the composition comprises an HLA-PEPTIDE target attached to a solid support. Exemplary solid supports include, but are not limited to, beads, wells, membranes, tubes, columns, plates, sepharose, magnetic beads, and chips. Exemplary solid supports are described in, e.g., Catalysts 2018, 8, 92; doi:10.3390/catal8020092, which is hereby incorporated by reference in its entirety.

[00181] The HLA-PEPTIDE target may be attached to the solid support by any suitable methods known in the art. In some cases, the HLA-PEPTIDE target is covalently attached to the solid support.

[00182] In some cases, the HLA-PEPTIDE target is attached to the solid support by way of an affinity binding pair. Affinity binding pairs generally involved specific interactions between two molecules. A ligand having an affinity for its binding partner molecule can be covalently attached to the solid support, and thus used as bait for immobilizing Common affinity binding pairs include, e.g., streptavidin and biotin, avidin and biotin; polyhistidine tags with metal ions such as copper, nickel, zinc, and cobalt; and the like.

[00183] The HLA-PEPTIDE target may comprise a detectable label.

[00184] Pharmaceutical compositions comprising HLA-PEPTIDE targets.

[00185] The composition comprising an HLA-PEPTIDE target may be a pharmaceutical composition. Such a composition may comprise multiple HLA-PEPTIDE targets. Exemplary

pharmaceutical compositions are described herein. The composition may be capable of eliciting an immune response. The composition may comprise an adjuvant. Suitable adjuvants include, but are not limited to 1018 ISS, alum, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel vector system, PLG microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon (Aquila Biotech, Worcester, Mass., USA) which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox. Quil or Superfos. Adjuvants such as incomplete Freund's or GM-CSF are useful. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Dupuis M, et al., Cell Immunol. 1998; 186(1):18-27; Allison A C; Dev Biol Stand. 1998; 92:3-11). Also cytokines can be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-alpha), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12) (Gabrilovich D I, et al., J Immunother Emphasis Tumor Immunol. 1996 (6):414-418).

HLA-PEPTIDE ABPs

[00186] Also provided herein are ABPs that specifically bind to HLA-PEPTIDE target as disclosed herein.

[00187] The HLA-PEPTIDE target may be expressed on the surface of any suitable target cell including a tumor cell.

[00188] The ABP can specifically bind to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA-restricted peptide is located in the peptide binding groove of an $\alpha 1/\alpha 2$ heterodimer portion of the HLA Class I molecule.

[00189] In some aspects, the ABP does not bind HLA class I in the absence of HLA-restricted peptide. In some aspects, the ABP does not bind HLA-restricted peptide in the absence of human MHC class I. In some aspects, the ABP binds tumor cells presenting human MHC class I

being complexed with HLA - restricted peptide, optionally wherein the HLA restricted peptide is a tumor antigen characterizing the cancer.

[00190] An ABP can bind to each portion of an HLA-PEPTIDE complex (i.e., HLA and peptide representing each portion of the complex), which when bound together form a novel target and protein surface for interaction with and binding by the ABP, distinct from a surface presented by the peptide alone or HLA subtype alone. Generally the novel target and protein surface formed by binding of HLA to peptide does not exist in the absence of each portion of the HLA-PEPTIDE complex.

[00191] An ABP can be capable of specifically binding a complex comprising HLA and an HLA-restricted peptide (HLA-PEPTIDE), e.g., derived from a tumor. In some aspects, the ABP does not bind HLA in an absence of the HLA-restricted peptide derived from the tumor. In some aspects, the ABP does not bind the HLA-restricted peptide derived from the tumor in an absence of HLA. In some aspects, the ABP binds a complex comprising HLA and HLA-restricted peptide when naturally presented on a cell such as a tumor cell.

[00192] In some embodiments, an ABP provided herein modulates binding of HLA-PEPTIDE to one or more ligands of HLA-PEPTIDE.

[00193] The ABP may specifically bind to any one of the HLA-PEPTIDE targets as disclosed in Table A. In some embodiments, the ABP specifically binds to a HLA-PEPTIDE target which is a target shown in Table A, with the proviso that the isolated HLA-PEPTIDE target is not any one of Target nos. 6364-6369, 6386-6389, 6500, 6521-6524, or 6578 and is not an HLA-PEPTIDE target found in Table B or Table C. In some embodiments, the HLA-restricted peptide is not from a gene selected from WT1 or MART1.

[00194] In more particular embodiments, the ABP specifically binds to an HLA-PEPTIDE target selected from any one of HLA subtype A*02:01 complexed with an HLA-restricted peptide comprising the sequence LLASSILCA, HLA subtype A*01:01 complexed with an HLA-restricted peptide comprising the sequence EVDPIGHLY, HLA subtype B*44:02 complexed with an HLA-restricted peptide comprising the sequence GEMSSNSTAL , HLA subtype A*02:01 complexed with an HLA-restricted peptide comprising the sequence GVYDGEEHSV , HLA subtype *01:01 complexed with an HLA-restricted peptide comprising the sequence EVDPIGHVY , and HLA subtype HLA-A*01:01 complexed with an HLA-restricted peptide comprising the sequence NTDNNLAVY .

[00195] In some embodiments, an ABP is an ABP that competes with an illustrative ABP provided herein. In some aspects, the ABP that competes with the illustrative ABP provided herein binds the same epitope as an illustrative ABP provided herein.

[00196] In some embodiments, the ABPs described herein are referred to herein as "variants." In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining ABPs. In some embodiments, a variant is derived from any of the sequences provided herein, wherein one or more conservative amino acid substitutions are made. In some embodiments, a variant is derived from any of the sequences provided herein, wherein one or more nonconservative amino acid substitutions are made. Conservative amino acid substitutions are described herein. Exemplary nonconservative amino acid substitutions include those described in J Immunol. 2008 May 1;180(9):6116-31, which is hereby incorporated by reference in its entirety. In preferred embodiments, the non-conservative amino acid substitution does not interfere with or inhibit the biological activity of the functional variant. In yet more preferred embodiments, the non-conservative amino acid substitution enhances the biological activity of the functional variant, such that the biological activity of the functional variant is increased as compared to the parent ABP.

ABPs comprising an antibody or antigen-binding fragment thereof

[00197] An ABP may comprise an antibody or antigen-binding fragment thereof.

[00198] In some embodiments, the ABPs provided herein comprise a light chain. In some aspects, the light chain is a kappa light chain. In some aspects, the light chain is a lambda light chain.

[00199] In some embodiments, the ABPs provided herein comprise a heavy chain. In some aspects, the heavy chain is an IgA. In some aspects, the heavy chain is an IgD. In some aspects, the heavy chain is an IgE. In some aspects, the heavy chain is an IgG. In some aspects, the heavy chain is an IgM. In some aspects, the heavy chain is an IgG1. In some aspects, the heavy chain is an IgG2. In some aspects, the heavy chain is an IgG3. In some aspects, the heavy chain is an IgG4. In some aspects, the heavy chain is an IgA1. In some aspects, the heavy chain is an IgA2.

[00200] In some embodiments, the ABPs provided herein comprise an antibody fragment. In some embodiments, the ABPs provided herein consist of an antibody fragment. In some embodiments, the ABPs provided herein consist essentially of an antibody fragment. In some aspects, the ABP fragment is an Fv fragment. In some aspects, the ABP fragment is a Fab fragment. In some aspects, the ABP fragment is a $F(ab')_2$ fragment. In some aspects, the ABP fragment is a Fab' fragment. In some aspects, the ABP fragment is an scFv (sFv) fragment. In some aspects, the ABP fragment is an scFv-Fc fragment. In some aspects, the ABP fragment is a fragment of a single domain ABP.

[00201] In some embodiments, an ABP fragment provided herein is derived from an illustrative ABP provided herein. In some embodiments, an ABP fragments provided herein is not derived from an illustrative ABP provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining ABP fragments.

[00202] In some embodiments, an ABP fragment provided herein retains the ability to bind the HLA-PEPTIDE target, as measured by one or more assays or biological effects described herein. In some embodiments, an ABP fragment provided herein retains the ability to prevent HLA-PEPTIDE from interacting with one or more of its ligands, as described herein.

[00203] In some embodiments, the ABPs provided herein are monoclonal ABPs. In some embodiments, the ABPs provided herein are polyclonal ABPs.

[00204] In some embodiments, the ABPs provided herein comprise a chimeric ABP. In some embodiments, the ABPs provided herein consist of a chimeric ABP. In some embodiments, the ABPs provided herein consist essentially of a chimeric ABP. In some embodiments, the ABPs provided herein comprise a humanized ABP. In some embodiments, the ABPs provided herein consist of a humanized ABP. In some embodiments, the ABPs provided herein consist essentially of a humanized ABP. In some embodiments, the ABPs provided herein comprise a human ABP. In some embodiments, the ABPs provided herein consist of a human ABP. In some embodiments, the ABPs provided herein consist essentially of a human ABP.

[00205] In some embodiments, the ABPs provided herein comprise an alternative scaffold. In some embodiments, the ABPs provided herein consist of an alternative scaffold. In some embodiments, the ABPs provided herein consist essentially of an alternative scaffold. Any suitable alternative scaffold may be used. In some aspects, the alternative scaffold is selected from an Adnectin™, an iMab, an Anticalin®, an EETI-II/AGRP, a Kunitz domain, a thioredoxin peptide aptamer, an Affibody®, a DARPin, an Affilin, a Tetranectin, a Fynomer, and an Avimer.

[00206] Also disclosed herein is an isolated humanized, human, or chimeric ABP that competes for binding to an HLA-PEPTIDE with an ABP disclosed herein.

[00207] Also disclosed herein is an isolated humanized, human, or chimeric ABP that binds an HLA-PEPTIDE epitope bound by an ABP disclosed herein.

[00208] In certain aspects, an ABP comprises a human Fc region comprising at least one modification that reduces binding to a human Fc receptor.

[00209] It is known that when an ABP is expressed in cells, the ABP is modified after translation. Examples of the posttranslational modification include cleavage of lysine at the C terminus of the heavy chain by a carboxypeptidase; modification of glutamine or glutamic acid at the N terminus of the heavy chain and the light chain to pyroglutamic acid by pyroglutamylation; glycosylation; oxidation; deamidation; and glycation, and it is known that such posttranslational modifications occur in various ABPs (*See* Journal of Pharmaceutical Sciences, 2008, Vol. 97, p. 2426-2447, incorporated by reference in its entirety). In some embodiments, an ABP is an ABP or antigen-binding fragment thereof which has undergone posttranslational modification. Examples of an ABP or antigen-binding fragment thereof which have undergone posttranslational modification include an ABP or antigen-binding fragments thereof which have undergone pyroglutamylation at the N terminus of the heavy chain variable region and/or deletion of lysine at the C terminus of the heavy chain. It is known in the art that such posttranslational modification due to pyroglutamylation at the N terminus and deletion of lysine at the C terminus does not have any influence on the activity of the ABP or fragment thereof (Analytical Biochemistry, 2006, Vol. 348, p. 24-39, incorporated by reference in its entirety).

Monospecific and Multispecific HLA-PEPTIDE ABPs

[00210] In some embodiments, the ABPs provided herein are monospecific ABPs.

[00211] In some embodiments, the ABPs provided herein are multispecific ABPs.

[00212] In some embodiments, a multispecific ABP provided herein binds more than one antigen. In some embodiments, a multispecific ABP binds 2 antigens. In some embodiments, a multispecific ABP binds 3 antigens. In some embodiments, a multispecific ABP binds 4 antigens. In some embodiments, a multispecific ABP binds 5 antigens.

[00213] In some embodiments, a multispecific ABP provided herein binds more than one epitope on a HLA-PEPTIDE antigen. In some embodiments, a multispecific ABP binds 2

epitopes on a HLA-PEPTIDE antigen. In some embodiments, a multispecific ABP binds 3 epitopes on a HLA-PEPTIDE antigen.

[00214] Many multispecific ABP constructs are known in the art, and the ABPs provided herein may be provided in the form of any suitable multispecific suitable construct.

[00215] In some embodiments, the multispecific ABP comprises an immunoglobulin comprising at least two different heavy chain variable regions each paired with a common light chain variable region (i.e., a "common light chain ABP"). The common light chain variable region forms a distinct antigen-binding domain with each of the two different heavy chain variable regions. *See* Merchant et al., *Nature Biotechnol.*, 1998, 16:677-681, incorporated by reference in its entirety.

[00216] In some embodiments, the multispecific ABP comprises an immunoglobulin comprising an ABP or fragment thereof attached to one or more of the N- or C-termini of the heavy or light chains of such immunoglobulin. *See* Coloma and Morrison, *Nature Biotechnol.*, 1997, 15:159-163, incorporated by reference in its entirety. In some aspects, such ABP comprises a tetravalent bispecific ABP.

[00217] In some embodiments, the multispecific ABP comprises a hybrid immunoglobulin comprising at least two different heavy chain variable regions and at least two different light chain variable regions. *See* Milstein and Cuello, *Nature*, 1983, 305:537-540; and Staerz and Bevan, *Proc. Natl. Acad. Sci. USA*, 1986, 83:1453-1457; each of which is incorporated by reference in its entirety.

[00218] In some embodiments, the multispecific ABP comprises immunoglobulin chains with alterations to reduce the formation of side products that do not have multispecificity. In some aspects, the ABPs comprise one or more "knobs-into-holes" modifications as described in U.S. Pat. No. 5,731,168, incorporated by reference in its entirety.

[00219] In some embodiments, the multispecific ABP comprises immunoglobulin chains with one or more electrostatic modifications to promote the assembly of Fc hetero-multimers. *See* WO 2009/089004, incorporated by reference in its entirety.

[00220] In some embodiments, the multispecific ABP comprises a bispecific single chain molecule. *See* Traunecker et al., *EMBO J.*, 1991, 10:3655-3659; and Gruber et al., *J. Immunol.*, 1994, 152:5368-5374; each of which is incorporated by reference in its entirety.

[00221] In some embodiments, the multispecific ABP comprises a heavy chain variable domain and a light chain variable domain connected by a polypeptide linker, where the length of

the linker is selected to promote assembly of multispecific ABP with the desired multispecificity. For example, monospecific scFvs generally form when a heavy chain variable domain and light chain variable domain are connected by a polypeptide linker of more than 12 amino acid residues. *See* U.S. Pat. Nos. 4,946,778 and 5,132,405, each of which is incorporated by reference in its entirety. In some embodiments, reduction of the polypeptide linker length to less than 12 amino acid residues prevents pairing of heavy and light chain variable domains on the same polypeptide chain, thereby allowing pairing of heavy and light chain variable domains from one chain with the complementary domains on another chain. The resulting ABP therefore has multispecificity, with the specificity of each binding site contributed by more than one polypeptide chain. Polypeptide chains comprising heavy and light chain variable domains that are joined by linkers between 3 and 12 amino acid residues form predominantly dimers (termed diabodies). With linkers between 0 and 2 amino acid residues, trimers (termed triabodies) and tetramers (termed tetrabodies) are favored. However, the exact type of oligomerization appears to depend on the amino acid residue composition and the order of the variable domain in each polypeptide chain (e.g., V_H-linker-V_L vs. V_L-linker-V_H), in addition to the linker length. A skilled person can select the appropriate linker length based on the desired multispecificity.

Fc Region and Variants

[00222] In certain embodiments, an ABP provided herein comprises an Fc region. An Fc region can be wild-type or a variant thereof. In certain embodiments, an ABP provided herein comprises an Fc region with one or more amino acid substitutions, insertions, or deletions in comparison to a naturally occurring Fc region. In some aspects, such substitutions, insertions, or deletions yield ABP with altered stability, glycosylation, or other characteristics. In some aspects, such substitutions, insertions, or deletions yield a glycosylated ABP.

[00223] A "variant Fc region" or "engineered Fc region" comprises an amino acid sequence that differs from that of a native-sequence Fc region by virtue of at least one amino acid modification, preferably one or more amino acid substitution(s). Preferably, the variant Fc region has at least one amino acid substitution compared to a native-sequence Fc region or to the Fc region of a parent polypeptide, e.g., from about one to about ten amino acid substitutions, and preferably from about one to about five amino acid substitutions in a native-sequence Fc region or in the Fc region of the parent polypeptide. The variant Fc region herein will preferably possess at least about 80% homology with a native-sequence Fc region and/or with an Fc region

of a parent polypeptide, and most preferably at least about 90% homology therewith, more preferably at least about 95% homology therewith.

[00224] The term "Fc-region-comprising ABP" refers to an ABP that comprises an Fc region. The C-terminal lysine (residue 447 according to the EU numbering system) of the Fc region may be removed, for example, during purification of the ABP or by recombinant engineering the nucleic acid encoding the ABP. Accordingly, an ABP having an Fc region can comprise an ABP with or without K447.

[00225] In some aspects, the Fc region of an ABP provided herein is modified to yield an ABP with altered affinity for an Fc receptor, or an ABP that is more immunologically inert. In some embodiments, the ABP variants provided herein possess some, but not all, effector functions. Such ABPs may be useful, for example, when the half-life of the ABP is important *in vivo*, but when certain effector functions (e.g., complement activation and ADCC) are unnecessary or deleterious.

[00226] In some embodiments, the Fc region of an ABP provided herein is a human IgG4 Fc region comprising one or more of the hinge stabilizing mutations S228P and L235E. *See* Aalberse et al., *Immunology*, 2002, 105:9-19, incorporated by reference in its entirety. In some embodiments, the IgG4 Fc region comprises one or more of the following mutations: E233P, F234V, and L235A. *See* Armour et al., *Mol. Immunol.*, 2003, 40:585-593, incorporated by reference in its entirety. In some embodiments, the IgG4 Fc region comprises a deletion at position G236.

[00227] In some embodiments, the Fc region of an ABP provided herein is a human IgG1 Fc region comprising one or more mutations to reduce Fc receptor binding. In some aspects, the one or more mutations are in residues selected from S228 (e.g., S228A), L234 (e.g., L234A), L235 (e.g., L235A), D265 (e.g., D265A), and N297 (e.g., N297A). In some aspects, the ABP comprises a PVA236 mutation. PVA236 means that the amino acid sequence ELLG, from amino acid position 233 to 236 of IgG1 or EFLG of IgG4, is replaced by PVA. *See* U.S. Pat. No. 9,150,641, incorporated by reference in its entirety.

[00228] In some embodiments, the Fc region of an ABP provided herein is modified as described in Armour et al., *Eur. J. Immunol.*, 1999, 29:2613-2624; WO 1999/058572; and/or U.K. Pat. App. No. 98099518; each of which is incorporated by reference in its entirety.

[00229] In some embodiments, the Fc region of an ABP provided herein is a human IgG2 Fc region comprising one or more of mutations A330S and P331S.

[00230] In some embodiments, the Fc region of an ABP provided herein has an amino acid substitution at one or more positions selected from 238, 265, 269, 270, 297, 327 and 329. *See* U.S. Pat. No. 6,737,056, incorporated by reference in its entirety. Such Fc mutants include Fc mutants with substitutions at two or more of amino acid positions 265, 269, 270, 297 and 327, including the so-called "DANA" Fc mutant with substitution of residues 265 and 297 with alanine. *See* U.S. Pat. No. 7,332,581, incorporated by reference in its entirety. In some embodiments, the ABP comprises an alanine at amino acid position 265. In some embodiments, the ABP comprises an alanine at amino acid position 297.

[00231] In certain embodiments, an ABP provided herein comprises an Fc region with one or more amino acid substitutions which improve ADCC, such as a substitution at one or more of positions 298, 333, and 334 of the Fc region. In some embodiments, an ABP provided herein comprises an Fc region with one or more amino acid substitutions at positions 239, 332, and 330, as described in Lazar et al., *Proc. Natl. Acad. Sci. USA*, 2006,103:4005-4010, incorporated by reference in its entirety.

[00232] In some embodiments, an ABP provided herein comprises one or more alterations that improves or diminishes C1q binding and/or CDC. *See* U.S. Pat. No. 6,194,551; WO 99/51642; and Idusogie et al., *J. Immunol.*, 2000, 164:4178-4184; each of which is incorporated by reference in its entirety.

[00233] In some embodiments, an ABP provided herein comprises one or more alterations to increase half-life. ABPs with increased half-lives and improved binding to the neonatal Fc receptor (FcRn) are described, for example, in Hinton et al., *J. Immunol.*, 2006, 176:346-356; and U.S. Pat. Pub. No. 2005/0014934; each of which is incorporated by reference in its entirety. Such Fc variants include those with substitutions at one or more of Fc region residues: 238, 250, 256, 265, 272, 286, 303, 305, 307, 311, 312, 314, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424, 428, and 434 of an IgG.

[00234] In some embodiments, an ABP provided herein comprises one or more Fc region variants as described in U.S. Pat. Nos. 7,371,826 5,648,260, and 5,624,821; Duncan and Winter, *Nature*, 1988, 322:738-740; and WO 94/29351; each of which is incorporated by reference in its entirety.

Antibodies specific for A*02:01_LLASSILCA (G7)

[00235] In some aspects, provided herein are ABPs comprising antibodies or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA

Class I molecule of the HLA-PEPTIDE target is HLA subtype A*02:01 and the HLA-restricted peptide of the HLA-PEPTIDE target comprises the sequence LLASSILCA (SEQ ID NO: 2737) ("G7").

Sequences of G7-specific antibodies

[00236] The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise one or more sequences, as described in further detail.

CDRs

[00237] The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise one or more antibody complementarity determining region (CDR) sequences, e.g., may comprise three heavy chain CDRs (CDR-H1, CDR-H2, CDR-H3) and three light chain CDRs (CDR-L1, CDR-L2, CDR-L3). The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a particular heavy chain CDR3 (CDR-H3) sequence and a particular light chain CDR3 (CDR-L3) sequence. In some embodiments, the CDR-H3 is SEQ ID NO: 3030 and the CDR-L3 is SEQ ID NO: 3048. In some embodiments, the CDR-H3 is SEQ ID NO: 3025 and the CDR-L3 is SEQ ID NO: 3043. In some embodiments, the CDR-H3 is SEQ ID NO: 3026 and the CDR-L3 is SEQ ID NO: 3044. In some embodiments, the CDR-H3 is SEQ ID NO: 3027 and the CDR-L3 is SEQ ID NO: 3045. In some embodiments, the CDR-H3 is SEQ ID NO: 3028 and the CDR-L3 is SEQ ID NO: 3046. In some embodiments, the CDR-H3 is SEQ ID NO: 3029 and the CDR-L3 is SEQ ID NO: 3047. In some embodiments, the CDR-H3 is SEQ ID NO: 3031 and the CDR-L3 is SEQ ID NO: 3049. In some embodiments, the CDR-H3 is SEQ ID NO: 3032 and the CDR-L3 is SEQ ID NO: 3050.

[00238] The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3010, a CDR-H2 that is SEQ ID NO: 3017, a CDR-H3 that is SEQ ID NO: 3025, a CDR-L1 that is SEQ ID NO: 3033, a CDR-L2 that is SEQ ID NO: 2970, and a CDR-L3 that is SEQ ID NO: 3043. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3011, a CDR-H2 that is SEQ ID NO: 3018, a CDR-H3 that is SEQ ID NO: 3026, a CDR-L1 that is SEQ ID NO: 3034, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 3044. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3012, a CDR-H2 that is SEQ ID NO: 3019, a CDR-H3 that is SEQ ID NO: 3027, a CDR-L1 that is SEQ ID NO: 3035, a CDR-L2 that is SEQ ID NO: 3039, and a CDR-L3 that is SEQ ID NO: 3045. The ABP specific for A*02:01_

LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3013, a CDR-H2 that is SEQ ID NO: 3020, a CDR-H3 that is SEQ ID NO: 3028, a CDR-L1 that is SEQ ID NO: 3036, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 3046. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 2879, a CDR-H2 that is SEQ ID NO: 3021, a CDR-H3 that is SEQ ID NO: 3029, a CDR-L1 that is SEQ ID NO: 2934, a CDR-L2 that is SEQ ID NO: 3040, and a CDR-L3 that is SEQ ID NO: 3047. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3014, a CDR-H2 that is SEQ ID NO: 3022, a CDR-H3 that is SEQ ID NO: 3030, a CDR-L1 that is SEQ ID NO: 3037, a CDR-L2 that is SEQ ID NO: 3041, and a CDR-L3 that is SEQ ID NO: 3048. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3015, a CDR-H2 that is SEQ ID NO: 3023, a CDR-H3 that is SEQ ID NO: 3031, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 3042, and a CDR-L3 that is SEQ ID NO: 3049. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a CDR-H1 that is SEQ ID NO: 3016, a CDR-H2 that is SEQ ID NO: 3024, a CDR-H3 that is SEQ ID NO: 3032, a CDR-L1 that is SEQ ID NO: 3038, a CDR-L2 that is SEQ ID NO: 3041, and a CDR-L3 that is SEQ ID NO: 3050.

VL

[00239] The ABP specific for *02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VL sequence. The VL sequence may be SEQ ID NO: 3002. The VL sequence may be SEQ ID NO: 3003. The VL sequence may be SEQ ID NO: 3004. The VL sequence may be SEQ ID NO: 3005. The VL sequence may be SEQ ID NO: 3006. The VL sequence may be SEQ ID NO: 3007. The VL sequence may be SEQ ID NO: 3008. The VL sequence may be SEQ ID NO: 3009.

VH

[00240] The ABP specific for *02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence. The VH sequence may be SEQ ID NO: 2994. The VH sequence may be SEQ ID NO: 2995. The VH sequence may be SEQ ID NO: 2996. The VH sequence may be SEQ ID NO: 2997. The VH sequence may be SEQ ID NO: 2998. The VH sequence may be SEQ ID NO: 2999. The VH sequence may be SEQ ID NO: 3000. The VH sequence may be SEQ ID NO: 3001.

VH-VL combinations

[00241] The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2994 and a VL sequence that is SEQ ID NO: 3002. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2995 and a VL sequence that is SEQ ID NO: 3003. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2996 and a VL sequence that is SEQ ID NO: 3004. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2997 and a VL sequence that is SEQ ID NO: 3005. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2998 and a VL sequence that is SEQ ID NO: 3006. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 2999 and a VL sequence that is SEQ ID NO: 3007. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 3000 and a VL sequence that is SEQ ID NO: 3008. The ABP specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a VH sequence that is SEQ ID NO: 3001 and a VL sequence that is SEQ ID NO: 3009.

Antibodies specific for A*01:01_ NTDNNLAVY (G2)

[00242] In some aspects, provided herein are ABPs comprising antibodies or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA Class I molecule of the HLA-PEPTIDE target is HLA subtype A*01:01 and the HLA-restricted peptide of the HLA-PEPTIDE target comprises the sequence NTDNNLAVY (SEQ ID NO: 23) ("G2").

Sequences of G2-specific antibodies

[00243] The ABP specific for A*01:01_ NTDNNLAVY (SEQ ID NO: 23) may comprise one or more sequences, as described in further detail.

CDRs

[00244] The ABP specific for A*01:01_ NTDNNLAVY (SEQ ID NO: 23) may comprise one or more antibody complementarity determining region (CDR) sequences, e.g., may comprise three heavy chain CDRs (CDR-H1, CDR-H2, CDR-H3) and three light chain CDRs (CDR-L1, CDR-L2, CDR-L3). The ABP specific for A*01:01_ NTDNNLAVY (SEQ ID

NO: 23) may comprise a particular heavy chain CDR3 (CDR-H3) sequence and a particular light chain CDR3 (CDR-L3) sequence. In some embodiments, the CDR-H3 is SEQ ID NO: 2902 and the CDR-L3 is SEQ ID NO: 2971. In some embodiments, the CDR-H3 is SEQ ID NO: 2903 and the CDR-L3 is SEQ ID NO: 2972. In some embodiments, the CDR-H3 is SEQ ID NO: 2903 and the CDR-L3 is SEQ ID NO: 2973. In some embodiments, the CDR-H3 is SEQ ID NO: 2904 and the CDR-L3 is SEQ ID NO: 2974. In some embodiments, the CDR-H3 is SEQ ID NO: 2905 and the CDR-L3 is SEQ ID NO: 2975. In some embodiments, the CDR-H3 is SEQ ID NO: 2906 and the CDR-L3 is SEQ ID NO: 2976. In some embodiments, the CDR-H3 is SEQ ID NO: 2907 and the CDR-L3 is SEQ ID NO: 2976. In some embodiments, the CDR-H3 is SEQ ID NO: 2908 and the CDR-L3 is SEQ ID NO: 2977. In some embodiments, the CDR-H3 is SEQ ID NO: 2909 and the CDR-L3 is SEQ ID NO: 2972. In some embodiments, the CDR-H3 is SEQ ID NO: 2910 and the CDR-L3 is SEQ ID NO: 2978. In some embodiments, the CDR-H3 is SEQ ID NO: 2911 and the CDR-L3 is SEQ ID NO: 2976. In some embodiments, the CDR-H3 is SEQ ID NO: 2912 and the CDR-L3 is SEQ ID NO: 2978. In some embodiments, the CDR-H3 is SEQ ID NO: 2913 and the CDR-L3 is SEQ ID NO: 2979. In some embodiments, the CDR-H3 is SEQ ID NO: 2914 and the CDR-L3 is SEQ ID NO: 2980. In some embodiments, the CDR-H3 is SEQ ID NO: 2903 and the CDR-L3 is SEQ ID NO: 2981. In some embodiments, the CDR-H3 is SEQ ID NO: 2915 and the CDR-L3 is SEQ ID NO: 2982. In some embodiments, the CDR-H3 is SEQ ID NO: 2916 and the CDR-L3 is SEQ ID NO: 2973. In some embodiments, the CDR-H3 is SEQ ID NO: 2917 and the CDR-L3 is SEQ ID NO: 2972. In some embodiments, the CDR-H3 is SEQ ID NO: 2917 and the CDR-L3 is SEQ ID NO: 2972. In some embodiments, the CDR-H3 is SEQ ID NO: 2918 and the CDR-L3 is SEQ ID NO: 2974. In some embodiments, the CDR-H3 is SEQ ID NO: 2919 and the CDR-L3 is SEQ ID NO: 2983. In some embodiments, the CDR-H3 is SEQ ID NO: 2920 and the CDR-L3 is SEQ ID NO: 2984. In some embodiments, the CDR-H3 is SEQ ID NO: 2921 and the CDR-L3 is SEQ ID NO: 2972. In some embodiments, the CDR-H3 is SEQ ID NO: 2922 and the CDR-L3 is SEQ ID NO: 2985. In some embodiments, the CDR-H3 is SEQ ID NO: 2923 and the CDR-L3 is SEQ ID NO: 2986. In some embodiments, the CDR-H3 is SEQ ID NO: 2924 and the CDR-L3 is SEQ ID NO: 2987. In some embodiments, the CDR-H3 is SEQ ID NO: 2925 and the CDR-L3 is SEQ ID NO: 2973. In some embodiments, the CDR-H3 is SEQ ID NO: 2926 and the CDR-L3 is SEQ ID NO: 2988. In some embodiments, the CDR-H3 is SEQ ID NO: 2927 and the CDR-

L3 is SEQ ID NO: 2989. In some embodiments, the CDR-H3 is SEQ ID NO: 2928 and the CDR-L3 is SEQ ID NO: 2981. In some embodiments, the CDR-H3 is SEQ ID NO: 2929 and the CDR-L3 is SEQ ID NO: 2990. In some embodiments, the CDR-H3 is SEQ ID NO: 2930 and the CDR-L3 is SEQ ID NO: 2989. In some embodiments, the CDR-H3 is SEQ ID NO: 2931 and the CDR-L3 is SEQ ID NO: 2991. In some embodiments, the CDR-H3 is SEQ ID NO: 2932 and the CDR-L3 is SEQ ID NO: 2992. In some embodiments, the CDR-H3 is SEQ ID NO: 2933 and the CDR-L3 is SEQ ID NO: 2993.

[00245] The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2851, a CDR-H2 that is SEQ ID NO: 2880, a CDR-H3 that is SEQ ID NO: 2902, a CDR-L1 that is SEQ ID NO: 2934, a CDR-L2 that is SEQ ID NO: 2955, and a CDR-L3 that is SEQ ID NO: 2971. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2852, a CDR-H2 that is SEQ ID NO: 2881, a CDR-H3 that is SEQ ID NO: 2903, a CDR-L1 that is SEQ ID NO: 2935, a CDR-L2 that is SEQ ID NO: 2956, and a CDR-L3 that is SEQ ID NO: 2972. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2853, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2903, a CDR-L1 that is SEQ ID NO: 2936, a CDR-L2 that is SEQ ID NO: 2957, and a CDR-L3 that is SEQ ID NO: 2973. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2854, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2904, a CDR-L1 that is SEQ ID NO: 2937, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2974. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2855, a CDR-H2 that is SEQ ID NO: 2883, a CDR-H3 that is SEQ ID NO: 2905, a CDR-L1 that is SEQ ID NO: 2937, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2975. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2855, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2906, a CDR-L1 that is SEQ ID NO: 2938, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2976. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2856, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2907, a CDR-L1 that is SEQ ID NO: 2939, a CDR-L2 that is SEQ ID NO: 2959, and a CDR-L3 that is SEQ ID NO: 2976. The ABP specific for

A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2857, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2908, a CDR-L1 that is SEQ ID NO: 2940, a CDR-L2 that is SEQ ID NO: 2960, and a CDR-L3 that is SEQ ID NO: 2977. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2858, a CDR-H2 that is SEQ ID NO: 2884, a CDR-H3 that is SEQ ID NO: 2909, a CDR-L1 that is SEQ ID NO: 2935, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2972. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2859, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2910, a CDR-L1 that is SEQ ID NO: 2941, a CDR-L2 that is SEQ ID NO: 2961, and a CDR-L3 that is SEQ ID NO: 2978. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2852, a CDR-H2 that is SEQ ID NO: 2885, a CDR-H3 that is SEQ ID NO: 2911, a CDR-L1 that is SEQ ID NO: 2942, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2976. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2860, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2912, a CDR-L1 that is SEQ ID NO: 2943, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2978. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2861, a CDR-H2 that is SEQ ID NO: 2886, a CDR-H3 that is SEQ ID NO: 2913, a CDR-L1 that is SEQ ID NO: 2944, a CDR-L2 that is SEQ ID NO: 2963, and a CDR-L3 that is SEQ ID NO: 2979. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2862, a CDR-H2 that is SEQ ID NO: 2887, a CDR-H3 that is SEQ ID NO: 2914, a CDR-L1 that is SEQ ID NO: 2945, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2980. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2855, a CDR-H2 that is SEQ ID NO: 2888, a CDR-H3 that is SEQ ID NO: 2903, a CDR-L1 that is SEQ ID NO: 2941, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2981. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2855, a CDR-H2 that is SEQ ID NO: 2889, a CDR-H3 that is SEQ ID NO: 2915, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2982. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a

CDR-H1 that is SEQ ID NO: 2863, a CDR-H2 that is SEQ ID NO: 2883, a CDR-H3 that is SEQ ID NO: 2916, a CDR-L1 that is SEQ ID NO: 2947, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2973. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2856, a CDR-H2 that is SEQ ID NO: 2890, a CDR-H3 that is SEQ ID NO: 2917, a CDR-L1 that is SEQ ID NO: 2934, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2972. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2864, a CDR-H2 that is SEQ ID NO: 2891, a CDR-H3 that is SEQ ID NO: 2917, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 2964, and a CDR-L3 that is SEQ ID NO: 2972. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2865, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2918, a CDR-L1 that is SEQ ID NO: 2941, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2974. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2866, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2919, a CDR-L1 that is SEQ ID NO: 2948, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2983. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2867, a CDR-H2 that is SEQ ID NO: 2892, a CDR-H3 that is SEQ ID NO: 2920, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2984. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2868, a CDR-H2 that is SEQ ID NO: 2893, a CDR-H3 that is SEQ ID NO: 2921, a CDR-L1 that is SEQ ID NO: 2949, a CDR-L2 that is SEQ ID NO: 2965, and a CDR-L3 that is SEQ ID NO: 2972. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2869, a CDR-H2 that is SEQ ID NO: 2894, a CDR-H3 that is SEQ ID NO: 2922, a CDR-L1 that is SEQ ID NO: 2950, a CDR-L2 that is SEQ ID NO: 2966, and a CDR-L3 that is SEQ ID NO: 2985. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2870, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2923, a CDR-L1 that is SEQ ID NO: 2943, a CDR-L2 that is SEQ ID NO: 2967, and a CDR-L3 that is SEQ ID NO: 2986. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO:

2871, a CDR-H2 that is SEQ ID NO: 2895, a CDR-H3 that is SEQ ID NO: 2924, a CDR-L1 that is SEQ ID NO: 2951, a CDR-L2 that is SEQ ID NO: 2968, and a CDR-L3 that is SEQ ID NO: 2987. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2872, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2925, a CDR-L1 that is SEQ ID NO: 2952, a CDR-L2 that is SEQ ID NO: 2969, and a CDR-L3 that is SEQ ID NO: 2973. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2873, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2926, a CDR-L1 that is SEQ ID NO: 2943, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2988. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2852, a CDR-H2 that is SEQ ID NO: 2882, a CDR-H3 that is SEQ ID NO: 2927, a CDR-L1 that is SEQ ID NO: 2935, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2989. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2874, a CDR-H2 that is SEQ ID NO: 2896, a CDR-H3 that is SEQ ID NO: 2928, a CDR-L1 that is SEQ ID NO: 2938, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2981. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2875, a CDR-H2 that is SEQ ID NO: 2897, a CDR-H3 that is SEQ ID NO: 2929, a CDR-L1 that is SEQ ID NO: 2953, a CDR-L2 that is SEQ ID NO: 2961, and a CDR-L3 that is SEQ ID NO: 2990. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2876, a CDR-H2 that is SEQ ID NO: 2898, a CDR-H3 that is SEQ ID NO: 2930, a CDR-L1 that is SEQ ID NO: 2941, a CDR-L2 that is SEQ ID NO: 2962, and a CDR-L3 that is SEQ ID NO: 2989. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2877, a CDR-H2 that is SEQ ID NO: 2899, a CDR-H3 that is SEQ ID NO: 2931, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 2964, and a CDR-L3 that is SEQ ID NO: 2991. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2878, a CDR-H2 that is SEQ ID NO: 2900, a CDR-H3 that is SEQ ID NO: 2932, a CDR-L1 that is SEQ ID NO: 2946, a CDR-L2 that is SEQ ID NO: 2958, and a CDR-L3 that is SEQ ID NO: 2992. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a CDR-H1 that is SEQ ID NO: 2879, a CDR-H2 that is SEQ ID NO: 2901, a CDR-H3 that is

SEQ ID NO: 2933, a CDR-L1 that is SEQ ID NO: 2954, a CDR-L2 that is SEQ ID NO: 2970, and a CDR-L3 that is SEQ ID NO: 2993.

VL

[00246] The ABP specific for A*01:01_ NTDNNLAVY (SEQ ID NO: 23) may comprise a VL sequence. The VL sequence may be SEQ ID NO: 2816. The VL sequence may be SEQ ID NO: 2817. The VL sequence may be SEQ ID NO: 2818. The VL sequence may be SEQ ID NO: 2819. The VL sequence may be SEQ ID NO: 2820. The VL sequence may be SEQ ID NO: 2821. The VL sequence may be SEQ ID NO: 2822. The VL sequence may be SEQ ID NO: 2823. The VL sequence may be SEQ ID NO: 2824. The VL sequence may be SEQ ID NO: 2825. The VL sequence may be SEQ ID NO: 2826. The VL sequence may be SEQ ID NO: 2827. The VL sequence may be SEQ ID NO: 2828. The VL sequence may be SEQ ID NO: 2829. The VL sequence may be SEQ ID NO: 2830. The VL sequence may be SEQ ID NO: 2831. The VL sequence may be SEQ ID NO: 2832. The VL sequence may be SEQ ID NO: 2833. The VL sequence may be SEQ ID NO: 2834. The VL sequence may be SEQ ID NO: 2835. The VL sequence may be SEQ ID NO: 2836. The VL sequence may be SEQ ID NO: 2837. The VL sequence may be SEQ ID NO: 2838. The VL sequence may be SEQ ID NO: 2839. The VL sequence may be SEQ ID NO: 2840. The VL sequence may be SEQ ID NO: 2841. The VL sequence may be SEQ ID NO: 2842. The VL sequence may be SEQ ID NO: 2843. The VL sequence may be SEQ ID NO: 2844. The VL sequence may be SEQ ID NO: 2845. The VL sequence may be SEQ ID NO: 2846. The VL sequence may be SEQ ID NO: 2847. The VL sequence may be SEQ ID NO: 2848. The VL sequence may be SEQ ID NO: 2849. The VL sequence may be SEQ ID NO: 2850.

VH

[00247] The ABP specific for A*01:01_ NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence. The VH sequence may be SEQ ID NO: 2781. The VH sequence may be SEQ ID NO: 2782. The VH sequence may be SEQ ID NO: 2783. The VH sequence may be SEQ ID NO: 2784. The VH sequence may be SEQ ID NO: 2785. The VH sequence may be SEQ ID NO: 2786. The VH sequence may be SEQ ID NO: 2787. The VH sequence may be SEQ ID NO: 2788. The VH sequence may be SEQ ID NO: 2789. The VH sequence may be SEQ ID NO: 2790. The VH sequence may be SEQ ID NO: 2791. The VH sequence may be SEQ ID NO: 2792. The VH sequence may be SEQ ID NO: 2793. The VH sequence may be SEQ

ID NO: 2794. The VH sequence may be SEQ ID NO: 2795. The VH sequence may be SEQ ID NO: 2796. The VH sequence may be SEQ ID NO: 2797. The VH sequence may be SEQ ID NO: 2798. The VH sequence may be SEQ ID NO: 2799. The VH sequence may be SEQ ID NO: 2800. The VH sequence may be SEQ ID NO: 2801. The VH sequence may be SEQ ID NO: 2802. The VH sequence may be SEQ ID NO: 2803. The VH sequence may be SEQ ID NO: 2804. The VH sequence may be SEQ ID NO: 2805. The VH sequence may be SEQ ID NO: 2806. The VH sequence may be SEQ ID NO: 2807. The VH sequence may be SEQ ID NO: 2808. The VH sequence may be SEQ ID NO: 2809. The VH sequence may be SEQ ID NO: 2810. The VH sequence may be SEQ ID NO: 2811. The VH sequence may be SEQ ID NO: 2812. The VH sequence may be SEQ ID NO: 2813. The VH sequence may be SEQ ID NO: 2814. The VH sequence may be SEQ ID NO: 2815.

VH-VL combinations

[00248] The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2781 and a VL sequence that is SEQ ID NO: 2816. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2782 and a VL sequence that is SEQ ID NO: 2817. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2783 and a VL sequence that is SEQ ID NO: 2818. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2784 and a VL sequence that is SEQ ID NO: 2819. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2785 and a VL sequence that is SEQ ID NO: 2820. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2786 and a VL sequence that is SEQ ID NO: 2821. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2787 and a VL sequence that is SEQ ID NO: 2822. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2788 and a VL sequence that is SEQ ID NO: 2823. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2789 and a VL sequence that is SEQ ID NO: 2824. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2790 and a VL sequence that is SEQ ID NO: 2825. The ABP specific for

A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2791 and a VL sequence that is SEQ ID NO: 2826. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2792 and a VL sequence that is SEQ ID NO: 2827. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2793 and a VL sequence that is SEQ ID NO: 2828. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2794 and a VL sequence that is SEQ ID NO: 2829. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2795 and a VL sequence that is SEQ ID NO: 2830. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2796 and a VL sequence that is SEQ ID NO: 2831. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2797 and a VL sequence that is SEQ ID NO: 2832. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2798 and a VL sequence that is SEQ ID NO: 2833. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2799 and a VL sequence that is SEQ ID NO: 2834. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2800 and a VL sequence that is SEQ ID NO: 2835. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2801 and a VL sequence that is SEQ ID NO: 2836. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2802 and a VL sequence that is SEQ ID NO: 2837. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2803 and a VL sequence that is SEQ ID NO: 2838. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2804 and a VL sequence that is SEQ ID NO: 2839. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2805 and a VL sequence that is SEQ ID NO: 2840. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2806 and a VL sequence that is SEQ ID NO: 2841. The ABP specific for

A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2807 and a VL sequence that is SEQ ID NO: 2842. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2808 and a VL sequence that is SEQ ID NO: 2843. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2809 and a VL sequence that is SEQ ID NO: 2844. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2810 and a VL sequence that is SEQ ID NO: 2845. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2811 and a VL sequence that is SEQ ID NO: 2846. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2812 and a VL sequence that is SEQ ID NO: 2847. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2813 and a VL sequence that is SEQ ID NO: 2848. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2814 and a VL sequence that is SEQ ID NO: 2849. The ABP specific for A*01:01_NTDNNLAVY (SEQ ID NO: 23) may comprise a VH sequence that is SEQ ID NO: 2815 and a VL sequence that is SEQ ID NO: 2850.

Receptors

[00249] Among the provided ABPs, e.g., HLA-PEPTIDE ABPs, are receptors. The receptors can include antigen receptors and other chimeric receptors that specifically bind an HLA-PEPTIDE target disclosed herein. The receptor may be a T cell receptor (TCR). The receptor may be a chimeric antigen receptor (CAR).

[00250] TCRs can be soluble or membrane-bound. Among the antigen receptors are functional non-TCR antigen receptors, such as chimeric antigen receptors (CARs). Also provided are cells expressing the receptors and uses thereof in adoptive cell therapy, such as treatment of diseases and disorders associated with HLA-PEPTIDE expression, including cancer.

[00251] Exemplary antigen receptors, including CARs, and methods for engineering and introducing such receptors into cells, include those described, for example, in international patent application publication numbers WO200014257, WO2013126726, WO2012/129514, WO2014031687, WO2013/166321, WO2013/071154, WO2013/123061 U.S. patent application

publication numbers US2002131960, US2013287748, US20130149337, U.S. Pat. Nos. 6,451,995, 7,446,190, 8,252,592, 8,339,645, 8,398,282, 7,446,179, 6,410,319, 7,070,995, 7,265,209, 7,354,762, 7,446,191, 8,324,353, and 8,479,118, and European patent application number EP2537416, and/or those described by Sadelain et al., Cancer Discov. 2013 April; 3(4): 388-398; Davila et al. (2013) PLoS ONE 8(4): e61338; Turtle et al., Curr. Opin. Immunol., 2012 October; 24(5): 633-39; Wu et al., Cancer, 2012 Mar. 18(2): 160-75. In some aspects, the antigen receptors include a CAR as described in U.S. Pat. No. 7,446,190, and those described in International Patent Application Publication No.: WO/2014055668 A1. Exemplary of the CARs include CARs as disclosed in any of the aforementioned publications, such as WO2014031687, U.S. Pat. No. 8,339,645, U.S. Pat. No. 7,446,179, US 2013/0149337, U.S. Pat. No. 7,446,190, U.S. Pat. No. 8,389,282, e.g., and in which the antigen-binding portion, e.g., scFv, is replaced by an antibody, e.g., as provided herein.

[00252] Among the chimeric receptors are chimeric antigen receptors (CARs). The chimeric receptors, such as CARs, generally include an extracellular antigen binding domain that includes, is, or is comprised within, one of the provided anti-HLA-PEPTIDE ABPs such as anti-HLA-PEPTIDE antibodies. Thus, the chimeric receptors, e.g., CARs, typically include in their extracellular portions one or more HLA-PEPTIDE-ABPs, such as one or more antigen-binding fragment, domain, or portion, or one or more antibody variable domains, and/or antibody molecules, such as those described herein. In some embodiments, the CAR includes a HLA-PEPTIDE-binding portion or portions of the ABP (e.g., antibody) molecule, such as a variable heavy (VH) chain region and/or variable light (VL) chain region of the antibody, e.g., an scFv antibody fragment.

TCRs

[00253] In an aspect, the ABPs provided herein, e.g., ABPs that specifically bind HLA-PEPTIDE targets disclosed herein, include T cell receptors (TCRs). The TCRs may be isolated and purified.

[00254] In a majority of T-cells, the TCR is a heterodimer polypeptide having an alpha (α) chain and beta- (β) chain, encoded by TRA and TRB, respectively. The alpha chain generally comprises an alpha variable region, encoded by TRAV, an alpha joining region, encoded by TRAJ, and an alpha constant region, encoded by TRAC. The beta chain generally comprises a beta variable region, encoded by TRBV, a beta diversity region, encoded by TRBD, a beta joining region, encoded by TRBJ, and a beta constant region, encoded by TRBC. The TCR-

alpha chain is generated by VJ recombination, and the beta chain receptor is generated by V(D)J recombination. Additional TCR diversity stems from junctional diversity. Several bases may be deleted and others added (called N and P nucleotides) at each of the junctions. In a minority of T-cells, the TCRs include gamma and delta chains. The TCR gamma chain is generated by VJ recombination, and the TCR delta chain is generated by V(D)J recombination (Kenneth Murphy, Paul Travers, and Mark Walport, Janeway's Immunology 7th edition, Garland Science, 2007, which is herein incorporated by reference in its entirety). The antigen binding site of a TCR generally comprises six complementarity determining regions (CDRs). The alpha chain contributes three CDRs, alpha CDR1, alpha CDR2, and αCDR3. The beta chain also contributes three CDR: beta CDR1, beta CDR2, and βCDR3. The αCDR3 and βCDR3 are the regions most affected by V(D)J recombination and account for most of the variation in a TCR repertoire.

[00255] TCRs can specifically recognize HLA-PEPTIDE targets, such as an HLA-PEPTIDE target disclosed in Table A; thus TCRs can be ABPs that specifically bind to HLA-PEPTIDE. TCRs can be soluble, e.g., similar to an antibody secreted by a B cell. TCRs can also be membrane-bound, e.g., on a cell such as a T cell or NK cell. Thus, TCRs can be used in a context that corresponds to soluble antibodies and/or membrane-bound CARs.

[00256] Any of the TCRs disclosed herein may comprise an alpha variable region, an alpha joining region, optionally an alpha constant region, a beta variable region, optionally a beta diversity region, a beta joining region, and optionally a beta constant region.

[00257] In some embodiments, the TCR or CAR is a recombinant TCR or CAR. The recombinant TCR or CAR may include any of the TCRs identified herein but include one or more modifications. Exemplary modifications, e.g., amino acid substitutions, are described herein. Amino acid substitutions described herein may be made with reference to IMGT nomenclature and amino acid numbering as found at www.imgt.org.

[00258] The recombinant TCR or CAR may be a human TCR or CAR, comprising fully human sequences, e.g., natural human sequences. The recombinant TCR or CAR may retain its natural human variable domain sequences but contain modifications to the α constant region, β constant region, or both α and β constant regions. Such modifications to the TCR constant regions may improve TCR assembly and expression for TCR gene therapy by, e.g., driving preferential pairings of the exogenous TCR chains.

[00259] In some embodiments, the α and β constant regions are modified by substituting the entire human constant region sequences for mouse constant region sequences. Such

"murinized" TCRs and methods of making them are described in Cancer Res. 2006 Sep 1;66(17):8878-86, which is hereby incorporated by reference in its entirety.

[00260] In some embodiments, the α and β constant regions are modified by making one or more amino acid substitutions in the human TCR α constant (TRAC) region, the TCR β constant (TRBC) region, or the TRAC and TRAB regions, which swap particular human residues for murine residues (human ➔ murine amino acid exchange). The one or more amino acid substitutions in the TRAC region may include a Ser substitution at residue 90, an Asp substitution at residue 91, a Val substitution at residue 92, a Pro substitution at residue 93, or any combination thereof. The one or more amino acid substitutions in the human TRBC region may include a Lys substitution at residue 18, an Ala substitution at residue 22, an Ile substitution at residue 133, a His substitution at residue 139, or any combination of the above. Such targeted amino acid substitutions are described in J Immunol June 1, 2010, 184 (11) 6223-6231, which is hereby incorporated by reference in its entirety.

[00261] In some embodiments, the human TRAC contains an Asp substitution at residue 210 and the human TRBC contains a Lys substitution at residue 134. Such substitutions may promote the formation of a salt bridge between the alpha and beta chains and formation of the TCR interchain disulfide bond. These targeted substitutions are described in J Immunol June 1, 2010, 184 (11) 6232-6241, which is hereby incorporated by reference in its entirety.

[00262] In some embodiments, the human TRAC and human TRBC regions are modified to contain introduced cysteines which may improve preferential pairing of the exogenous TCR chains through formation of an additional disulfide bond. For example, the human TRAC may contain a Cys substitution at residue 48 and the human TRBC may contain a Cys substitution at residue 57, described in Cancer Res. 2007 Apr 15;67(8):3898-903 and Blood. 2007 Mar 15;109(6):2331-8, which are hereby incorporated by reference in their entirety.

[00263] The recombinant TCR or CAR may comprise other modifications to the α and β chains.

[00264] In some embodiments, the α and β chains are modified by linking the extracellular domains of the α and β chains to a complete human CD3ζ (CD3-zeta) molecule. Such modifications are described in J Immunol June 1, 2008, 180 (11) 7736-7746; Gene Ther. 2000 Aug;7(16):1369-77; and The Open Gene Therapy Journal, 2011, 4: 11-22, which are hereby incorporated by reference in their entirety.

[00265] In some embodiments, the α chain is modified by introducing hydrophobic amino acid substitutions in the transmembrane region of the α chain, as described in J Immunol June 1, 2012, 188 (11) 5538-5546; hereby incorporated by reference in their entirety.

[00266] The alpha or beta chain may be modified by altering any one of the N-glycosylation sites in the amino acid sequence, as described in J Exp Med. 2009 Feb 16; 206(2): 463–475; hereby incorporated by reference in its entirety.

[00267] The alpha and beta chain may each comprise a dimerization domain, e.g., a heterologous dimerization domain. Such a heterologous domain may be a leucine zipper, a 5H3 domain or hydrophobic proline rich counter domains, or other similar modalities, as known in the art. In one example, the alpha and beta chains may be modified by introducing 30mer segments to the carboxyl termini of the alpha and beta extracellular domains, wherein the segments selectively associate to form a stable leucine zipper. Such modifications are described in PNAS November 22, 1994. 91 (24) 11408-11412; https://doi.org/10.1073/pnas.91.24.11408; hereby incorporated by reference in its entirety.

[00268] TCRs identified herein may be modified to include mutations that result in increased affinity or half-life, such as those described in WO2012/013913, hereby incorporated by reference in its entirety.

[00269] The recombinant TCR or CAR may be a single chain TCR (scTCR). Such scTCR may comprise an α chain variable region sequence fused to the N terminus of a TCR α chain constant region extracellular sequence, a TCR β chain variable region fused to the N terminus of a TCR β chain constant region extracellular sequence, and a linker sequence linking the C terminus of the α segment to the N terminus of the β segment, or vice versa. In some embodiments, the constant region extracellular sequences of the α and β segments of the scTCR are linked by a disulfide bond. In some embodiments, the length of the linker sequence and the position of the disulfide bond being such that the variable region sequences of the α and β segments are mutually orientated substantially as in native αβ T cell receptors. Exemplary scTCRs are described in U.S. Patent No. 7,569,664, which is hereby incorporated by reference in its entirety.

[00270] In some cases, the variable regions of the scTCR may be covalently joined by a short peptide linker, such as described in Gene Therapy volume 7, pages 1369–1377 (2000). The short peptide linker may be a serine rich or glycine rich linker. For example, the linker

may be $(Gly_4Ser)_3$, as described in Cancer Gene Therapy (2004) 11, 487–496, incorporated by reference in its entirety.

[00271] The recombinant TCR or antigen binding fragment thereof may be expressed as a fusion protein. For instance, the TCR or antigen binding fragment thereof may be fused with a toxin. Such fusion proteins are described in Cancer Res. 2002 Mar 15;62(6):1757-60. The TCR or antigen binding fragment thereof may be fused with an antibody Fc region. Such fusion proteins are described in J Immunol May 1, 2017, 198 (1 Supplement) 120.9.

[00272] In some embodiments, the recombinant receptor such as a TCR or CAR, such as the antibody portion thereof, further includes a spacer, which may be or include at least a portion of an immunoglobulin constant region or variant or modified version thereof, such as a hinge region, e.g., an IgG4 hinge region, and/or a CH1/CL and/or Fc region. In some embodiments, the constant region or portion is of a human IgG, such as IgG4 or IgG1. In some aspects, the portion of the constant region serves as a spacer region between the antigen-recognition component, e.g., scFv, and transmembrane domain. The spacer can be of a length that provides for increased responsiveness of the cell following antigen binding, as compared to in the absence of the spacer. In some examples, the spacer is at or about 12 amino acids in length or is no more than 12 amino acids in length. Exemplary spacers include those having at least about 10 to 229 amino acids, about 10 to 200 amino acids, about 10 to 175 amino acids, about 10 to 150 amino acids, about 10 to 125 amino acids, about 10 to 100 amino acids, about 10 to 75 amino acids, about 10 to 50 amino acids, about 10 to 40 amino acids, about 10 to 30 amino acids, about 10 to 20 amino acids, or about 10 to 15 amino acids, and including any integer between the endpoints of any of the listed ranges. In some embodiments, a spacer region has about 12 amino acids or less, about 119 amino acids or less, or about 229 amino acids or less. Exemplary spacers include IgG4 hinge alone, IgG4 hinge linked to CH2 and CH3 domains, or IgG4 hinge linked to the CH3 domain. Exemplary spacers include, but are not limited to, those described in Hudecek et al. (2013) Clin. Cancer Res., 19:3153 or international patent application publication number WO2014031687. In some embodiments, the constant region or portion is of IgD.

[00273] The antigen recognition domain of a receptor such as a TCR or CAR can be linked to one or more intracellular signaling components, such as signaling components that mimic activation through an antigen receptor complex, such as a TCR complex, in the case of a CAR, and/or signal via another cell surface receptor. Thus, in some embodiments, the HLA-PEPTIDE-specific binding component (e.g., ABP such as antibody or TCR) is linked to one or more

transmembrane and intracellular signaling domains. In some embodiments, the transmembrane domain is fused to the extracellular domain. In one embodiment, a transmembrane domain that naturally is associated with one of the domains in the receptor, e.g., CAR, is used. In some instances, the transmembrane domain is selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex.

[00274] The transmembrane domain in some embodiments is derived either from a natural or from a synthetic source. Where the source is natural, the domain in some aspects is derived from any membrane-bound or transmembrane protein. Transmembrane regions include those derived from (i.e. comprise at least the transmembrane region(s) of) the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CDS, CD9, CD 16, CD22, CD33, CD37, CD64, CD80, CD86, CD 134, CD137, and/or CD 154. Alternatively the transmembrane domain in some embodiments is synthetic. In some aspects, the synthetic transmembrane domain comprises predominantly hydrophobic residues such as leucine and valine. In some aspects, a triplet of phenylalanine, tryptophan and valine will be found at each end of a synthetic transmembrane domain. In some embodiments, the linkage is by linkers, spacers, and/or transmembrane domain(s).

[00275] Among the intracellular signaling domains are those that mimic or approximate a signal through a natural antigen receptor, a signal through such a receptor in combination with a costimulatory receptor, and/or a signal through a costimulatory receptor alone. In some embodiments, a short oligo- or polypeptide linker, for example, a linker of between 2 and 10 amino acids in length, such as one containing glycines and serines, e.g., glycine-serine doublet, is present and forms a linkage between the transmembrane domain and the cytoplasmic signaling domain of the receptor.

[00276] The receptor, e.g., the TCR or CAR, can include at least one intracellular signaling component or components. In some embodiments, the receptor includes an intracellular component of a TCR complex, such as a TCR CD3 chain that mediates T-cell activation and cytotoxicity, e.g., CD3 zeta chain. Thus, in some aspects, the HLA-PEPTIDE-binding ABP (e.g., antibody) is linked to one or more cell signaling modules. In some embodiments, cell signaling modules include CD3 transmembrane domain, CD3 intracellular signaling domains, and/or other CD transmembrane domains. In some embodiments, the receptor, e.g., CAR, further includes a portion of one or more additional molecules such as Fc receptor-gamma, CD8, CD4, CD25, or

CD16. For example, in some aspects, the CAR includes a chimeric molecule between CD3-zeta or Fc receptor-gamma and CD8, CD4, CD25 or CD16.

[00277] In some embodiments, upon ligation of the TCR or CAR, the cytoplasmic domain or intracellular signaling domain of the receptor activates at least one of the normal effector functions or responses of the immune cell, e.g., T cell engineered to express the receptor. For example, in some contexts, the receptor induces a function of a T cell such as cytolytic activity or T-helper activity, such as secretion of cytokines or other factors. In some embodiments, a truncated portion of an intracellular signaling domain of an antigen receptor component or costimulatory molecule is used in place of an intact immunostimulatory chain, for example, if it transduces the effector function signal. In some embodiments, the intracellular signaling domain or domains include the cytoplasmic sequences of the T cell receptor (TCR), and in some aspects also those of co-receptors that in the natural context act in concert with such receptor to initiate signal transduction following antigen receptor engagement, and/or any derivative or variant of such molecules, and/or any synthetic sequence that has the same functional capability.

[00278] In the context of a natural TCR, full activation generally requires not only signaling through the TCR, but also a costimulatory signal. Thus, in some embodiments, to promote full activation, a component for generating secondary or co-stimulatory signal is also included in the receptor. In other embodiments, the receptor does not include a component for generating a costimulatory signal. In some aspects, an additional receptor is expressed in the same cell and provides the component for generating the secondary or costimulatory signal.

[00279] T cell activation is in some aspects described as being mediated by two classes of cytoplasmic signaling sequences: those that initiate antigen-dependent primary activation through the TCR (primary cytoplasmic signaling sequences), and those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal (secondary cytoplasmic signaling sequences). In some aspects, the receptor includes one or both of such signaling components.

[00280] In some aspects, the receptor includes a primary cytoplasmic signaling sequence that regulates primary activation of the TCR complex. Primary cytoplasmic signaling sequences that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs. Examples of ITAM containing primary cytoplasmic signaling sequences include those derived from TCR or CD3 zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CDS, CD22, CD79a, CD79b, and CD66d. In some

embodiments, cytoplasmic signaling molecule(s) in the CAR contain(s) a cytoplasmic signaling domain, portion thereof, or sequence derived from CD3 zeta.

[00281] In some embodiments, the receptor includes a signaling domain and/or transmembrane portion of a costimulatory receptor, such as CD28, 4-1BB, OX40, DAP10, and ICOS. In some aspects, the same receptor includes both the activating and costimulatory components.

[00282] In some embodiments, the activating domain is included within one receptor, whereas the costimulatory component is provided by another receptor recognizing another antigen. In some embodiments, the receptors include activating or stimulatory receptors, and costimulatory receptors, both expressed on the same cell (see WO2014/055668). In some aspects, the HLA-PEPTIDE-targeting receptor is the stimulatory or activating receptor; in other aspects, it is the costimulatory receptor. In some embodiments, the cells further include inhibitory receptors (e.g., iCARs, see Fedorov et al., Sci. Transl. Medicine, 5(215) (December, 2013), such as a receptor recognizing an antigen other than HLA-PEPTIDE, whereby an activating signal delivered through the HLA-PEPTIDE-targeting receptor is diminished or inhibited by binding of the inhibitory receptor to its ligand, e.g., to reduce off-target effects.

[00283] In certain embodiments, the intracellular signaling domain comprises a CD28 transmembrane and signaling domain linked to a CD3 (e.g., CD3-zeta) intracellular domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD28 and CD137 (4-1BB, TNFRSF9) co-stimulatory domains, linked to a CD3 zeta intracellular domain.

[00284] In some embodiments, the receptor encompasses one or more, e.g., two or more, costimulatory domains and an activation domain, e.g., primary activation domain, in the cytoplasmic portion. Exemplary receptors include intracellular components of CD3-zeta, CD28, and 4-1BB.

[00285] In some embodiments, the CAR or other antigen receptor such as a TCR further includes a marker, such as a cell surface marker, which may be used to confirm transduction or engineering of the cell to express the receptor, such as a truncated version of a cell surface receptor, such as truncated EGFR (tEGFR). In some aspects, the marker includes all or part (e.g., truncated form) of CD34, a NGFR, or epidermal growth factor receptor (e.g., tEGFR). In some embodiments, the nucleic acid encoding the marker is operably linked to a polynucleotide encoding for a linker sequence, such as a cleavable linker sequence or a ribosomal skip sequence, e.g., T2A. See WO2014031687. In some embodiments, introduction of a construct

encoding the CAR and EGFRt separated by a T2A ribosome switch can express two proteins from the same construct, such that the EGFRt can be used as a marker to detect cells expressing such construct. In some embodiments, a marker, and optionally a linker sequence, can be any as disclosed in published patent application No. WO2014031687. For example, the marker can be a truncated EGFR (tEGFR) that is, optionally, linked to a linker sequence, such as a T2A ribosomal skip sequence.

[00286] In some embodiments, the marker is a molecule, e.g., cell surface protein, not naturally found on T cells or not naturally found on the surface of T cells, or a portion thereof.

[00287] In some embodiments, the molecule is a non-self molecule, e.g., non-self protein, i.e., one that is not recognized as "self" by the immune system of the host into which the cells will be adoptively transferred.

[00288] In some embodiments, the marker serves no therapeutic function and/or produces no effect other than to be used as a marker for genetic engineering, e.g., for selecting cells successfully engineered. In other embodiments, the marker may be a therapeutic molecule or molecule otherwise exerting some desired effect, such as a ligand for a cell to be encountered in vivo, such as a costimulatory or immune checkpoint molecule to enhance and/or dampen responses of the cells upon adoptive transfer and encounter with ligand.

[00289] The TCR or CAR may comprise one or modified synthetic amino acids in place of one or more naturally-occurring amino acids. Exemplary modified amino acids include, but are not limited to, aminocyclohexane carboxylic acid, norleucine, α-amino n-decanoic acid, homoserine, S-acetylaminomethylcysteine, trans-3- and trans-4-hydroxyproline, 4-aminophenylalanine, 4- nitrophenylalanine, 4-chlorophenylalanine, 4-carboxyphenylalanine, (3-phenylserine (3-hydroxyphenylalanine, phenylglycine, α-naphthylalanine, cyclohexylalanine, cyclohexylglycine, indoline-2-carboxylic acid, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, aminomalonic acid, aminomalonic acid monoamide, N' -benzyl-N'-methyl-lysine, N',N' -dibenzyl-lysine, 6- hydroxylysine, ornithine, α-aminocyclopentane carboxylic acid, α-aminocyclohexane carboxylic acid, α-aminocycloheptane carboxylic acid, α-(2-amino-2-norbomane)-carboxylic acid, α,γ -diaminobutyric acid, α,γ -diaminopropionic acid, homophenylalanine, and α-tertbutylglycine.

[00290] In some cases, CARs are referred to as first, second, and/or third generation CARs. In some aspects, a first generation CAR is one that solely provides a CD3-chain induced signal upon antigen binding; in some aspects, a second-generation CARs is one that provides such a

signal and costimulatory signal, such as one including an intracellular signaling domain from a costimulatory receptor such as CD28 or CD137; in some aspects, a third generation CAR in some aspects is one that includes multiple costimulatory domains of different costimulatory receptors.

[00291] In some embodiments, the chimeric antigen receptor includes an extracellular portion containing an antibody or fragment described herein. In some aspects, the chimeric antigen receptor includes an extracellular portion containing an antibody or fragment described herein and an intracellular signaling domain. In some embodiments, an antibody or fragment includes an scFv or a single-domain VH antibody and the intracellular domain contains an ITAM. In some aspects, the intracellular signaling domain includes a signaling domain of a zeta chain of a CD3-zeta (CD3) chain. In some embodiments, the chimeric antigen receptor includes a transmembrane domain linking the extracellular domain and the intracellular signaling domain.

[00292] In some aspects, the transmembrane domain contains a transmembrane portion of CD28. The extracellular domain and transmembrane can be linked directly or indirectly. In some embodiments, the extracellular domain and transmembrane are linked by a spacer, such as any described herein. In some embodiments, the chimeric antigen receptor contains an intracellular domain of a T cell costimulatory molecule, such as between the transmembrane domain and intracellular signaling domain. In some aspects, the T cell costimulatory molecule is CD28 or 41BB.

[00293] In some embodiments, the CAR contains an antibody, e.g., an antibody fragment, a transmembrane domain that is or contains a transmembrane portion of CD28 or a functional variant thereof, and an intracellular signaling domain containing a signaling portion of CD28 or functional variant thereof and a signaling portion of CD3 zeta or functional variant thereof. In some embodiments, the CAR contains an antibody, e.g., antibody fragment, a transmembrane domain that is or contains a transmembrane portion of CD28 or a functional variant thereof, and an intracellular signaling domain containing a signaling portion of a 4-1BB or functional variant thereof and a signaling portion of CD3 zeta or functional variant thereof. In some such embodiments, the receptor further includes a spacer containing a portion of an Ig molecule, such as a human Ig molecule, such as an Ig hinge, e.g. an IgG4 hinge, such as a hinge-only spacer.

[00294] In some embodiments, the transmembrane domain of the receptor, e.g., the CAR, is a transmembrane domain of human CD28 or variant thereof, e.g., a 27-amino acid transmembrane domain of a human CD28 (Accession No.: P10747.1).

[00295] In some embodiments, the chimeric antigen receptor contains an intracellular domain of a T cell costimulatory molecule. In some aspects, the T cell costimulatory molecule is CD28 or 41BB.

[00296] In some embodiments, the intracellular signaling domain comprises an intracellular costimulatory signaling domain of human CD28 or functional variant or portion thereof, such as a 41 amino acid domain thereof and/or such a domain with an LL to GG substitution at positions 186-187 of a native CD28 protein. In some embodiments, the intracellular domain comprises an intracellular costimulatory signaling domain of 41BB or functional variant or portion thereof, such as a 42-amino acid cytoplasmic domain of a human 4-1BB (Accession No. Q07011.1) or functional variant or portion thereof.

[00297] In some embodiments, the intracellular signaling domain comprises a human CD3 zeta stimulatory signaling domain or functional variant thereof, such as a 112 AA cytoplasmic domain of isoform 3 of human CD3.zeta. (Accession No.: P20963.2) or a CD3 zeta signaling domain as described in U.S. Pat. No. 7,446,190 or U.S. Pat. No. 8,911,993.

[00298] In some aspects, the spacer contains only a hinge region of an IgG, such as only a hinge of IgG4 or IgG1. In other embodiments, the spacer is an Ig hinge, e.g., and IgG4 hinge, linked to a CH2 and/or CH3 domains. In some embodiments, the spacer is an Ig hinge, e.g., an IgG4 hinge, linked to CH2 and CH3 domains. In some embodiments, the spacer is an Ig hinge, e.g., an IgG4 hinge, linked to a CH3 domain only. In some embodiments, the spacer is or comprises a glycine-serine rich sequence or other flexible linker such as known flexible linkers.

[00299] For example, in some embodiments, the CAR includes an antibody or fragment thereof, such as any of the HLA-PEPTIDE antibodies, including sdAbs (e.g. containing only the VH region) and scFvs, described herein, a spacer such as any of the Ig-hinge containing spacers, a CD28 transmembrane domain, a CD28 intracellular signaling domain, and a CD3 zeta signaling domain. In some embodiments, the CAR includes an antibody or fragment, such as any of the HLA-PEPTIDE antibodies, including sdAbs and scFvs described herein, a spacer such as any of the Ig-hinge containing spacers, a CD28 transmembrane domain, a CD28 intracellular signaling domain, and a CD3 zeta signaling domain.

Target-specific TCRs to A*02:01_LLASSILCA (SEQ ID NO: 2737) [G7]

[00300] In some aspects, provided herein are ABPs comprising TCRs or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA Class I molecule of the HLA-PEPTIDE target is HLA subtype A*02:01 and the HLA-restricted

peptide of the HLA-PEPTIDE target comprises the sequence LLASSILCA (SEQ ID NO: 2737) ("G7").

[00301] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 sequence. The αCDR3 sequence may be SEQ ID NO: 4277, 4278, 4279, 4280, or 4281.

[00302] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a βCDR3 sequence. The βCDR3 sequence may be any one of SEQ ID NOS 4291-4295.

[00303] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a particular αCDR3 sequence and a particular βCDR3 sequence. The αCDR3 may be SEQ ID NO: 4277 and the βCDR3 may be SEQ ID NO: 4291. The αCDR3 may be SEQ ID NO: 4278 and the βCDR3 may be SEQ ID NO: 4292. The αCDR3 may be SEQ ID NO: 4279 and the βCDR3 may be SEQ ID NO: 4293. The αCDR3 may be SEQ ID NO: 4280 and the βCDR3 may be SEQ ID NO: 4294. The αCDR3 may be SEQ ID NO: 4281 and the βCDR3 may be SEQ ID NO: 4295.

[00304] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 that is SEQ ID NO: 4277 and a beta CDR 3 that is SEQ ID NO: 4291. The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 that is SEQ ID NO: 4278 and a beta CDR 3 that is SEQ ID NO: 4292. The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 that is SEQ ID NO: 4279 and a beta CDR 3 that is SEQ ID NO: 4293. The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 that is SEQ ID NO: 4280 and a beta CDR 3 that is SEQ ID NO: 4294. The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an αCDR3 that is SEQ ID NO: 4281 and a beta CDR 3 that is SEQ ID NO: 4295.

[00305] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a TRAV, a TRAJ, a TRBV, optionally a TRBD, and a TRBJ amino acid sequence, optionally a TRAC sequence and optionally a TRBC sequence. Such TCR may comprise TRAV19, TRAJ4, TRBV6-5, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV5, TRAJ13, TRBV7-9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV3, TRAJ39, TRBV7-9, and TRBJ2-2. Such TCR may comprise TRAV38-2DV8, TRAJ21, TRBV9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV4, TRAJ9, TRBV27, and TRBJ1-5.

[00306] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise an alpha VJ sequence. The alpha VJ sequence may be any one of SEQ ID NOS 4306-4310.

[00307] The TCR specific for A*02:01_ LLASSILCA (SEQ ID NO: 2737) may comprise a beta V(D)J sequence. The beta V(D)J sequence may be any one of SEQ ID NOS 4321-4325.

[00308] In some embodiments, the alpha VJ sequence is SEQ ID NO: 4306 and the beta V(D)J sequence is SEQ ID NO: 4321. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4307 and the beta V(D)J sequence is SEQ ID NO: 4322. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4308 and the beta V(D)J sequence is SEQ ID NO: 4323. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4309 and the beta V(D)J sequence is SEQ ID NO: 4324. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4310 and the beta V(D)J sequence is SEQ ID NO: 4325.

[00309]

Target-specific TCRs to A*01:01_ EVDPIGHLY (SEQ ID NO: 3051)

[00310] In some aspects, provided herein are ABPs comprising TCRs or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA Class I molecule of the HLA-PEPTIDE target is HLA subtype A*01:01 and the HLA-restricted peptide of the HLA-PEPTIDE target comprises the sequence EVDPIGHLY (SEQ ID NO: 3051).

[00311] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise an αCDR3 sequence. The αCDR3 sequence may be any one of SEQ ID NOS 3052-3350 or 4273-4276.

[00312] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise a βCDR3 sequence. The βCDR3 sequence may be any one of SEQ ID NOS 3351-3655 or 4287-4290.

[00313] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise a particular αCDR3 sequence and a particular βCDR3 sequence. The αCDR3 may be SEQ ID NO: 4273 and the βCDR3 may be SEQ ID NO: 4287. The αCDR3 may be SEQ ID NO: 4274 and the βCDR3 may be SEQ ID NO: 4288. The αCDR3 may be SEQ ID NO: 4275 and the βCDR3 may be SEQ ID NO: 4289. The αCDR3 may be SEQ ID NO: 4276 and the βCDR3 may be SEQ ID NO: 4290. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3351. The αCDR3 may be SEQ ID NO: 3053 and the βCDR3

may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3054 and the βCDR3 may be SEQ ID NO: 3353. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3055 and the βCDR3 may be SEQ ID NO: 3354. The αCDR3 may be SEQ ID NO: 3056 and the βCDR3 may be SEQ ID NO: 3355. The αCDR3 may be SEQ ID NO: 3057 and the βCDR3 may be SEQ ID NO: 3356. The αCDR3 may be SEQ ID NO: 3058 and the βCDR3 may be SEQ ID NO: 3357. The αCDR3 may be SEQ ID NO: 3059 and the βCDR3 may be SEQ ID NO: 3358. The αCDR3 may be SEQ ID NO: 3060 and the βCDR3 may be SEQ ID NO: 3359. The αCDR3 may be SEQ ID NO: 3061 and the βCDR3 may be SEQ ID NO: 3360. The αCDR3 may be SEQ ID NO: 3062 and the βCDR3 may be SEQ ID NO: 3361. The αCDR3 may be SEQ ID NO: 3063 and the βCDR3 may be SEQ ID NO: 3362. The αCDR3 may be SEQ ID NO: 3053 and the βCDR3 may be SEQ ID NO: 3351. The αCDR3 may be SEQ ID NO: 3057 and the βCDR3 may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3064 and the βCDR3 may be SEQ ID NO: 3363. The αCDR3 may be SEQ ID NO: 3065 and the βCDR3 may be SEQ ID NO: 3364. The αCDR3 may be SEQ ID NO: 3054 and the βCDR3 may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3066 and the βCDR3 may be SEQ ID NO: 3365. The αCDR3 may be SEQ ID NO: 3067 and the βCDR3 may be SEQ ID NO: 3366. The αCDR3 may be SEQ ID NO: 3068 and the βCDR3 may be SEQ ID NO: 3367. The αCDR3 may be SEQ ID NO: 3069 and the βCDR3 may be SEQ ID NO: 3368. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3356. The αCDR3 may be SEQ ID NO: 3070 and the βCDR3 may be SEQ ID NO: 3369. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3355. The αCDR3 may be SEQ ID NO: 3071 and the βCDR3 may be SEQ ID NO: 3370. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3353. The αCDR3 may be SEQ ID NO: 3072 and the βCDR3 may be SEQ ID NO: 3371. The αCDR3 may be SEQ ID NO: 3073 and the βCDR3 may be SEQ ID NO: 3372. The αCDR3 may be SEQ ID NO: 3057 and the βCDR3 may be SEQ ID NO: 3351. The αCDR3 may be SEQ ID NO: 3074 and the βCDR3 may be SEQ ID NO: 3373. The αCDR3 may be SEQ ID NO: 3075 and the βCDR3 may be SEQ ID NO: 3374. The αCDR3 may be SEQ ID NO: 3076 and the βCDR3 may be SEQ ID NO: 3375. The αCDR3 may be SEQ ID NO: 3077 and the βCDR3 may be SEQ ID NO: 3376. The αCDR3 may be SEQ ID NO: 3078 and the βCDR3 may be SEQ ID NO: 3377. The αCDR3 may be SEQ ID NO: 3079 and the βCDR3 may be SEQ ID NO: 3378. The αCDR3 may be SEQ ID NO: 3080 and the βCDR3 may be SEQ ID

NO: 3379. The αCDR3 may be SEQ ID NO: 3081 and the βCDR3 may be SEQ ID NO: 3380. The αCDR3 may be SEQ ID NO: 3082 and the βCDR3 may be SEQ ID NO: 3381. The αCDR3 may be SEQ ID NO: 3083 and the βCDR3 may be SEQ ID NO: 3382. The αCDR3 may be SEQ ID NO: 3084 and the βCDR3 may be SEQ ID NO: 3383. The αCDR3 may be SEQ ID NO: 3085 and the βCDR3 may be SEQ ID NO: 3384. The αCDR3 may be SEQ ID NO: 3086 and the βCDR3 may be SEQ ID NO: 3385. The αCDR3 may be SEQ ID NO: 3087 and the βCDR3 may be SEQ ID NO: 3386. The αCDR3 may be SEQ ID NO: 3088 and the βCDR3 may be SEQ ID NO: 3387. The αCDR3 may be SEQ ID NO: 3089 and the βCDR3 may be SEQ ID NO: 3388. The αCDR3 may be SEQ ID NO: 3052 and the βCDR3 may be SEQ ID NO: 3389. The αCDR3 may be SEQ ID NO: 3056 and the βCDR3 may be SEQ ID NO: 3351. The αCDR3 may be SEQ ID NO: 3090 and the βCDR3 may be SEQ ID NO: 3390. The αCDR3 may be SEQ ID NO: 3091 and the βCDR3 may be SEQ ID NO: 3391. The αCDR3 may be SEQ ID NO: 3092 and the βCDR3 may be SEQ ID NO: 3392. The αCDR3 may be SEQ ID NO: 3093 and the βCDR3 may be SEQ ID NO: 3393. The αCDR3 may be SEQ ID NO: 3053 and the βCDR3 may be SEQ ID NO: 3356. The αCDR3 may be SEQ ID NO: 3094 and the βCDR3 may be SEQ ID NO: 3394. The αCDR3 may be SEQ ID NO: 3054 and the βCDR3 may be SEQ ID NO: 3363. The αCDR3 may be SEQ ID NO: 3095 and the βCDR3 may be SEQ ID NO: 3395. The αCDR3 may be SEQ ID NO: 3054 and the βCDR3 may be SEQ ID NO: 3351. The αCDR3 may be SEQ ID NO: 3096 and the βCDR3 may be SEQ ID NO: 3396. The αCDR3 may be SEQ ID NO: 3053 and the βCDR3 may be SEQ ID NO: 3355. The αCDR3 may be SEQ ID NO: 3097 and the βCDR3 may be SEQ ID NO: 3397. The αCDR3 may be SEQ ID NO: 3098 and the βCDR3 may be SEQ ID NO: 3398. The αCDR3 may be SEQ ID NO: 3099 and the βCDR3 may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3100 and the βCDR3 may be SEQ ID NO: 3399. The αCDR3 may be SEQ ID NO: 3053 and the βCDR3 may be SEQ ID NO: 3353. The αCDR3 may be SEQ ID NO: 3101 and the βCDR3 may be SEQ ID NO: 3400. The αCDR3 may be SEQ ID NO: 3102 and the βCDR3 may be SEQ ID NO: 3401. The αCDR3 may be SEQ ID NO: 3058 and the βCDR3 may be SEQ ID NO: 3352. The αCDR3 may be SEQ ID NO: 3103 and the βCDR3 may be SEQ ID NO: 3402. The αCDR3 may be SEQ ID NO: 3104 and the βCDR3 may be SEQ ID NO: 3403. The αCDR3 may be SEQ ID NO: 3105 and the βCDR3 may be SEQ ID NO: 3404. The αCDR3 may be SEQ ID NO: 3106 and the βCDR3 may be SEQ ID NO: 3405. The αCDR3 may be SEQ ID NO: 3107 and the βCDR3 may be SEQ ID NO: 3406. The

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and the βCDR3 may be SEQ ID NO: 3595. The αCDR3 may be SEQ ID NO: 3308 and the βCDR3 may be SEQ ID NO: 3612. The αCDR3 may be SEQ ID NO: 3309 and the βCDR3 may be SEQ ID NO: 3613. The αCDR3 may be SEQ ID NO: 3310 and the βCDR3 may be SEQ ID NO: 3614. The αCDR3 may be SEQ ID NO: 3311 and the βCDR3 may be SEQ ID NO: 3615. The αCDR3 may be SEQ ID NO: 3312 and the βCDR3 may be SEQ ID NO: 3616. The αCDR3 may be SEQ ID NO: 3313 and the βCDR3 may be SEQ ID NO: 3617. The αCDR3 may be SEQ ID NO: 3314 and the βCDR3 may be SEQ ID NO: 3618. The αCDR3 may be SEQ ID NO: 3289 and the βCDR3 may be SEQ ID NO: 3619. The αCDR3 may be SEQ ID NO: 3315 and the βCDR3 may be SEQ ID NO: 3620. The αCDR3 may be SEQ ID NO: 3316 and the βCDR3 may be SEQ ID NO: 3621. The αCDR3 may be SEQ ID NO: 3317 and the βCDR3 may be SEQ ID NO: 3622. The αCDR3 may be SEQ ID NO: 3318 and the βCDR3 may be SEQ ID NO: 3623. The αCDR3 may be SEQ ID NO: 3319 and the βCDR3 may be SEQ ID NO: 3624. The αCDR3 may be SEQ ID NO: 3320 and the βCDR3 may be SEQ ID NO: 3625. The αCDR3 may be SEQ ID NO: 3321 and the βCDR3 may be SEQ ID NO: 3626. The αCDR3 may be SEQ ID NO: 3322 and the βCDR3 may be SEQ ID NO: 3627. The αCDR3 may be SEQ ID NO: 3323 and the βCDR3 may be SEQ ID NO: 3628. The αCDR3 may be SEQ ID NO: 3324 and the βCDR3 may be SEQ ID NO: 3629. The αCDR3 may be SEQ ID NO: 3325 and the βCDR3 may be SEQ ID NO: 3602. The αCDR3 may be SEQ ID NO: 3326 and the βCDR3 may be SEQ ID NO: 3630. The αCDR3 may be SEQ ID NO: 3327 and the βCDR3 may be SEQ ID NO: 3631. The αCDR3 may be SEQ ID NO: 3328 and the βCDR3 may be SEQ ID NO: 3632. The αCDR3 may be SEQ ID NO: 3289 and the βCDR3 may be SEQ ID NO: 3598. The αCDR3 may be SEQ ID NO: 3329 and the βCDR3 may be SEQ ID NO: 3633. The αCDR3 may be SEQ ID NO: 3330 and the βCDR3 may be SEQ ID NO: 3634. The αCDR3 may be SEQ ID NO: 3331 and the βCDR3 may be SEQ ID NO: 3635. The αCDR3 may be SEQ ID NO: 3332 and the βCDR3 may be SEQ ID NO: 3636. The αCDR3 may be SEQ ID NO: 3333 and the βCDR3 may be SEQ ID NO: 3637. The αCDR3 may be SEQ ID NO: 3334 and the βCDR3 may be SEQ ID NO: 3638. The αCDR3 may be SEQ ID NO: 3335 and the βCDR3 may be SEQ ID NO: 3639. The αCDR3 may be SEQ ID NO: 3336 and the βCDR3 may be SEQ ID NO: 3640. The αCDR3 may be SEQ ID NO: 3337 and the βCDR3 may be SEQ ID NO: 3641. The αCDR3 may be SEQ ID NO: 3338 and the βCDR3 may be SEQ ID NO: 3642. The αCDR3 may be SEQ ID NO: 3290 and the βCDR3 may be SEQ ID NO: 3596. The αCDR3 may be SEQ ID NO: 3339 and the βCDR3

may be SEQ ID NO: 3643. The αCDR3 may be SEQ ID NO: 3290 and the βCDR3 may be SEQ ID NO: 3601. The αCDR3 may be SEQ ID NO: 3340 and the βCDR3 may be SEQ ID NO: 3644. The αCDR3 may be SEQ ID NO: 3289 and the βCDR3 may be SEQ ID NO: 3611. The αCDR3 may be SEQ ID NO: 3341 and the βCDR3 may be SEQ ID NO: 3645. The αCDR3 may be SEQ ID NO: 3342 and the βCDR3 may be SEQ ID NO: 3646. The αCDR3 may be SEQ ID NO: 3343 and the βCDR3 may be SEQ ID NO: 3647. The αCDR3 may be SEQ ID NO: 3142 and the βCDR3 may be SEQ ID NO: 3648. The αCDR3 may be SEQ ID NO: 3344 and the βCDR3 may be SEQ ID NO: 3649. The αCDR3 may be SEQ ID NO: 3345 and the βCDR3 may be SEQ ID NO: 3650. The αCDR3 may be SEQ ID NO: 3290 and the βCDR3 may be SEQ ID NO: 3614. The αCDR3 may be SEQ ID NO: 3346 and the βCDR3 may be SEQ ID NO: 3651. The αCDR3 may be SEQ ID NO: 3347 and the βCDR3 may be SEQ ID NO: 3652. The αCDR3 may be SEQ ID NO: 3348 and the βCDR3 may be SEQ ID NO: 3653. The αCDR3 may be SEQ ID NO: 3349 and the βCDR3 may be SEQ ID NO: 3654. The αCDR3 may be SEQ ID NO: 3350 and the βCDR3 may be SEQ ID NO: 3655.

[00314] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise a TRAV, a TRAJ, a TRBV, optionally a TRBD, and a TRBJ amino acid sequence, optionally a TRAC sequence and optionally a TRBC sequence. Such TCR may comprise TRAV24, TRAJ31, TRBV3-1, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV3, TRAJ6, TRBV19, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ26, TRBV27, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV20, TRAJ15, TRBV27, and TRBJ2-3. Such TCR may comprise TRAV12-3, TRAJ20, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV19, TRAJ40, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ4, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV12-3, TRAJ20, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV1-1, TRAJ4, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV12-1, TRAJ17, TRBV6-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV4, TRAJ47, TRBV20-1, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV21, TRAJ6, TRBV5-4, and TRBJ2-1. Such TCR may comprise TRAV12-1, TRAJ11, TRBV11-3, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ31, TRBV5-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ33, TRBV5-1, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV34, TRAJ40, TRBV9, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV29DV5, TRAJ29, TRBV7-9, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV19, TRAJ40, TRBV20-1,

TRBD2, and TRBJ1-2. Such TCR may comprise TRAV4, TRAJ47, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ54, TRBV5-1, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ42, TRBV7-9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ4, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ40, TRBV29-1, and TRBJ2-2. Such TCR may comprise TRAV29DV5, TRAJ49, TRBV10-2, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ40, TRBV27, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ11, TRBV5-4, and TRBJ2-2. Such TCR may comprise TRAV12-3, TRAJ20, TRBV20-1, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV26-2, TRAJ49, TRBV19, and TRBJ1-5. Such TCR may comprise TRAV12-3, TRAJ20, TRBV6-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV17, TRAJ34, TRBV11-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV12-3, TRAJ20, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ26, TRBV5-6, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV29DV5, TRAJ4, TRBV27, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV4, TRAJ47, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV13-1, TRAJ49, TRBV27, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ10, TRBV25-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV29DV5, TRAJ39, TRBV7-9, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ47, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV39, TRAJ41, TRBV13, and TRBJ1-4. Such TCR may comprise TRAV17, TRAJ53, TRBV29-1, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV26-1, TRAJ42, TRBV19, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV8-6, TRAJ50, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV19, TRAJ10, TRBV7-9, and TRBJ2-7. Such TCR may comprise TRAV8-4, TRAJ42, TRBV3-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV12-1, TRAJ47, TRBV5-8, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV29DV5, TRAJ42, TRBV10-3, and TRBJ2-7. Such TCR may comprise TRAV13-2, TRAJ20, TRBV27, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV10, TRAJ9, TRBV3-1, TRBD1, and TRBJ1-3. Such TCR may comprise TRAV19, TRAJ27, TRBV27, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV9-2, TRAJ20, TRBV12-4, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV12-2, TRAJ20, TRBV7-6, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV12-1, TRAJ17, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV30, TRAJ58, TRBV19, and TRBJ2-7. Such TCR may comprise TRAV8-1, TRAJ43, TRBV7-8, TRBD2, and TRBJ2-1.

Such TCR may comprise TRAV13-1, TRAJ9, TRBV9, TRBD1, and TRBJ2-5. Such TCR may comprise TRAV12-1, TRAJ29, TRBV6-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV19, TRAJ40, TRBV20-1, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV21, TRAJ43, TRBV7-3, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ4, TRBV5-1, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV26-2, TRAJ32, TRBV24-1, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ4, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV19, TRAJ15, TRBV7-8, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV19, TRAJ40, TRBV6-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV12-2, TRAJ13, TRBV25-1, and TRBJ2-7. Such TCR may comprise TRAV29DV5, TRAJ54, TRBV7-8, and TRBJ2-1. Such TCR may comprise TRAV19, TRAJ53, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV23DV6, TRAJ36, TRBV9, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV19, TRAJ40, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV8-6, TRAJ32, TRBV19, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV1-1, TRAJ13, TRBV14, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ6, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ44, TRBV9, and TRBJ2-7. Such TCR may comprise TRAV29DV5, TRAJ3, TRBV3-1, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV17, TRAJ39, TRBV7-2, and TRBJ1-2. Such TCR may comprise TRAV26-2, TRAJ12, TRBV7-9, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV29DV5, TRAJ22, TRBV11-3, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ20, TRBV12-4, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV12-3, TRAJ3, TRBV27, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV27, TRAJ33, TRBV6-5, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV13-1, TRAJ22, TRBV12-4, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV26-1, TRAJ34, TRBV27, and TRBJ1-2. Such TCR may comprise TRAV10, TRAJ4, TRBV7-9, TRBD1, and TRBJ2-4. Such TCR may comprise TRAV21, TRAJ6, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV12-3, TRAJ20, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ26, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV12-2, TRAJ20, TRBV18, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV9-2, TRAJ23, TRBV11-3, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ6, TRBV6-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV12-3, TRAJ20, TRBV7-8, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV9-2, TRAJ23, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV24,

TRAJ45, TRBV5-4, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV13-1, TRAJ3, TRBV27, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV20, TRAJ20, TRBV7-2, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV8-4, TRAJ42, TRBV9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV1-2, TRAJ31, TRBV7-9, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV12-1, TRAJ13, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ4, TRBV28, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ4, TRBV27, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV3, TRAJ9, TRBV7-9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV26-1, TRAJ42, TRBV19, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ47, TRBV19, and TRBJ1-1. Such TCR may comprise TRAV26-1, TRAJ34, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ31, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ11, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV17, TRAJ34, TRBV6-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV13-2, TRAJ47, TRBV19, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV29DV5, TRAJ28, TRBV27, TRBD2, and TRBJ2-4. Such TCR may comprise TRAV13-2, TRAJ17, TRBV27, TRBD2, and TRBJ1-5. Such TCR may comprise TRAV38-2DV8, TRAJ57, TRBV5-4, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV17, TRAJ32, TRBV7-8, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ39, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-3, TRAJ20, TRBV7-9, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV1-1, TRAJ4, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ9, TRBV2, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV19, TRAJ32, TRBV9, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV8-3, TRAJ6, TRBV9, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV19, TRAJ40, TRBV7-9, and TRBJ2-7. Such TCR may comprise TRAV5, TRAJ37, TRBV5-6, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ33, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV29DV5, TRAJ3, TRBV20-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV1-1, TRAJ4, TRBV20-1, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ6, TRBV10-3, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ23, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV12-2, TRAJ20, TRBV11-2, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV1-2, TRAJ15, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ9, TRBV5-4, and TRBJ1-6. Such TCR may comprise TRAV8-6, TRAJ12, TRBV7-9,

TRBD1, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ31, TRBV11-2, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ41, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV25, TRAJ28, TRBV7-2, TRBD2, and TRBJ2-6. Such TCR may comprise TRAV21, TRAJ33, TRBV10-3, TRBD1, and TRBJ1-3. Such TCR may comprise TRAV21, TRAJ49, TRBV5-1, TRBD1, and TRBJ2-5. Such TCR may comprise TRAV1-1, TRAJ34, TRBV6-6, and TRBJ1-5. Such TCR may comprise TRAV24, TRAJ6, TRBV7-2, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV1-1, TRAJ15, TRBV6-6, and TRBJ1-5. Such TCR may comprise TRAV21, TRAJ15, TRBV29-1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ43, TRBV12-4, and TRBJ1-5. Such TCR may comprise TRAV21, TRAJ30, TRBV9, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV21, TRAJ31, TRBV5-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV26-1, TRAJ45, TRBV19, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ43, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ31, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV29DV5, TRAJ28, TRBV4-1, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV26-2, TRAJ44, TRBV27, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ31, TRBV9, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV21, TRAJ36, TRBV9, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ9, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV8-3, TRAJ15, TRBV4-1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ43, TRBV24-1, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV29DV5, TRAJ40, TRBV7-9, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV30, TRAJ32, TRBV28, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV38-2DV8, TRAJ26, TRBV7-9, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV12-1, TRAJ6, TRBV20-1, TRBD1, and TRBJ1-3. Such TCR may comprise TRAV21, TRAJ47, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV38-2DV8, TRAJ45, TRBV29-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ15, TRBV7-2, and TRBJ1-1. Such TCR may comprise TRAV12-2, TRAJ29, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV3, TRAJ6, TRBV28, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ9, TRBV10-3, TRBD1, and TRBJ1-3. Such TCR may comprise TRAV1-2, TRAJ15, TRBV7-9, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV8-6, TRAJ40, TRBV15, and TRBJ2-5. Such TCR may comprise TRAV38-2DV8, TRAJ57, TRBV13, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV8-6, TRAJ10, TRBV7-9, and TRBJ1-1. Such TCR may comprise

TRAV21, TRAJ20, TRBV5-4, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV13-1, TRAJ28, TRBV7-8, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV21, TRAJ9, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV1-2, TRAJ15, TRBV2, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV35, TRAJ26, TRBV27, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV38-2DV8, TRAJ43, TRBV5-1, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV5, TRAJ32, TRBV19, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV13-1, TRAJ21, TRBV5-1, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV12-2, TRAJ45, TRBV12-4, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ31, TRBV12-5, and TRBJ2-2. Such TCR may comprise TRAV24, TRAJ52, TRBV27, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ52, TRBV19, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV36DV7, TRAJ44, TRBV7-9, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV3, TRAJ29, TRBV11-2, TRBD1, and TRBJ2-5. Such TCR may comprise TRAV1-1, TRAJ15, TRBV13, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV29DV5, TRAJ52, TRBV11-3, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV12-1, TRAJ6, TRBV19, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ13, TRBV27, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV17, TRAJ43, TRBV12-3, and TRBJ1-4. Such TCR may comprise TRAV12-3, TRAJ20, TRBV12-4, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ52, TRBV4-1, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ23, TRBV19, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV1-1, TRAJ30, TRBV13, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV12-2, TRAJ43, TRBV12-4, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV24, TRAJ10, TRBV5-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV5, TRAJ9, TRBV4-1, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ40, TRBV7-8, and TRBJ1-1. Such TCR may comprise TRAV13-1, TRAJ45, TRBV9, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV12-1, TRAJ26, TRBV4-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV26-2, TRAJ45, TRBV19, and TRBJ1-2. Such TCR may comprise TRAV22, TRAJ23, TRBV5-4, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ42, TRBV28, and TRBJ2-7. Such TCR may comprise TRAV17, TRAJ52, TRBV7-8, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV12-1, TRAJ39, TRBV3-1, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV21, TRAJ9, TRBV5-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV1-1, TRAJ5, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV23DV6, TRAJ13,

TRBV6-5, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV8-6, TRAJ12, TRBV24-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV1-2, TRAJ28, TRBV27, and TRBJ2-3. Such TCR may comprise TRAV29DV5, TRAJ34, TRBV4-1, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV12-1, TRAJ21, TRBV28, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV9-2, TRAJ29, TRBV5-8, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV27, TRAJ40, TRBV7-6, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ31, TRBV7-8, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ30, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ30, TRBV20-1, and TRBJ2-1. Such TCR may comprise TRAV1-1, TRAJ26, TRBV12-5, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV1-2, TRAJ33, TRBV9, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV26-1, TRAJ50, TRBV27, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV40, TRAJ41, TRBV6-5, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV12-2, TRAJ31, TRBV7-9, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV5, TRAJ43, TRBV5-1, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV24, TRAJ52, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV1-2, TRAJ11, TRBV7-6, TRBD1, and TRBJ1-3. Such TCR may comprise TRAV21, TRAJ33, TRBV5-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ39, TRBV10-3, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ20, TRBV14, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV29DV5, TRAJ48, TRBV7-9, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV13-1, TRAJ22, TRBV29-1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ33, TRBV10-3, and TRBJ2-1. Such TCR may comprise TRAV39, TRAJ49, TRBV24-1, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV13-1, TRAJ23, TRBV27, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ9, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ33, TRBV9, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ28, TRBV19, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV10, TRAJ8, TRBV5-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ48, TRBV27, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV12-2, TRAJ4, TRBV7-2, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ31, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ33, TRBV9, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ6, TRBV6-6, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV21, TRAJ29, TRBV5-1, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV41, TRAJ41, TRBV7-9, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV21,

TRAJ33, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV17, TRAJ39, TRBV27, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV13-2, TRAJ13, TRBV9, and TRBJ1-3. Such TCR may comprise TRAV21, TRAJ33, TRBV5-1, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV17, TRAJ57, TRBV9, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV5, TRAJ44, TRBV7-9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV3, TRAJ39, TRBV27, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV1-2, TRAJ4, TRBV11-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV38-2DV8, TRAJ40, TRBV7-8, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV8-3, TRAJ41, TRBV7-9, and TRBJ1-1. Such TCR may comprise TRAV5, TRAJ4, TRBV11-2, and TRBJ2-1. Such TCR may comprise TRAV24, TRAJ49, TRBV6-5, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV4, TRAJ45, TRBV24-1, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV29DV5, TRAJ48, TRBV20-1, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV26-2, TRAJ44, TRBV6-1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ27, TRBV7-9, and TRBJ1-6. Such TCR may comprise TRAV26-1, TRAJ49, TRBV7-9, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ5, TRBV7-8, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ33, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ20, TRBV27, TRBD1, and TRBJ2-4. Such TCR may comprise TRAV39, TRAJ42, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV1-2, TRAJ39, TRBV27, TRBD2, and TRBJ1-4. Such TCR may comprise TRAV1-1, TRAJ34, TRBV9, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV25, TRAJ34, TRBV29-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV39, TRAJ39, TRBV30, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ6, TRBV20-1, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV8-6, TRAJ30, TRBV9, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV21, TRAJ18, TRBV27, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV12-3, TRAJ23, TRBV11-3, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV12-1, TRAJ47, TRBV5-6, and TRBJ1-2. Such TCR may comprise TRAV22, TRAJ31, TRBV5-6, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ33, TRBV14, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV1-2, TRAJ31, TRBV2, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV1-2, TRAJ5, TRBV20-1, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ33, TRBV5-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV16, TRAJ28, TRBV7-9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV13-1, TRAJ12, TRBV20-1, TRBD2, and TRBJ1-1. Such TCR may comprise

TRAV17, TRAJ52, TRBV29-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV36DV7, TRAJ49, TRBV15, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV12-3, TRAJ58, TRBV12-4, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV16, TRAJ18, TRBV27, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ33, TRBV27, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV12-2, TRAJ48, TRBV27, and TRBJ2-6. Such TCR may comprise TRAV21, TRAJ33, TRBV2, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV29DV5, TRAJ37, TRBV5-4, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ20, TRBV24-1, TRBD1, and TRBJ1-4. Such TCR may comprise TRAV12-2, TRAJ6, TRBV15, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV12-1, TRAJ42, TRBV27, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV1-1, TRAJ23, TRBV25-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV38-1, TRAJ28, TRBV5-1, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ33, TRBV2, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ31, TRBV5-1, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV8-6, TRAJ42, TRBV27, and TRBJ1-1. Such TCR may comprise TRAV40, TRAJ32, TRBV7-6, and TRBJ2-2. Such TCR may comprise TRAV5, TRAJ5, TRBV20-1, TRBD1, and TRBJ2-5. Such TCR may comprise TRAV12-1, TRAJ40, TRBV4-1, and TRBJ2-5. Such TCR may comprise TRAV13-2, TRAJ53, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV12-2, TRAJ48, TRBV5-6, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV12-3, TRAJ15, TRBV20-1, and TRBJ2-7. Such TCR may comprise TRAV12-3, TRAJ23, TRBV13, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV13-2, TRAJ9, TRBV7-3, and TRBJ1-6. Such TCR may comprise TRAV21, TRAJ45, TRBV5-1, and TRBJ1-1. Such TCR may comprise TRAV25, TRAJ31, TRBV29-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV34, TRAJ37, TRBV28, and TRBJ1-1. Such TCR may comprise TRAV1-2, TRAJ9, TRBV9, TRBD1, and TRBJ2-6. Such TCR may comprise TRAV21, TRAJ36, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ34, TRBV6-1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ26, TRBV11-3, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV17, TRAJ36, TRBV5-4, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ49, TRBV4-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV12-1, TRAJ13, TRBV9, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV24, TRAJ7, TRBV7-9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ20, TRBV9, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV13-2, TRAJ49, TRBV6-1, TRBD1, and TRBJ2-5. Such TCR

may comprise TRAV21, TRAJ33, TRBV5-5, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV12-1, TRAJ39, TRBV4-2, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV26-2, TRAJ30, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV20, TRAJ45, TRBV5-4, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ31, TRBV7-8, TRBD2, and TRBJ1-2. Such TCR may comprise TRAV38-2DV8, TRAJ48, TRBV2, TRBD1, and TRBJ1-5. Such TCR may comprise TRAV25, TRAJ15, TRBV9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ49, TRBV5-4, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ12, TRBV27, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV38-2DV8, TRAJ54, TRBV24-1, and TRBJ2-2. Such TCR may comprise TRAV17, TRAJ52, TRBV27, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ28, TRBV9, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ36, TRBV4-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ31, TRBV5-4, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ33, TRBV5-1, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV12-1, TRAJ43, TRBV6-5, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ41, TRBV9, and TRBJ2-2. Such TCR may comprise TRAV19, TRAJ40, TRBV20-1, and TRBJ2-7. Such TCR may comprise TRAV12-2, TRAJ52, TRBV6-1, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV26-1, TRAJ57, TRBV2, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ36, TRBV12-4, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV8-4, TRAJ34, TRBV7-9, and TRBJ2-7. Such TCR may comprise TRAV19, TRAJ32, TRBV7-9, and TRBJ1-2. Such TCR may comprise TRAV21, TRAJ6, TRBV3-1, TRBD2, and TRBJ1-4. Such TCR may comprise TRAV13-2, TRAJ29, TRBV5-1, and TRBJ2-2. Such TCR may comprise TRAV14DV4, TRAJ26, TRBV7-9, TRBD1, and TRBJ2-5. Such TCR may comprise TRAV35, TRAJ44, TRBV27, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ24, TRBV27, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV25, TRAJ21, TRBV28, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV3, TRAJ36, TRBV28, and TRBJ1-5. Such TCR may comprise TRAV26-2, TRAJ52, TRBV5-6, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV8-6, TRAJ40, TRBV9, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV21, TRAJ42, TRBV28, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV12-1, TRAJ32, TRBV20-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV24, TRAJ24, TRBV28, TRBD2, and TRBJ2-5. Such TCR may comprise TRAV21, TRAJ36, TRBV9, TRBD2, and TRBJ1-1. Such TCR may comprise TRAV12-1, TRAJ26, TRBV2, and TRBJ1-6. Such TCR

may comprise TRAV21, TRAJ31, TRBV29-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV39, TRAJ33, TRBV6-1, and TRBJ1-5. Such TCR may comprise TRAV3, TRAJ38, TRBV27, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV10, TRAJ33, TRBV30, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ20, TRBV2, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV13-1, TRAJ20, TRBV5-1, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV27, TRAJ45, TRBV27, TRBD1, and TRBJ1-6. Such TCR may comprise TRAV21, TRAJ18, TRBV9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV26-2, TRAJ28, TRBV27, and TRBJ1-5. Such TCR may comprise TRAV12-1, TRAJ34, TRBV9, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV13-2, TRAJ40, TRBV4-1, and TRBJ1-3. Such TCR may comprise TRAV12-1, TRAJ34, TRBV4-2, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV13-2, TRAJ46, TRBV7-9, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ36, TRBV9, TRBD2, and TRBJ2-7. Such TCR may comprise TRAV1-2, TRAJ20, TRBV11-3, TRBD1, and TRBJ2-3. Such TCR may comprise TRAV3, TRAJ6, TRBV12-4, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV25, TRAJ32, TRBV19, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV21, TRAJ33, TRBV9, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV19, TRAJ53, TRBV7-7, TRBD1, and TRBJ2-1. Such TCR may comprise TRAV12-1, TRAJ20, TRBV10-3, TRBD2, and TRBJ2-3. Such TCR may comprise TRAV12-1, TRAJ34, TRBV6-5, TRBD1, and TRBJ2-7. Such TCR may comprise TRAV26-2, TRAJ43, TRBV25-1, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV8-6, TRAJ20, TRBV7-9, TRBD1, and TRBJ2-2. Such TCR may comprise TRAV3, TRAJ18, TRBV20-1, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV21, TRAJ40, TRBV11-3, TRBD1, and TRBJ1-2. Such TCR may comprise TRAV2, TRAJ10, TRBV6-5, TRBD2, and TRBJ2-7.

[00315] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise an alpha VJ sequence. The alpha VJ sequence may be any one of SEQ ID NOS 3656-3961 or 4302-4305.

[00316] The TCR specific for A*01:01 _ EVDPIGHLY (SEQ ID NO: 3051) may comprise a beta V(D)J sequence. The beta V(D)J sequence may be any one of SEQ ID NOS 3962-4269 or 4317-4320.

[00317] In some embodiments, the alpha VJ sequence is SEQ ID NO: 3656 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3657 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the

alpha VJ sequence is SEQ ID NO: 3658 and the beta V(D)J sequence is SEQ ID NO: 3964. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3660 and the beta V(D)J sequence is SEQ ID NO: 3965. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3661 and the beta V(D)J sequence is SEQ ID NO: 3966. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3662 and the beta V(D)J sequence is SEQ ID NO: 3967. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3663 and the beta V(D)J sequence is SEQ ID NO: 3968. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3664 and the beta V(D)J sequence is SEQ ID NO: 3969. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3665 and the beta V(D)J sequence is SEQ ID NO: 3970. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3666 and the beta V(D)J sequence is SEQ ID NO: 3971. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3667 and the beta V(D)J sequence is SEQ ID NO: 3972. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3668 and the beta V(D)J sequence is SEQ ID NO: 3973. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3657 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3662 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3669 and the beta V(D)J sequence is SEQ ID NO: 3974. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3670 and the beta V(D)J sequence is SEQ ID NO: 3975. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3658 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3671 and the beta V(D)J sequence is SEQ ID NO: 3976. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3672 and the beta V(D)J sequence is SEQ ID NO: 3977. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3673 and the beta V(D)J sequence is SEQ ID NO: 3978. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3674 and the beta V(D)J sequence is SEQ ID NO: 3979. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3967. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3675 and the beta V(D)J sequence is SEQ ID NO: 3980. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3966. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3676 and the beta V(D)J sequence is SEQ ID NO: 3981. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3964. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3677 and the beta V(D)J sequence is SEQ ID NO: 3982. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3678 and the beta V(D)J sequence is SEQ ID NO: 3983. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3662 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3679 and the beta V(D)J sequence is SEQ ID NO: 3984. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3680 and the beta V(D)J sequence is SEQ ID NO: 3985. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3681 and the beta V(D)J sequence is SEQ ID NO: 3986. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3682 and the beta V(D)J sequence is SEQ ID NO: 3987. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3683 and the beta V(D)J sequence is SEQ ID NO: 3988. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3684 and the beta V(D)J sequence is SEQ ID NO: 3989. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3685 and the beta V(D)J sequence is SEQ ID NO: 3990. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3686 and the beta V(D)J sequence is SEQ ID NO: 3991. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3687 and the beta V(D)J sequence is SEQ ID NO: 3992. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3688 and the beta V(D)J sequence is SEQ ID NO: 3993. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3689 and the beta V(D)J sequence is SEQ ID NO: 3994. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3690 and the beta V(D)J sequence is SEQ ID NO: 3995. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3691 and the beta V(D)J sequence is SEQ ID NO: 3996. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3692 and the beta V(D)J sequence is SEQ ID NO: 3997. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3693 and the beta V(D)J sequence is SEQ ID NO: 3998. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3694 and the beta V(D)J sequence is SEQ ID NO: 3999. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3695 and the beta V(D)J sequence is SEQ ID NO: 4000. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3661 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3696 and the beta V(D)J sequence is SEQ ID NO: 4001. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3697 and the beta V(D)J sequence is SEQ ID NO: 4002. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3698 and the beta V(D)J sequence is SEQ ID NO: 4003. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3699 and the beta V(D)J sequence is SEQ ID NO: 4004. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3700 and the beta V(D)J sequence is SEQ ID NO: 3967. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3701 and the beta V(D)J sequence is SEQ ID NO: 4005. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3658 and the beta V(D)J sequence is SEQ ID NO: 3974. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3702 and the beta V(D)J sequence is SEQ ID NO: 4006. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3658 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3703 and the beta V(D)J sequence is SEQ ID NO: 4007. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3657 and the beta V(D)J sequence is SEQ ID NO: 3966. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3704 and the beta V(D)J sequence is SEQ ID NO: 4008. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3705 and the beta V(D)J sequence is SEQ ID NO: 4009. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3706 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3707 and the beta V(D)J sequence is SEQ ID NO: 4010. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3657 and the beta V(D)J sequence is SEQ ID NO: 3964. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3708 and the beta V(D)J sequence is SEQ ID NO: 4011. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3709 and the beta V(D)J sequence is SEQ ID NO: 4012. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3663 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3710 and the beta V(D)J sequence is SEQ ID NO: 4013. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3711 and the beta V(D)J sequence is SEQ ID NO: 4014. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3712 and the beta V(D)J sequence is SEQ ID NO: 4015. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3713 and the beta V(D)J sequence is SEQ ID NO: 4016. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3714 and the beta V(D)J sequence is SEQ ID NO: 4017. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3715 and the beta V(D)J sequence is SEQ ID NO: 4018. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3716 and the beta V(D)J sequence is SEQ ID NO: 4019. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3717 and the beta V(D)J sequence is SEQ ID NO: 4020. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3718 and the beta V(D)J sequence is SEQ ID NO: 4021. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3719 and the beta V(D)J sequence is SEQ ID NO: 4022. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3720 and the beta V(D)J sequence is SEQ ID NO: 4023. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3663 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3965. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3677 and the beta V(D)J sequence is SEQ ID NO: 4024. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3721 and the beta V(D)J sequence is SEQ ID NO: 4025. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3722 and the beta V(D)J sequence is SEQ ID NO: 4026. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3663 and the beta V(D)J sequence is SEQ ID NO: 3966. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 4027. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3722 and the beta V(D)J sequence is SEQ ID NO: 3964. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3723 and the beta V(D)J sequence is SEQ ID NO: 4028. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3724 and the beta V(D)J sequence is SEQ ID NO: 4029. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3725 and the beta V(D)J sequence is SEQ ID NO: 4030. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3726 and the beta V(D)J sequence is SEQ ID NO: 4031. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3727 and the beta V(D)J sequence is SEQ ID NO: 4032. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3728 and the beta V(D)J sequence is SEQ ID NO: 4033. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3729 and the beta V(D)J sequence is SEQ ID NO: 4034. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3658 and the beta V(D)J sequence is SEQ ID NO: 3978. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3730 and the beta V(D)J sequence is SEQ ID NO: 4035. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3731 and the beta V(D)J sequence is SEQ ID NO: 4036. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3732 and the beta V(D)J sequence is SEQ ID NO: 4037. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3719 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3665 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3664 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3676 and the beta V(D)J sequence is SEQ ID NO: 3966. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3733 and the beta V(D)J sequence is SEQ ID NO: 4038. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3734 and the beta V(D)J sequence is SEQ ID NO: 4039. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3735 and the beta V(D)J sequence is SEQ ID NO: 4040. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3736 and the beta V(D)J sequence is SEQ ID NO: 4041. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3737 and the beta V(D)J sequence is SEQ ID NO: 4042. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3738 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3659 and the beta V(D)J sequence is SEQ ID NO: 3973. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3660 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3739 and the beta V(D)J sequence is SEQ ID NO: 4043. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3740 and the beta V(D)J sequence is SEQ ID NO: 4044. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3741 and the beta V(D)J sequence is SEQ ID NO: 4045. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3657 and the beta V(D)J sequence is SEQ ID NO: 3992. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3742 and the beta V(D)J sequence is SEQ ID NO: 4046. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3666 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3711 and the beta V(D)J sequence is SEQ ID NO: 3963. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3660 and the beta V(D)J sequence is SEQ ID NO: 3962. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3663 and the beta V(D)J sequence is SEQ ID NO: 3964. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3743 and the beta V(D)J sequence is SEQ ID NO: 4047. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3744 and the beta V(D)J sequence is SEQ ID NO: 4048. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3745 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3746 and the beta V(D)J sequence is SEQ ID NO: 4050. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3747 and the beta V(D)J sequence is SEQ ID NO: 4051. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3748 and the beta V(D)J sequence is SEQ ID NO: 4052. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3749 and the beta V(D)J sequence is SEQ ID NO: 4053. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3750 and the beta V(D)J sequence is SEQ ID NO: 4054. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3751 and the beta V(D)J sequence is SEQ ID NO: 4055. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3752 and the beta V(D)J sequence is SEQ ID NO: 4056. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3753 and the beta V(D)J sequence is SEQ ID NO: 4057. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3754 and the beta V(D)J sequence is SEQ ID NO: 4058. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3755 and the beta V(D)J sequence is SEQ ID NO: 4057. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3756 and the beta V(D)J sequence is SEQ ID NO: 4059. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3757 and the beta V(D)J sequence is SEQ ID NO: 4060. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3758 and the beta V(D)J sequence is SEQ ID NO: 4061. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3759 and the beta V(D)J sequence is SEQ ID NO: 4062. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3760 and the beta V(D)J sequence is SEQ ID NO: 4063. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3761 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3748 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3762 and the beta V(D)J sequence is SEQ ID NO: 4064. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3763 and the beta V(D)J sequence is SEQ ID NO: 4065. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3764 and the beta V(D)J sequence is SEQ ID NO: 4066. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3765 and the beta V(D)J sequence is SEQ ID NO: 4067. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3746 and the beta V(D)J sequence is SEQ ID NO: 4053. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3766 and the beta V(D)J sequence is SEQ ID NO: 4068. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3761 and the beta V(D)J sequence is SEQ ID NO: 4069. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3767 and the beta V(D)J sequence is SEQ ID NO: 4070. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3768 and the beta V(D)J sequence is SEQ ID NO: 4071. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3769 and the beta V(D)J sequence is SEQ ID NO: 4072. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3770 and the beta V(D)J sequence is SEQ ID NO: 4073. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3771 and the beta V(D)J sequence is SEQ ID NO: 4074. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3772 and the beta V(D)J sequence is SEQ ID NO: 4075. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3773 and the beta V(D)J sequence is SEQ ID NO: 4076. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3774 and the beta V(D)J sequence is SEQ ID NO: 4077. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3775 and the beta V(D)J sequence is SEQ ID NO: 4078. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3746 and the beta V(D)J sequence is SEQ ID NO: 4055. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3745 and the beta V(D)J sequence is SEQ ID NO: 4051. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3776 and the beta V(D)J sequence is SEQ ID NO: 4079. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3777 and the beta V(D)J sequence is SEQ ID NO: 4080. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3778 and the beta V(D)J sequence is SEQ ID NO: 4081. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3779 and the beta V(D)J sequence is SEQ ID NO: 4082. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3780 and the beta V(D)J sequence is SEQ ID NO: 4083. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3746 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3781 and the beta V(D)J sequence is SEQ ID NO: 4084. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3782 and the beta V(D)J sequence is SEQ ID NO: 4085. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3783 and the beta V(D)J sequence is SEQ ID NO: 4086. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3784 and the beta V(D)J sequence is SEQ ID NO: 4087. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3785 and the beta V(D)J sequence is SEQ ID NO: 4088. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3786 and the beta V(D)J sequence is SEQ ID NO: 4089. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3787 and the beta V(D)J sequence is SEQ ID NO: 4090. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3788 and the beta V(D)J sequence is SEQ ID NO: 4091. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3789 and the beta V(D)J sequence is SEQ ID NO: 4092. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3790 and the beta V(D)J sequence is SEQ ID NO: 4093. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3791 and the beta V(D)J sequence is SEQ ID NO: 4094. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3755 and the beta V(D)J sequence is SEQ ID NO: 4095. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3792 and the beta V(D)J sequence is SEQ ID NO: 4096. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3793 and the beta V(D)J sequence is SEQ ID NO: 4097. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3794 and the beta V(D)J sequence is SEQ ID NO: 4098. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3795 and the beta V(D)J sequence is SEQ ID NO: 4099. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3796 and the beta V(D)J sequence is SEQ ID NO: 4100. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3797 and the beta V(D)J sequence is SEQ ID NO: 4101. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3798 and the beta V(D)J sequence is SEQ ID NO: 4102. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3799 and the beta V(D)J sequence is SEQ ID NO: 4095. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3800 and the beta V(D)J sequence is SEQ ID NO: 4103. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3801 and the beta V(D)J sequence is SEQ ID NO: 4104. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3802 and the beta V(D)J sequence is SEQ ID NO: 4105. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3803 and the beta V(D)J sequence is SEQ ID NO: 4106. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3804 and the beta V(D)J sequence is SEQ ID NO: 4107. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3805 and the beta V(D)J sequence is SEQ ID NO: 4108. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3806 and the beta V(D)J sequence is SEQ ID NO: 4109. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3807 and the beta V(D)J sequence is SEQ ID NO: 4110. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3808 and the beta V(D)J sequence is SEQ ID NO: 4111. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3809 and the beta V(D)J sequence is SEQ ID NO: 4112. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3810 and the beta V(D)J sequence is SEQ ID NO: 4113. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3746 and the beta V(D)J sequence is SEQ ID NO: 4062. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3811 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3812 and the beta V(D)J sequence is SEQ ID NO: 4114. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3747 and the beta V(D)J sequence is SEQ ID NO: 4049. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3813 and the beta V(D)J sequence is SEQ ID NO: 4115. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3814 and the beta V(D)J sequence is SEQ ID NO: 4116. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3815 and the beta V(D)J sequence is SEQ ID NO: 4117. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3816 and the beta V(D)J sequence is SEQ ID NO: 4118. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3817 and the beta V(D)J sequence is SEQ ID NO: 4119. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3818 and the beta V(D)J sequence is SEQ ID NO: 4120. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3758 and the beta V(D)J sequence is SEQ ID NO: 4053. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3819 and the beta V(D)J sequence is SEQ ID NO: 4121. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3820 and the beta V(D)J sequence is SEQ ID NO: 4122. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3821 and the beta V(D)J sequence is SEQ ID NO: 4123. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3822 and the beta V(D)J sequence is SEQ ID NO: 4124. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3823 and the beta V(D)J sequence is SEQ ID NO: 4125. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3824 and the beta V(D)J sequence is SEQ ID NO: 4126. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3825 and the beta V(D)J sequence is SEQ ID NO: 4127. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3826 and the beta V(D)J sequence is SEQ ID NO: 4128. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3827 and the beta V(D)J sequence is SEQ ID NO: 4129. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4130. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3829 and the beta V(D)J sequence is SEQ ID NO: 4131. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3830 and the beta V(D)J sequence is SEQ ID NO: 4132. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3831 and the beta V(D)J sequence is SEQ ID NO: 4133. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3832 and the beta V(D)J sequence is SEQ ID NO: 4134. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4131. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3833 and the beta V(D)J sequence is SEQ ID NO: 4135. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3834 and the beta V(D)J sequence is SEQ ID NO: 4136. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3835 and the beta V(D)J sequence is SEQ ID NO: 4137. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3836 and the beta V(D)J sequence is SEQ ID NO: 4138. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3837 and the beta V(D)J sequence is SEQ ID NO: 4139. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3838 and the beta V(D)J sequence is SEQ ID NO: 4140. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3839 and the beta V(D)J sequence is SEQ ID NO: 4141. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3840 and the beta V(D)J sequence is SEQ ID NO: 4142. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3841 and the beta V(D)J sequence is SEQ ID NO: 4143. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4138. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3842 and the beta V(D)J sequence is SEQ ID NO: 4144. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3843 and the beta V(D)J sequence is SEQ ID NO: 4145. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3844 and the beta V(D)J sequence is SEQ ID NO: 4133. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4143. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3845 and the beta V(D)J sequence is SEQ ID NO: 4146. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3846 and the beta V(D)J sequence is SEQ ID NO: 4147. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4145. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3847 and the beta V(D)J sequence is SEQ ID NO: 4148. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3848 and the beta V(D)J sequence is SEQ ID NO: 4149. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3849 and the beta V(D)J sequence is SEQ ID NO: 4150. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3850 and the beta V(D)J sequence is SEQ ID NO: 4151. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3851 and the beta V(D)J sequence is SEQ ID NO: 4152. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3852 and the beta V(D)J sequence is SEQ ID NO: 4153. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3853 and the beta V(D)J sequence is SEQ ID NO: 4154. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3854 and the beta V(D)J sequence is SEQ ID NO: 4155. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3855 and the beta V(D)J sequence is SEQ ID NO: 4156. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3831 and the beta V(D)J sequence is SEQ ID NO: 4157. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3856 and the beta V(D)J sequence is SEQ ID NO: 4158. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3857 and the beta V(D)J sequence is SEQ ID NO: 4159. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3858 and the beta V(D)J sequence is SEQ ID NO: 4160. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3859 and the beta V(D)J sequence is SEQ ID NO: 4161. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4137. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3860 and the beta V(D)J sequence is SEQ ID NO: 4162. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3861 and the beta V(D)J sequence is SEQ ID NO: 4163. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3862 and the beta V(D)J sequence is SEQ ID NO: 4164. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3863 and the beta V(D)J sequence is SEQ ID NO: 4165. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3864 and the beta V(D)J sequence is SEQ ID NO: 4166. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3865 and the beta V(D)J sequence is SEQ ID NO: 4167. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3866 and the beta V(D)J sequence is SEQ ID NO: 4168. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3867 and the beta V(D)J sequence is SEQ ID NO: 4169. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3868 and the beta V(D)J sequence is SEQ ID NO: 4170. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3869 and the beta V(D)J sequence is SEQ ID NO: 4171. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3870 and the beta V(D)J sequence is SEQ ID NO: 4172. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3871 and the beta V(D)J sequence is SEQ ID NO: 4173. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4132. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3872 and the beta V(D)J sequence is SEQ ID NO: 4174. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3873 and the beta V(D)J sequence is SEQ ID NO: 4175. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4176. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3874 and the beta V(D)J sequence is SEQ ID NO: 4177. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3875 and the beta V(D)J sequence is SEQ ID NO: 4178. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3876 and the beta V(D)J sequence is SEQ ID NO: 4179. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3877 and the beta V(D)J sequence is SEQ ID NO: 4180. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3878 and the beta V(D)J sequence is SEQ ID NO: 4181. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3879 and the beta V(D)J sequence is SEQ ID NO: 4182. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4141. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3880 and the beta V(D)J sequence is SEQ ID NO: 4183. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4184. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3881 and the beta V(D)J sequence is SEQ ID NO: 4185. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3830 and the beta V(D)J sequence is SEQ ID NO: 4135. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3882 and the beta V(D)J sequence is SEQ ID NO: 4186. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3883 and the beta V(D)J sequence is SEQ ID NO: 4187. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3884 and the beta V(D)J sequence is SEQ ID NO: 4188. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3885 and the beta V(D)J sequence is SEQ ID NO: 4189. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4190. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3841 and the beta V(D)J sequence is SEQ ID NO: 4130. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3886 and the beta V(D)J sequence is SEQ ID NO: 4191. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3887 and the beta V(D)J sequence is SEQ ID NO: 4192. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3888 and the beta V(D)J sequence is SEQ ID NO: 4193. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3889 and the beta V(D)J sequence is SEQ ID NO: 4194. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3890 and the beta V(D)J sequence is SEQ ID NO: 4195. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3891 and the beta V(D)J sequence is SEQ ID NO: 4196. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3892 and the beta V(D)J sequence is SEQ ID NO: 4197. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3893 and the beta V(D)J sequence is SEQ ID NO: 4198. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3894 and the beta V(D)J sequence is SEQ ID NO: 4199. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3895 and the beta V(D)J sequence is SEQ ID NO: 4200. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3896 and the beta V(D)J sequence is SEQ ID NO: 4201. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3897 and the beta V(D)J sequence is SEQ ID NO: 4202. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3898 and the beta V(D)J sequence is SEQ ID NO: 4203. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3899 and the beta V(D)J sequence is SEQ ID NO: 4204. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3900 and the beta V(D)J sequence is SEQ ID NO: 4205. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3901 and the beta V(D)J sequence is SEQ ID NO: 4206. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3902 and the beta V(D)J sequence is SEQ ID NO: 4207. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3903 and the beta V(D)J sequence is SEQ ID NO: 4208. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3904 and the beta V(D)J sequence is SEQ ID NO: 4209. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3905 and the beta V(D)J sequence is SEQ ID NO: 4210. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3830 and the beta V(D)J sequence is SEQ ID NO: 4211. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3906 and the beta V(D)J sequence is SEQ ID NO: 4212. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3828 and the beta V(D)J sequence is SEQ ID NO: 4213. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3907 and the beta V(D)J sequence is SEQ ID NO: 4214. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3908 and the beta V(D)J sequence is SEQ ID NO: 4215. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3909 and the beta V(D)J sequence is SEQ ID NO: 4216. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3910 and the beta V(D)J sequence is SEQ ID NO: 4217. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3911 and the beta V(D)J sequence is SEQ ID NO: 4218. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3912 and the beta V(D)J sequence is SEQ ID NO: 4219. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3913 and the beta V(D)J sequence is SEQ ID NO: 4220. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3914 and the beta V(D)J sequence is SEQ ID NO: 4221. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3915 and the beta V(D)J sequence is SEQ ID NO: 4222. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3916 and the beta V(D)J sequence is SEQ ID NO: 4223. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3917 and the beta V(D)J sequence is SEQ ID NO: 4224. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3899 and the beta V(D)J sequence is SEQ ID NO: 4208. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3918 and the beta V(D)J sequence is SEQ ID NO: 4225. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3919 and the beta V(D)J sequence is SEQ ID NO: 4226. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3920 and the beta V(D)J sequence is SEQ ID NO: 4227. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3921 and the beta V(D)J sequence is SEQ ID NO: 4228. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3922 and the beta V(D)J sequence is SEQ ID NO: 4229. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3923 and the beta V(D)J sequence is SEQ ID NO: 4230. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3924 and the beta V(D)J sequence is SEQ ID NO: 4231. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3899 and the beta V(D)J sequence is SEQ ID NO: 4232. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3925 and the beta V(D)J sequence is SEQ ID NO: 4233. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3926 and the beta V(D)J sequence is SEQ ID NO: 4234. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3927 and the beta V(D)J sequence is SEQ ID NO: 4235. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3928 and the beta V(D)J sequence is SEQ ID NO: 4236. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3929 and the beta V(D)J sequence is SEQ ID NO: 4237. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3930 and the beta V(D)J sequence is SEQ ID NO: 4238. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3931 and the beta V(D)J sequence is SEQ ID NO: 4239. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3932 and the beta V(D)J sequence is SEQ ID NO: 4240. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3933 and the beta V(D)J sequence is SEQ ID NO: 4241. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3934 and the beta V(D)J sequence is SEQ ID NO: 4242. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3935 and the beta V(D)J sequence is SEQ ID NO: 4215. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3936 and the beta V(D)J sequence is SEQ ID NO: 4243. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3937 and the beta V(D)J sequence is SEQ ID NO: 4244. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3938 and the beta V(D)J sequence is SEQ ID NO: 4245. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3899 and the beta V(D)J sequence is SEQ ID NO: 4211. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3939 and the beta V(D)J sequence is SEQ ID NO: 4246. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3940 and the beta V(D)J sequence is SEQ ID NO: 4247. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3941 and the beta V(D)J sequence is SEQ ID NO: 4248. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3942 and the beta V(D)J sequence is SEQ ID NO: 4249. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3943 and the beta V(D)J sequence is SEQ ID NO: 4250. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3944 and the beta V(D)J sequence is SEQ ID NO: 4251. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3945 and the beta V(D)J sequence is SEQ ID NO: 4252. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3946 and the beta V(D)J sequence is SEQ ID NO: 4253. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3947 and the beta V(D)J sequence is SEQ ID NO: 4254. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3948 and the beta V(D)J sequence is SEQ ID NO: 4255. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3900 and the beta V(D)J sequence is SEQ ID NO: 4209. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3949 and the beta V(D)J sequence is SEQ ID NO: 4256. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3900 and the beta V(D)J sequence is SEQ ID NO: 4214. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3950 and the beta V(D)J sequence is SEQ ID NO: 4257. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3899 and the beta V(D)J sequence is SEQ ID NO: 4224. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3951 and the beta V(D)J sequence is SEQ ID NO: 4258. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3952 and the beta V(D)J sequence is SEQ ID NO: 4259. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3953 and the beta V(D)J sequence is SEQ ID NO: 4260. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3751 and the beta V(D)J sequence is SEQ ID NO: 4261. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3954 and the beta V(D)J sequence is SEQ ID NO: 4262. In some embodiments, the alpha VJ sequence

is SEQ ID NO: 3955 and the beta V(D)J sequence is SEQ ID NO: 4263. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3956 and the beta V(D)J sequence is SEQ ID NO: 4264. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3957 and the beta V(D)J sequence is SEQ ID NO: 4265. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3958 and the beta V(D)J sequence is SEQ ID NO: 4266. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3959 and the beta V(D)J sequence is SEQ ID NO: 4267. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3960 and the beta V(D)J sequence is SEQ ID NO: 4268. In some embodiments, the alpha VJ sequence is SEQ ID NO: 3961 and the beta V(D)J sequence is SEQ ID NO: 4269. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4302 and the beta V(D)J sequence is SEQ ID NO: 4317. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4303 and the beta V(D)J sequence is SEQ ID NO: 4318. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4304 and the beta V(D)J sequence is SEQ ID NO: 4319. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4305 and the beta V(D)J sequence is SEQ ID NO: 4320.

Target-specific TCRs to B*44:02_GEMSSNSTAL (SEQ ID NO: 4272)

[00318] In some aspects, provided herein are ABPs comprising TCRs or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA Class I molecule of the HLA-PEPTIDE target is HLA subtype B*44:02 and the HLA-restricted peptide of the HLA-PEPTIDE target comprises the sequence GEMSSNSTAL (SEQ ID NO: 4272).

[00319] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise an αCDR3 sequence. The αCDR3 sequence may be any one of SEQ ID NOS 4284-4286 or 3138.

[00320] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise a βCDR3 sequence. The βCDR3 sequence may be any one of SEQ ID NOS 4298-4301.

[00321] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise a particular αCDR3sequence and a particular βCDR3 sequence. The αCDR3 may be SEQ ID NO: 4284 and the βCDR3 may be SEQ ID NO: 4298. The αCDR3 may be SEQ ID NO: 4285 and the βCDR3 may be SEQ ID NO: 4299. The αCDR3 may be SEQ ID NO:

4286 and the βCDR3 may be SEQ ID NO: 4300. The αCDR3 may be SEQ ID NO: 3138 and the βCDR3 may be SEQ ID NO: 4301.

[00322] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise a TRAV, a TRAJ, a TRBV, optionally a TRBD, and a TRBJ amino acid sequence, optionally a TRAC sequence and optionally a TRBC sequence. Such TCR may comprise TRAV19, TRAJ39, TRBV7-6, TRBD1, and TRBJ1-1. Such TCR may comprise TRAV36DV7, TRAJ34, TRBV7-6, TRBD2, and TRBJ2-2. Such TCR may comprise TRAV24, TRAJ15, TRBV7-6, TRBD2, and TRBJ2-1. Such TCR may comprise TRAV8-4, TRAJ12, TRBV12-4, TRBD2, and TRBJ2-3.

[00323] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise an alpha VJ sequence. The alpha VJ sequence may be any one of SEQ ID NOS 4313-4316.

[00324] The TCR specific for B*44:02_GEMSSNSTAL (SEQ ID NO: 4272) may comprise a beta V(D)J sequence. The beta V(D)J sequence may be any one of SEQ ID NOS 4328-4331.

[00325] In some embodiments, the alpha VJ sequence is SEQ ID NO: 4313 and the beta V(D)J sequence is SEQ ID NO: 4328. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4314 and the beta V(D)J sequence is SEQ ID NO: 4329. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4315 and the beta V(D)J sequence is SEQ ID NO: 4330. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4316 and the beta V(D)J sequence is SEQ ID NO: 4331.

Target-specific TCRs to A*02:01_GVYDGEEHSV (SEQ ID NO: 4271)

[00326] In some aspects, provided herein are ABPs comprising TCRs or antigen-binding fragments thereof that specifically bind an HLA-PEPTIDE target, wherein the HLA Class I molecule of the HLA-PEPTIDE target is HLA subtype A*02:01 and the HLA-restricted peptide of the HLA-PEPTIDE target comprises the sequence GVYDGEEHSV (SEQ ID NO: 4271).

[00327] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise an αCDR3 sequence. The αCDR3 sequence may be any one of SEQ ID NOS 4282-4283.

[00328] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise a βCDR3 sequence. The βCDR3 sequence may be any one of SEQ ID NOS 4296-4297.

[00329] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise a particular αCDR3 sequence and a particular βCDR3 sequence. The αCDR3 may be SEQ ID NO: 4282 and the βCDR3 may be SEQ ID NO: 4296. The αCDR3 may be SEQ ID NO: 4283 and the βCDR3 may be SEQ ID NO: 4297.

[00330] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise a TRAV, a TRAJ, a TRBV, optionally a TRBD, and a TRBJ amino acid sequence, optionally a TRAC sequence and optionally a TRBC sequence. Such TCR may comprise TRAV13-1, TRAJ11, TRBV6-3, and TRBJ2-1. Such TCR may comprise TRAV14DV4, TRAJ54, TRBV4-3, TRBD1, and TRBJ2-4.

[00331] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise an alpha VJ sequence. The alpha VJ sequence may be any one of SEQ ID NOS 4311-4312.

[00332] The TCR specific for A*02:01_GVYDGEEHSV (SEQ ID NO: 4271) may comprise a beta V(D)J sequence. The beta V(D)J sequence may be any one of SEQ ID NOS 4326-4327.

[00333] In some embodiments, the alpha VJ sequence is SEQ ID NO: 4311 and the beta V(D)J sequence is SEQ ID NO: 4326. In some embodiments, the alpha VJ sequence is SEQ ID NO: 4312 and the beta V(D)J sequence is SEQ ID NO: 4327.

Engineered Cells

[00334] Also provided are cells such as cells that contain an antigen receptor, e.g., that contains an extracellular domain including an anti-HLA-PEPTIDE ABP (e.g., a CAR or TCR), described herein. Also provided are populations of such cells, and compositions containing such cells. In some embodiments, compositions or populations are enriched for such cells, such as in which cells expressing the HLA-PEPTIDE ABP make up at least 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or more than 99 percent of the total cells in the composition or cells of a certain type such as T cells or CD8+ or CD4+ cells. In some embodiments, a composition comprises at least one cell containing an antigen receptor disclosed herein. Among the compositions are pharmaceutical compositions and formulations for

administration, such as for adoptive cell therapy. Also provided are therapeutic methods for administering the cells and compositions to subjects, e.g., patients.

[00335] Thus also provided are genetically engineered cells expressing an ABP comprising a receptor, e.g., a TCR or CAR. The cells generally are eukaryotic cells, such as mammalian cells, and typically are human cells. In some embodiments, the cells are derived from the blood, bone marrow, lymph, or lymphoid organs, are cells of the immune system, such as cells of the innate or adaptive immunity, e.g., myeloid or lymphoid cells, including lymphocytes, typically T cells and/or NK cells. Other exemplary cells include stem cells, such as multipotent and pluripotent stem cells, including induced pluripotent stem cells (iPSCs). The cells typically are primary cells, such as those isolated directly from a subject and/or isolated from a subject and frozen. In some embodiments, the cells include one or more subsets of T cells or other cell types, such as whole T cell populations, CD4+ cells, CD8+ cells, and subpopulations thereof, such as those defined by function, activation state, maturity, potential for differentiation, expansion, recirculation, localization, and/or persistence capacities, antigen-specificity, type of antigen receptor, presence in a particular organ or compartment, marker or cytokine secretion profile, and/or degree of differentiation. With reference to the subject to be treated, the cells may be allogeneic and/or autologous. Among the methods include off-the-shelf methods. In some aspects, such as for off-the-shelf technologies, the cells are pluripotent and/or multipotent, such as stem cells, such as induced pluripotent stem cells (iPSCs). In some embodiments, the methods include isolating cells from the subject, preparing, processing, culturing, and/or engineering them, as described herein, and re-introducing them into the same patient, before or after cryopreservation.

[00336] Among the sub-types and subpopulations of T cells and/or of CD4+ and/or of CD8+ T cells are naive T (TN) cells, effector T cells (TEFF), memory T cells and sub-types thereof, such as stem cell memory T (TSCM), central memory T (TCM), effector memory T (TEM), or terminally differentiated effector memory T cells, tumor-infiltrating lymphocytes (TIL), immature T cells, mature T cells, helper T cells, cytotoxic T cells, mucosa-associated invariant T (MALT) cells, naturally occurring and adaptive regulatory T (Treg) cells, helper T cells, such as TH1 cells, TH2 cells, TH3 cells, TH17 cells, TH9 cells, TH22 cells, follicular helper T cells, alpha/beta T cells, and delta/gamma T cells.

[00337] In some embodiments, the cells are natural killer (NK) cells. In some embodiments, the cells are monocytes or granulocytes, e.g., myeloid cells, macrophages, neutrophils, dendritic cells, mast cells, eosinophils, and/or basophils.

[00338] The cells may be genetically modified to reduce expression or knock out endogenous TCRs. Such modifications are described in Mol Ther Nucleic Acids. 2012 Dec; 1(12): e63; Blood. 2011 Aug 11;118(6):1495-503; Blood. 2012 Jun 14; 119(24): 5697–5705; Torikai, Hiroki et al "HLA and TCR Knockout by Zinc Finger Nucleases: Toward "off-the-Shelf" Allogeneic T-Cell Therapy for CD19+ Malignancies.." Blood 116.21 (2010): 3766; Blood. 2018 Jan 18;131(3):311-322. doi: 10.1182/blood-2017-05-787598; and WO2016069283, which are incorporated by reference in their entirety.

[00339] The cells may be genetically modified to promote cytokine secretion. Such modifications are described in Hsu C, Hughes MS, Zheng Z, Bray RB, Rosenberg SA, Morgan RA. Primary human T lymphocytes engineered with a codon-optimized IL-15 gene resist cytokine withdrawal-induced apoptosis and persist long-term in the absence of exogenous cytokine. J Immunol. 2005;175:7226–34; Quintarelli C, Vera JF, Savoldo B, Giordano Attianese GM, Pule M, Foster AE, Co-expression of cytokine and suicide genes to enhance the activity and safety of tumor-specific cytotoxic T lymphocytes. Blood. 2007;110:2793–802; and Hsu C, Jones SA, Cohen CJ, Zheng Z, Kerstann K, Zhou J,Cytokine-independent growth and clonal expansion of a primary human CD8+ T-cell clone following retroviral transduction with the IL-15 gene. Blood. 2007;109:5168–77.

[00340] Mismatching of chemokine receptors on T cells and tumor-secreted chemokines has been shown to account for the suboptimal trafficking of T cells into the tumor microenvironment. To improve efficacy of therapy, the cells may be genetically modified to increase recognition of chemokines in tumor micro environment. Examples of such modifications are described in Moon, EKCarpenito, CSun, JWang, LCKapoor, VPredina, J Expression of a functional CCR2 receptor enhances tumor localization and tumor eradication by retargeted human T cells expressing a mesothelin-specific chimeric antibody receptor.Clin Cancer Res. 2011; 17: 4719-4730; and.Craddock, JALu, ABear, APule, MBrenner, MKRooney, CM et al. Enhanced tumor trafficking of GD2 chimeric antigen receptor T cells by expression of the chemokine receptor CCR2b.J Immunother. 2010; 33: 780-788.

[00341] The cells may be genetically modified to enhance expression of costimulatory/enhancing receptors, such as CD28 and 41BB.

[00342] Adverse effects of T cell therapy can include cytokine release syndrome and prolonged B-cell depletion. Introduction of a suicide/safety switch in the recipient cells may improve the safety profile of a cell-based therapy. Accordingly, the cells may be genetically modified to include a suicide/safety switch. The suicide/safety switch may be a gene that confers sensitivity to an agent, e.g., a drug, upon the cell in which the gene is expressed, and which causes the cell to die when the cell is contacted with or exposed to the agent. Exemplary suicide/safety switches are described in Protein Cell. 2017 Aug; 8(8): 573–589. The suicide/safety switch may be HSV-TK. The suicide/safety switch may be cytosine daminase, purine nucleoside phosphorylase, or nitroreductase. The suicide/safety switch may be RapaCIDe™, described in U.S. Patent Application Pub. No. US20170166877A1. The suicide/safety switch system may be CD20/Rituximab, described in Haematologica. 2009 Sep; 94(9): 1316–1320. These references are incorporated by reference in their entirety.

[00343] The TCR or CAR may be introduced into the recipient cell as a split receptor which assembles only in the presence of a heterodimerizing small molecule. Such systems are described in Science. 2015 Oct 16; 350(6258): aab4077, and in U.S. Patent No. 9,587,020, which are hereby incorporated by reference.

[00344] In some embodiments, the cells include one or more nucleic acids, e.g., a polynucleotide encoding a TCR or CAR disclosed herein, wherein the polynucleotide is introduced via genetic engineering, and thereby express recombinant or genetically engineered TCRs or CARs as disclosed herein. In some embodiments, the nucleic acids are heterologous, i.e., normally not present in a cell or sample obtained from the cell, such as one obtained from another organism or cell, which for example, is not ordinarily found in the cell being engineered and/or an organism from which such cell is derived. In some embodiments, the nucleic acids are not naturally occurring, such as a nucleic acid not found in nature, including one comprising chimeric combinations of nucleic acids encoding various domains from multiple different cell types.

[00345] The nucleic acids may include a codon-optimized nucleotide sequence. Without being bound to a particular theory or mechanism, it is believed that codon optimization of the nucleotide sequence increases the translation efficiency of the mRNA transcripts. Codon optimization of the nucleotide sequence may involve substituting a native codon for another codon that encodes the same amino acid, but can be translated by tRNA that is more readily available within a cell, thus increasing translation efficiency. Optimization of the nucleotide

sequence may also reduce secondary mRNA structures that would interfere with translation, thus increasing translation efficiency.

[00346] A construct or vector may be used to introduce the TCR or CAR into the recipient cell. Exemplary constructs are described herein. Polynucleotides encoding the alpha and beta chains of the TCR or CAR may in a single construct or in separate constructs. The polynucleotides encoding the alpha and beta chains may be operably linked to a promoter, e.g., a heterologous promoter. The heterologous promoter may be a strong promoter, e.g., EF1alpha, CMV, PGK1, Ubc, beta actin, CAG promoter, and the like. The heterologous promoter may be a weak promoter. The heterologous promoter may be an inducible promoter. Exemplary inducible promoters include, but are not limited to TRE, NFAT, GAL4, LAC, and the like. Other exemplary inducible expression systems are described in U.S. Patent Nos. 5,514,578; 6,245,531; 7,091,038 and European Patent No. 0517805, which are incorporated by reference in their entirety.

[00347] The construct for introducing the TCR or CAR into the recipient cell may also comprise a polynucleotide encoding a signal peptide (signal peptide element). The signal peptide may promote surface trafficking of the introduced TCR or CAR. Exemplary signal peptides include, but are not limited to CD8 signal peptide, immunoglobulin signal peptides, where specific examples include GM-CSF and IgG kappa. Such signal peptides are described in Trends Biochem Sci. 2006 Oct;31(10):563-71. Epub 2006 Aug 21; and An, et al. "Construction of a New Anti-CD19 Chimeric Antigen Receptor and the Anti-Leukemia Function Study of the Transduced T Cells." Oncotarget 7.9 (2016): 10638–10649. PMC. Web. 16 Aug. 2018; which are hereby incorporated by reference.

[00348] In some cases, e.g., cases where the alpha and beta chains are expressed from a single construct or open reading frame, or cases wherein a marker gene is included in the construct, the construct may comprise a ribosomal skip sequence. The ribosomal skip sequence may be a 2A peptide, e.g., a P2A or T2A peptide. Exemplary P2A and T2A peptides are described in Scientific Reports volume 7, Article number: 2193 (2017), hereby incorporated by reference in its entirety. In some cases, a FURIN/PACE cleavage site is introduced upstream of the 2A element. FURIN/PACE cleavage sites are described in, e.g., http://www.nuolan.net/substrates.html. The cleavage peptide may also be a factor Xa cleavage site. In cases where the alpha and beta chains are expressed from a single construct or open reading frame, the construct may comprise an internal ribosome entry site (IRES).

[00349] The construct may further comprise one or more marker genes. Exemplary marker genes include but are not limited to GFP, luciferase, HA, lacZ. The marker may be a selectable marker, such as an antibiotic resistance marker, a heavy metal resistance marker, or a biocide resistant marker, as is known to those of skill in the art. The marker may be a complementation marker for use in an auxotrophic host. Exemplary complementation markers and auxotrophic hosts are described in Gene. 2001 Jan 24;263(1-2):159-69. Such markers may be expressed via an IRES, a frameshift sequence, a 2A peptide linker, a fusion with the TCR or CAR, or expressed separately from a separate promoter.

[00350] Exemplary vectors or systems for introducing TCRs or CARs into recipient cells include, but are not limited to Adeno-associated virus, Adenovirus, Adenovirus + Modified vaccinia, Ankara virus (MVA), Adenovirus + Retrovirus, Adenovirus + Sendai virus, Adenovirus + Vaccinia virus, Alphavirus (VEE) Replicon Vaccine, Antisense oligonucleotide, Bifidobacterium longum, CRISPR-Cas9, E. coli, Flavivirus, Gene gun, Herpesviruses, Herpes simplex virus, Lactococcus lactis, Electroporation, Lentivirus, Lipofection, Listeria monocytogenes, Measles virus, Modified Vaccinia Ankara virus (MVA), mRNA Electroporation, Naked/Plasmid DNA, Naked/Plasmid DNA + Adenovirus, Naked/Plasmid DNA + Modified Vaccinia Ankara virus (MVA), Naked/Plasmid DNA + RNA transfer, Naked/Plasmid DNA + Vaccinia virus, Naked/Plasmid DNA + Vesicular stomatitis virus, Newcastle disease virus, Non-viral, PiggyBac™ (PB) Transposon, nanoparticle-based systems, Poliovirus, Poxvirus, Poxvirus + Vaccinia virus, Retrovirus, RNA transfer, RNA transfer + Naked/Plasmid DNA, RNA virus, Saccharomyces cerevisiae, Salmonella typhimurium, Semliki forest virus, Sendai virus, Shigella dysenteriae, Simian virus, siRNA, Sleeping Beauty transposon, Streptococcus mutans, Vaccinia virus, Venezuelan equine encephalitis virus replicon, Vesicular stomatitis virus, and Vibrio cholera.

[00351] In preferred embodiments, the TCR or CAR is introduced into the recipient cell via adeno associated virus (AAV), adenovirus, CRISPR-CAS9, herpesvirus, lentivirus, lipofection, mRNA electroporation, PiggyBac™ (PB) Transposon, retrovirus, RNA transfer, or Sleeping Beauty transposon.

[00352] In some embodiments, a vector for introducing a TCR or CAR into a recipient cell is a viral vector. Exemplary viral vectors include adenoviral vectors, adeno-associated viral (AAV) vectors, lentiviral vectors, herpes viral vectors, retroviral vectors, and the like. Such vectors are described herein.

[00353] Exemplary embodiments of TCR constructs for introducing a TCR or CAR into recipient cells is shown in FIG 2. In some embodiments, a TCR construct includes, from the 5'-3' direction, the following polynucleotide sequences: a promoter sequence, a signal peptide sequence, a TCR β variable (TCRβv) sequence, a TCR β constant ((TCRβc) sequence, a cleavage peptide (e.g., P2A), a signal peptide sequence, a TCR α variable (TCRαv) sequence, and a TCR α constant (TCRαc) sequence. In some embodiments, the TCRβc and TCRαc sequences of the construct include one or more murine regions, e.g., full murine constant sequences or human ➔ murine amino acid exchanges as described herein. In some embodiments, the construct further includes, 3' of the TCRαc sequence, a cleavage peptide sequence (e.g., T2A) followed by a reporter gene. In an embodiment, the construct includes, from the 5'-3' direction, the following polynucleotide sequences: a promoter sequence, a signal peptide sequence, a TCR β variable (TCRβv) sequence, a TCR β constant ((TCRβc) sequence containing one or more murine regions, a cleavage peptide (e.g., P2A), a signal peptide sequence, a TCR α variable (TCRαv) sequence, and a TCR α constant (TCRαc) sequence containing one or more murine regions, a cleavage peptide (e.g., T2A), and a reporter gene.

[00354] FIG. 3 depicts an exemplary construct backbone sequence for cloning TCRs into expression systems for therapy development.

[00355] FIG. 4 depicts an exemplary construct sequence for cloning an identified A*0201_ LLASSILCA-specific TCR into expression systems for therapy development.

[00356] FIG. 5 depicts an exemplary construct sequence for cloning an identified A*0101_ EVDPIGHLY-specific TCR into expression systems for therapy development.

Nucleotides, Vectors, Host Cells, and Related Methods

[00357] Also provided are isolated nucleic acids encoding HLA-PEPTIDE ABPs, vectors comprising the nucleic acids, and host cells comprising the vectors and nucleic acids, as well as recombinant techniques for the production of the ABPs.

[00358] The nucleic acids may be recombinant. The recombinant nucleic acids may be constructed outside living cells by joining natural or synthetic nucleic acid segments to nucleic acid molecules that can replicate in a living cell, or replication products thereof. For purposes herein, the replication can be in vitro replication or in vivo replication.

[00359] For recombinant production of an ABP, the nucleic acid(s) encoding it may be isolated and inserted into a replicable vector for further cloning (i.e., amplification of the DNA)

or expression. In some aspects, the nucleic acid may be produced by homologous recombination, for example as described in U.S. Patent No. 5,204,244, incorporated by reference in its entirety.

[00360] Many different vectors are known in the art. The vector components generally include one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence, for example as described in U.S. Patent No. 5,534,615, incorporated by reference in its entirety.

[00361] Exemplary vectors or constructs suitable for expressing an ABP, e.g., a TCR, CAR, antibody, or antigen binding fragment thereof, include, e.g., the pUC series (Fermentas Life Sciences), the pBluescript series (Stratagene, LaJolla, CA), the pET series (Novagen, Madison, WI), the pGEX series (Pharmacia Biotech, Uppsala, Sweden), and the pEX series (Clontech, Palo Alto, CA). Bacteriophage vectors, such as AGTlO, AGTl 1, AZapII (Stratagene), AEMBL4, and ANMl 149, are also suitable for expressing an ABP disclosed herein.

[00362] Illustrative examples of suitable host cells are provided below. These host cells are not meant to be limiting, and any suitable host cell may be used to produce the ABPs provided herein.

[00363] Suitable host cells include any prokaryotic (e.g., bacterial), lower eukaryotic (e.g., yeast), or higher eukaryotic (e.g., mammalian) cells. Suitable prokaryotes include eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *Escherichia* (*E. coli*), *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella* (*S. typhimurium*), *Serratia* (*S. marcescans*), *Shigella*, *Bacilli* (*B. subtilis* and *B. licheniformis*), *Pseudomonas* (*P. aeruginosa*), and *Streptomyces*. One useful *E. coli* cloning host is *E. coli* 294, although other strains such as *E. coli* B, *E. coli* X1776, and *E. coli* W3110 are also suitable.

[00364] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are also suitable cloning or expression hosts for HLA-PEPTIDE ABP-encoding vectors. *Saccharomyces cerevisiae*, or common baker's yeast, is a commonly used lower eukaryotic host microorganism. However, a number of other genera, species, and strains are available and useful, such as *Schizosaccharomyces pombe*, *Kluyveromyces* (*K. lactis*, *K. fragilis*, *K. bulgaricus K. wickeramii*, *K. waltii*, *K. drosophilarum*, *K. thermotolerans*, and *K. marxianus*), *Yarrowia*, *Pichia pastoris*, *Candida* (*C. albicans*), *Trichoderma reesia*, *Neurospora crassa*, *Schwanniomyces* (*S. occidentalis*), and filamentous fungi such as, for example *Penicillium*, *Tolypocladium*, and *Aspergillus* (*A. nidulans* and *A. niger*).

[00365] Useful mammalian host cells include COS-7 cells, HEK293 cells; baby hamster kidney (BHK) cells; Chinese hamster ovary (CHO); mouse sertoli cells; African green monkey kidney cells (VERO-76), and the like.

[00366] The host cells used to produce the HLA-PEPTIDE ABP may be cultured in a variety of media. Commercially available media such as, for example, Ham's F10, Minimal Essential Medium (MEM), RPMI-1640, and Dulbecco's Modified Eagle's Medium (DMEM) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., *Meth. Enz.*, 1979, 58:44; Barnes et al., *Anal. Biochem.*, 1980, 102:255; and U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, and 5,122,469; or WO 90/03430 and WO 87/00195 may be used. Each of the foregoing references is incorporated by reference in its entirety.

[00367] Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics, trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art.

[00368] The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[00369] When using recombinant techniques, the ABP can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the ABP is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, is removed, for example, by centrifugation or ultrafiltration. For example, Carter et al. (*Bio/Technology*, 1992, 10:163-167, incorporated by reference in its entirety) describes a procedure for isolating ABPs which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation.

[00370] In some embodiments, the ABP is produced in a cell-free system. In some aspects, the cell-free system is an *in vitro* transcription and translation system as described in Yin et al., *mAbs*, 2012, 4:217-225, incorporated by reference in its entirety. In some aspects, the cell-free system utilizes a cell-free extract from a eukaryotic cell or from a prokaryotic cell. In some

aspects, the prokaryotic cell is *E. coli*. Cell-free expression of the ABP may be useful, for example, where the ABP accumulates in a cell as an insoluble aggregate, or where yields from periplasmic expression are low.

[00371] Where the ABP is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon® or Millipore® Pellcon® ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

[00372] The ABP composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being a particularly useful purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the ABP. Protein A can be used to purify ABPs that comprise human γ1, γ2, or γ4 heavy chains (Lindmark et al., *J. Immunol. Meth.*, 1983, 62:1-13, incorporated by reference in its entirety). Protein G is useful for all mouse isotypes and for human γ3 (Guss et al., *EMBO J.*, 1986, 5:1567-1575, incorporated by reference in its entirety).

[00373] The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the ABP comprises a C_{H3} domain, the BakerBond ABX® resin is useful for purification.

[00374] Other techniques for protein purification, such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin Sepharose®, chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available, and can be applied by one of skill in the art.

[00375] Following any preliminary purification step(s), the mixture comprising the ABP of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5 to about 4.5, generally performed at low salt concentrations (e.g., from about 0 to about 0.25 M salt).

Methods of Making HLA-PEPTIDE ABPs

HLA-PEPTIDE Antigen Preparation

[00376] The HLA-PEPTIDE antigen used for isolation or creation of the ABPs provided herein may be intact HLA-PEPTIDE or a fragment of HLA-PEPTIDE. The HLA-PEPTIDE antigen may be, for example, in the form of isolated protein or a protein expressed on the surface of a cell.

[00377] In some embodiments, the HLA-PEPTIDE antigen is a non-naturally occurring variant of HLA-PEPTIDE, such as a HLA-PEPTIDE protein having an amino acid sequence or post-translational modification that does not occur in nature.

[00378] In some embodiments, the HLA-PEPTIDE antigen is truncated by removal of, for example, intracellular or membrane-spanning sequences, or signal sequences. In some embodiments, the HLA-PEPTIDE antigen is fused at its C-terminus to a human IgG1 Fc domain or a polyhistidine tag.

Methods of Identifying ABPs

[00379] ABPs that bind HLA-PEPTIDE can be identified using any method known in the art, e.g., phage display or immunization of a subject.

[00380] One method of identifying an antigen binding protein includes providing at least one HLA-PEPTIDE target; and binding the at least one target with an antigen binding protein, thereby identifying the antigen binding protein. The antigen binding protein can be present in a library comprising a plurality of distinct antigen binding proteins.

[00381] In some embodiments, the library is a phage display library. The phage display library can be developed so that it is substantially free of antigen binding proteins that non-specifically bind the HLA of the HLA-PEPTIDE target. The antigen binding protein can be present in a yeast display library comprising a plurality of distinct antigen binding proteins. The yeast display library can be developed so that it is substantially free of antigen binding proteins that non-specifically bind the HLA of the HLA-PEPTIDE target.

[00382] In some embodiments, the library is a yeast display library.

[00383] In some embodiments, the library is a TCR display library. Exemplary TCR display libraries and methods of using such TCR display libraries are described in WO 98/39482; WO 01/62908; WO 2004/044004; WO2005116646, WO2014018863, WO2015136072,

WO2017046198; and Helmut et al, (2000) PNAS 97 (26) 14578-14583, which are hereby incorporated by reference in their entirety.

[00384] In some aspects, the binding step is performed more than once, optionally at least three times, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10x.

[00385] In addition, the method can also include contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target to determine if the antigen binding protein selectively binds the HLA-PEPTIDE target.

[00386] Another method of identifying an antigen binding protein can include obtaining at least one HLA-PEPTIDE target; administering the HLA-PEPTIDE target to a subject (e.g., a mouse, rabbit or a llama), optionally in combination with an adjuvant; and isolating the antigen binding protein from the subject. Isolating the antigen binding protein can include screening the serum of the subject to identify the antigen binding protein. The method can also include contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target, e.g., to determine if the antigen binding protein selectively binds to the HLA-PEPTIDE target. An antigen binding protein that is identified can be humanized.

[00387] In some aspects, isolating the antigen binding protein comprises isolating a B cell from the subject that expresses the antigen binding protein. The B cell can be used to create a hybridoma. The B cell can also be used for cloning one or more of its CDRs. The B cell can also be immortalized, for example, by using EBV transformation. Sequences encoding an antigen binding protein can be cloned from immortalized B cells or can be cloned directly from B cells isolated from an immunized subject. A library that comprises the antigen binding protein of the B cell can also be created, optionally wherein the library is phage display or yeast display.

[00388] Another method of identifying an antigen binding protein can include obtaining a cell comprising the antigen binding protein; contacting the cell with an HLA-multimer (e.g., a tetramer) comprising at least one HLA-PEPTIDE target; and identifying the antigen binding protein via binding between the HLA-multimer and the antigen binding protein.

[00389] The cell can be, e.g., a T cell, optionally a CTL, or an NK cell, for example. The method can further include isolating the cell, optionally using flow cytometry, magnetic separation, or single cell separation. The method can further include sequencing the antigen binding protein.

[00390] Another method of identifying an antigen binding protein can include obtaining one or more cells comprising the antigen binding protein; activating the one or more cells with at

least one HLA-PEPTIDE target presented on at least one antigen presenting cell (APC); and identifying the antigen binding protein via selection of one or more cells activated by interaction with at least one HLA-PEPTIDE target.

[00391] The cell can be, e.g., a T cell, optionally a CTL, or an NK cell, for example. The method can further include isolating the cell, optionally using flow cytometry, magnetic separation, or single cell separation. The method can further include sequencing the antigen binding protein.

Methods of Making Monoclonal ABPs

[00392] Monoclonal ABPs may be obtained, for example, using the hybridoma method first described by Kohler et al., *Nature*, 1975, 256:495-497 (incorporated by reference in its entirety), and/or by recombinant DNA methods (*see e.g.,* U.S. Patent No. 4,816,567, incorporated by reference in its entirety). Monoclonal ABPs may also be obtained, for example, using phage or yeast-based libraries. *See e.g.,* U.S. Patent Nos. 8,258,082 and 8,691,730, each of which is incorporated by reference in its entirety.

[00393] In the hybridoma method, a mouse or other appropriate host animal is immunized to elicit lymphocytes that produce or are capable of producing ABPs that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes are then fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell. *See* Goding J.W., *Monoclonal ABPs: Principles and Practice* 3rd ed. (1986) Academic Press, San Diego, CA, incorporated by reference in its entirety.

[00394] The hybridoma cells are seeded and grown in a suitable culture medium that contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

[00395] Useful myeloma cells are those that fuse efficiently, support stable high-level production of ABP by the selected ABP-producing cells, and are sensitive media conditions, such as the presence or absence of HAT medium. Among these, preferred myeloma cell lines are murine myeloma lines, such as those derived from MOP-21 and MC-11 mouse tumors (available from the Salk Institute Cell Distribution Center, San Diego, CA), and SP-2 or X63-Ag8-653 cells

(available from the American Type Culture Collection, Rockville, MD). Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal ABPs. *See e.g.*, Kozbor, *J. Immunol.*, 1984, 133:3001, incorporated by reference in its entirety.

[00396] After the identification of hybridoma cells that produce ABPs of the desired specificity, affinity, and/or biological activity, selected clones may be subcloned by limiting dilution procedures and grown by standard methods. *See* Goding, *supra*. Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal.

[00397] DNA encoding the monoclonal ABPs may be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal ABPs). Thus, the hybridoma cells can serve as a useful source of DNA encoding ABPs with the desired properties. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as bacteria (e.g., *E. coli*), yeast (e.g., *Saccharomyces* or *Pichia sp.*), COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce ABP, to produce the monoclonal ABPs.

Methods of Making Chimeric ABPs

[00398] Illustrative methods of making chimeric ABPs are described, for example, in U.S. Pat. No. 4,816,567; and Morrison et al., *Proc. Natl. Acad. Sci. USA*, 1984, 81:6851-6855; each of which is incorporated by reference in its entirety. In some embodiments, a chimeric ABP is made by using recombinant techniques to combine a non-human variable region (e.g., a variable region derived from a mouse, rat, hamster, rabbit, or non-human primate, such as a monkey) with a human constant region.

Methods of Making Humanized ABPs

[00399] Humanized ABPs may be generated by replacing most, or all, of the structural portions of a non-human monoclonal ABP with corresponding human ABP sequences. Consequently, a hybrid molecule is generated in which only the antigen-specific variable, or CDR, is composed of non-human sequence. Methods to obtain humanized ABPs include those described in, for example, Winter and Milstein, *Nature*, 1991, 349:293-299; Rader et al., *Proc. Nat. Acad. Sci. U.S.A.*, 1998, 95:8910-8915; Steinberger et al., *J. Biol. Chem.*, 2000, 275:36073-

36078; Queen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1989, 86:10029-10033; and U.S. Patent Nos. 5,585,089, 5,693,761, 5,693,762, and 6,180,370; each of which is incorporated by reference in its entirety.

Methods of Making Human ABPs

[00400] Human ABPs can be generated by a variety of techniques known in the art, for example by using transgenic animals (e.g., humanized mice). *See, e.g.,* Jakobovits et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1993, 90:2551; Jakobovits et al., *Nature*, 1993, 362:255-258; Bruggermann et al., *Year in Immuno.*, 1993, 7:33; and U.S. Patent Nos. 5,591,669, 5,589,369 and 5,545,807; each of which is incorporated by reference in its entirety. Human ABPs can also be derived from phage-display libraries (*see e.g.,* Hoogenboom et al., *J. Mol. Biol.*, 1991, 227:381-388; Marks et al., *J. Mol. Biol.*, 1991, 222:581-597; and U.S. Pat. Nos. 5,565,332 and 5,573,905; each of which is incorporated by reference in its entirety). Human ABPs may also be generated by *in vitro* activated B cells (*see e.g.,* U.S. Patent. Nos. 5,567,610 and 5,229,275, each of which is incorporated by reference in its entirety). Human ABPs may also be derived from yeast-based libraries (*see e.g.,* U.S. Patent No. 8,691,730, incorporated by reference in its entirety).

Methods of Making ABP Fragments

[00401] The ABP fragments provided herein may be made by any suitable method, including the illustrative methods described herein or those known in the art. Suitable methods include recombinant techniques and proteolytic digestion of whole ABPs. Illustrative methods of making ABP fragments are described, for example, in Hudson et al., *Nat. Med.*, 2003, 9:129-134, incorporated by reference in its entirety. Methods of making scFv ABPs are described, for example, in Plückthun, in *The Pharmacology of Monoclonal ABPs*, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); WO 93/16185; and U.S. Pat. Nos. 5,571,894 and 5,587,458; each of which is incorporated by reference in its entirety.

Methods of Making Alternative Scaffolds

[00402] The alternative scaffolds provided herein may be made by any suitable method, including the illustrative methods described herein or those known in the art. For example, methods of preparing Adnectins™ are described in Emanuel et al., *mAbs*, 2011, 3:38-48, incorporated by reference in its entirety. Methods of preparing iMabs are described in U.S. Pat. Pub. No. 2003/0215914, incorporated by reference in its entirety. Methods of preparing Anticalins® are described in Vogt and Skerra, *Chem. Biochem.*, 2004, 5:191-199, incorporated by

reference in its entirety. Methods of preparing Kunitz domains are described in Wagner et al., *Biochem. & Biophys. Res. Comm.*, 1992, 186:118-1145, incorporated by reference in its entirety. Methods of preparing thioredoxin peptide aptamers are provided in Geyer and Brent, *Meth. Enzymol.*, 2000, 328:171-208, incorporated by reference in its entirety. Methods of preparing Affibodies are provided in Fernandez, *Curr. Opinion in Biotech.*, 2004, 15:364-373, incorporated by reference in its entirety. Methods of preparing DARPins are provided in Zahnd et al., *J. Mol. Biol.*, 2007, 369:1015-1028, incorporated by reference in its entirety. Methods of preparing Affilins are provided in Ebersbach et al., *J. Mol. Biol.*, 2007, 372:172-185, incorporated by reference in its entirety. Methods of preparing Tetranectins are provided in Graversen et al., *J. Biol. Chem.*, 2000, 275:37390-37396, incorporated by reference in its entirety. Methods of preparing Avimers are provided in Silverman et al., *Nature Biotech.*, 2005, 23:1556-1561, incorporated by reference in its entirety. Methods of preparing Fynomers are provided in Silacci et al., *J. Biol. Chem.*, 2014, 289:14392-14398, incorporated by reference in its entirety. Further information on alternative scaffolds is provided in Binz et al., *Nat. Biotechnol.*, 2005 23:1257-1268; and Skerra, *Current Opin. in Biotech.*, 2007 18:295-304, each of which is incorporated by reference in its entirety.

Methods of Making Multispecific ABPs

[00403] The multispecific ABPs provided herein may be made by any suitable method, including the illustrative methods described herein or those known in the art. Methods of making common light chain ABPs are described in Merchant et al., *Nature Biotechnol.*, 1998, 16:677-681, incorporated by reference in its entirety. Methods of making tetravalent bispecific ABPs are described in Coloma and Morrison, *Nature Biotechnol.*, 1997, 15:159-163, incorporated by reference in its entirety. Methods of making hybrid immunoglobulins are described in Milstein and Cuello, *Nature*, 1983, 305:537-540; and Staerz and Bevan, *Proc. Natl. Acad. Sci. USA*, 1986, 83:1453-1457; each of which is incorporated by reference in its entirety. Methods of making immunoglobulins with knobs-into-holes modification are described in U.S. Pat. No. 5,731,168, incorporated by reference in its entirety. Methods of making immunoglobulins with electrostatic modifications are provided in WO 2009/089004, incorporated by reference in its entirety. Methods of making bispecific single chain ABPs are described in Traunecker et al., *EMBO J.*, 1991, 10:3655-3659; and Gruber et al., *J. Immunol.*, 1994, 152:5368-5374; each of which is incorporated by reference in its entirety. Methods of making single-chain ABPs, whose linker length may be varied, are described in U.S. Pat. Nos. 4,946,778 and 5,132,405, each of which is

incorporated by reference in its entirety. Methods of making diabodies are described in Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 1993, 90:6444-6448, incorporated by reference in its entirety. Methods of making triabodies and tetrabodies are described in Todorovska et al., *J. Immunol. Methods*, 2001, 248:47-66, incorporated by reference in its entirety. Methods of making trispecific F(ab')3 derivatives are described in Tutt et al. *J. Immunol.*, 1991, 147:60-69, incorporated by reference in its entirety. Methods of making cross-linked ABPs are described in U.S. Patent No. 4,676,980; Brennan et al., *Science*, 1985, 229:81-83; Staerz, et al. *Nature*, 1985, 314:628-631; and EP 0453082; each of which is incorporated by reference in its entirety. Methods of making antigen-binding domains assembled by leucine zippers are described in Kostelny et al., *J. Immunol.*, 1992, 148:1547-1553, incorporated by reference in its entirety. Methods of making ABPs via the DNL approach are described in U.S. Pat. Nos. 7,521,056; 7,550,143; 7,534,866; and 7,527,787; each of which is incorporated by reference in its entirety. Methods of making hybrids of ABP and non-ABP molecules are described in WO 93/08829, incorporated by reference in its entirety, for examples of such ABPs. Methods of making DAF ABPs are described in U.S. Pat. Pub. No. 2008/0069820, incorporated by reference in its entirety. Methods of making ABPs via reduction and oxidation are described in Carlring et al., *PLoS One*, 2011, 6:e22533, incorporated by reference in its entirety. Methods of making DVD-Igs™ are described in U.S. Pat. No. 7,612,181, incorporated by reference in its entirety. Methods of making DARTs™ are described in Moore et al., *Blood*, 2011, 117:454-451, incorporated by reference in its entirety. Methods of making DuoBodies® are described in Labrijn et al., *Proc. Natl. Acad. Sci. USA*, 2013, 110:5145-5150; Gramer et al., *mAbs*, 2013, 5:962-972; and Labrijn et al., *Nature Protocols*, 2014, 9:2450-2463; each of which is incorporated by reference in its entirety. Methods of making ABPs comprising scFvs fused to the C-terminus of the C_{H3} from an IgG are described in Coloma and Morrison, *Nature Biotechnol.*, 1997, 15:159-163, incorporated by reference in its entirety. Methods of making ABPs in which a Fab molecule is attached to the constant region of an immunoglobulin are described in Miler et al., *J. Immunol.*, 2003, 170:4854-4861, incorporated by reference in its entirety. Methods of making CovX-Bodies are described in Doppalapudi et al., *Proc. Natl. Acad. Sci. USA*, 2010, 107:22611-22616, incorporated by reference in its entirety. Methods of making Fcab ABPs are described in Wozniak-Knopp et al., *Protein Eng. Des. Sel.*, 2010, 23:289-297, incorporated by reference in its entirety. Methods of making TandAb® ABPs are described in Kipriyanov et al., *J. Mol. Biol.*, 1999, 293:41-56 and Zhukovsky et al., *Blood*, 2013, 122:5116, each of which is incorporated by reference in its

entirety. Methods of making tandem Fabs are described in WO 2015/103072, incorporated by reference in its entirety. Methods of making Zybodies™ are described in LaFleur et al., *mAbs*, 2013, 5:208-218, incorporated by reference in its entirety.

Methods of Making Variants

[00404] Any suitable method can be used to introduce variability into a polynucleotide sequence(s) encoding an ABP, including error-prone PCR, chain shuffling, and oligonucleotide-directed mutagenesis such as trinucleotide-directed mutagenesis (TRIM). In some aspects, several CDR residues (e.g., 4-6 residues at a time) are randomized. CDR residues involved in antigen binding may be specifically identified, for example, using alanine scanning mutagenesis or modeling. CDR-H3 and CDR-L3 in particular are often targeted for mutation.

[00405] The introduction of diversity into the variable regions and/or CDRs can be used to produce a secondary library. The secondary library is then screened to identify ABP variants with improved affinity. Affinity maturation by constructing and reselecting from secondary libraries has been described, for example, in Hoogenboom et al., *Methods in Molecular Biology*, 2001, 178:1-37, incorporated by reference in its entirety.

Methods for Engineering Cells with ABPs

[00406] Also provided are methods, nucleic acids, compositions, and kits, for expressing the ABPs, including receptors comprising antibodies, CARs, and TCRs, and for producing genetically engineered cells expressing such ABPs. The genetic engineering generally involves introduction of a nucleic acid encoding the recombinant or engineered component into the cell, such as by retroviral transduction, transfection, or transformation.

[00407] In some embodiments, gene transfer is accomplished by first stimulating the cell, such as by combining it with a stimulus that induces a response such as proliferation, survival, and/or activation, e.g., as measured by expression of a cytokine or activation marker, followed by transduction of the activated cells, and expansion in culture to numbers sufficient for clinical applications.

[00408] In some contexts, overexpression of a stimulatory factor (for example, a lymphokine or a cytokine) may be toxic to a subject. Thus, in some contexts, the engineered cells include gene segments that cause the cells to be susceptible to negative selection in vivo, such as upon administration in adoptive immunotherapy. For example in some aspects, the cells are engineered so that they can be eliminated as a result of a change in the in vivo condition of the

patient to which they are administered. The negative selectable phenotype may result from the insertion of a gene that confers sensitivity to an administered agent, for example, a compound. Negative selectable genes include the Herpes simplex virus type I thymidine kinase (HSV-I TK) gene (Wigler et al., Cell II: 223, 1977) which confers ganciclovir sensitivity; the cellular hypoxanthine phosphribosyltransferase (HPRT) gene, the cellular adenine phosphoribosyltransferase (APRT) gene, bacterial cytosine deaminase, (Mullen et al., Proc. Natl. Acad. Sci. USA. 89:33 (1992)).

[00409] In some aspects, the cells further are engineered to promote expression of cytokines or other factors. Various methods for the introduction of genetically engineered components, e.g., antigen receptors, e.g., CARs, are well known and may be used with the provided methods and compositions. Exemplary methods include those for transfer of nucleic acids encoding the receptors, including via viral, e.g., retroviral or lentiviral, transduction, transposons, and electroporation.

[00410] In some embodiments, recombinant nucleic acids are transferred into cells using recombinant infectious virus particles, such as, e.g., vectors derived from simian virus 40 (SV40), adenoviruses, adeno-associated virus (AAV). In some embodiments, recombinant nucleic acids are transferred into T cells using recombinant lentiviral vectors or retroviral vectors, such as gamma-retroviral vectors (see, e.g., Koste et al. (2014) Gene Therapy 2014 Apr. 3. doi: 10.1038/gt.2014.25; Carlens et al. (2000) Exp Hematol 28(10): 1137-46; Alonso-Camino et al. (2013) Mol Ther Nucl Acids 2, e93; Park et al., Trends Biotechnol. 2011 Nov. 29(11): 550-557.

[00411] In some embodiments, the retroviral vector has a long terminal repeat sequence (LTR), e.g., a retroviral vector derived from the Moloney murine leukemia virus (MoMLV), myeloproliferative sarcoma virus (MPSV), murine embryonic stem cell virus (MESV), murine stem cell virus (MSCV), spleen focus forming virus (SFFV), or adeno-associated virus (AAV). Most retroviral vectors are derived from murine retroviruses. In some embodiments, the retroviruses include those derived from any avian or mammalian cell source. The retroviruses typically are amphotropic, meaning that they are capable of infecting host cells of several species, including humans. In one embodiment, the gene to be expressed replaces the retroviral gag, pol and/or env sequences. A number of illustrative retroviral systems have been described (e.g., U.S. Pat. Nos. 5,219,740; 6,207,453; 5,219,740; Miller and Rosman (1989) BioTechniques 7:980-990; Miller, A. D. (1990) Human Gene Therapy 1:5-14; Scarpa et al. (1991) Virology

180:849-852; Burns et al. (1993) Proc. Natl. Acad. Sci. USA 90:8033-8037; and Boris-Lawrie and Temin (1993) Cur. Opin. Genet. Develop. 3:102-109.

[00412] Methods of lentiviral transduction are known. Exemplary methods are described in, e.g., Wang et al. (2012) J. Immunother. 35(9): 689-701; Cooper et al. (2003) Blood. 101:1637-1644; Verhoeyen et al. (2009) Methods Mol Biol. 506: 97-114; and Cavalieri et al. (2003) Blood. 102(2): 497-505.

[00413] In some embodiments, recombinant nucleic acids are transferred into T cells via electroporation (see, e.g., Chicaybam et al, (2013) PLoS ONE 8(3): e60298; Van Tedeloo et al. (2000) Gene Therapy 7(16): 1431-1437; and Roth et al. (2018) Nature 559:405–409). In some embodiments, recombinant nucleic acids are transferred into T cells via transposition (see, e.g., Manuri et al. (2010) Hum Gene Ther 21(4): 427-437; Sharma et al. (2013) Molec Ther Nucl Acids 2, e74; and Huang et al. (2009) Methods Mol Biol 506: 115-126). Other methods of introducing and expressing genetic material in immune cells include calcium phosphate transfection (e.g., as described in Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.), protoplast fusion, cationic liposome-mediated transfection; tungsten particle-facilitated microparticle bombardment (Johnston, Nature, 346: 776-777 (1990)); and strontium phosphate DNA co-precipitation (Brash et al., Mol. Cell Biol., 7: 2031-2034 (1987)).

[00414] Other approaches and vectors for transfer of the nucleic acids encoding the recombinant products are those described, e.g., in international patent application, Publication No.: WO2014055668, and U.S. Pat. No. 7,446,190.

[00415] Among additional nucleic acids, e.g., genes for introduction are those to improve the efficacy of therapy, such as by promoting viability and/or function of transferred cells; genes to provide a genetic marker for selection and/or evaluation of the cells, such as to assess in vivo survival or localization; genes to improve safety, for example, by making the cell susceptible to negative selection in vivo as described by Lupton S. D. et al., Mol. and Cell Biol., 11:6 (1991); and Riddell et al., Human Gene Therapy 3:319-338 (1992); see also the publications of PCT/US91/08442 and PCT/US94/05601 by Lupton et al. describing the use of bifunctional selectable fusion genes derived from fusing a dominant positive selectable marker with a negative selectable marker. See, e.g., Riddell et al., U.S. Pat. No. 6,040,177, at columns 14-17.

Preparation of Engineered Cells

[00416] In some embodiments, preparation of the engineered cells includes one or more culture and/or preparation steps. The cells for introduction of the HLA-PEPTIDE-ABP, e.g., TCR or CAR, can be isolated from a sample, such as a biological sample, e.g., one obtained from or derived from a subject. In some embodiments, the subject from which the cell is isolated is one having the disease or condition or in need of a cell therapy or to which cell therapy will be administered. The subject in some embodiments is a human in need of a particular therapeutic intervention, such as the adoptive cell therapy for which cells are being isolated, processed, and/or engineered.

[00417] Accordingly, the cells in some embodiments are primary cells, e.g., primary human cells. The samples include tissue, fluid, and other samples taken directly from the subject, as well as samples resulting from one or more processing steps, such as separation, centrifugation, genetic engineering (e.g. transduction with viral vector), washing, and/or incubation. The biological sample can be a sample obtained directly from a biological source or a sample that is processed. Biological samples include, but are not limited to, body fluids, such as blood, plasma, serum, cerebrospinal fluid, synovial fluid, urine and sweat, tissue and organ samples, including processed samples derived therefrom.

[00418] In some aspects, the sample from which the cells are derived or isolated is blood or a blood-derived sample, or is or is derived from an apheresis or leukapheresis product. Exemplary samples include whole blood, peripheral blood mononuclear cells (PBMCs), leukocytes, bone marrow, thymus, tissue biopsy, tumor, leukemia, lymphoma, lymph node, gut associated lymphoid tissue, mucosa associated lymphoid tissue, spleen, other lymphoid tissues, liver, lung, stomach, intestine, colon, kidney, pancreas, breast, bone, prostate, cervix, testes, ovaries, tonsil, or other organ, and/or cells derived therefrom. Samples include, in the context of cell therapy, e.g., adoptive cell therapy, samples from autologous and allogeneic sources.

[00419] In some embodiments, the cells are derived from cell lines, e.g., T cell lines. The cells in some embodiments are obtained from a xenogeneic source, for example, from mouse, rat, non-human primate, or pig.

[00420] In some embodiments, isolation of the cells includes one or more preparation and/or non-affinity based cell separation steps. In some examples, cells are washed, centrifuged, and/or incubated in the presence of one or more reagents, for example, to remove unwanted components, enrich for desired components, lyse or remove cells sensitive to particular reagents.

In some examples, cells are separated based on one or more property, such as density, adherent properties, size, sensitivity and/or resistance to particular components.

[00421] In some examples, cells from the circulating blood of a subject are obtained, e.g., by apheresis or leukapheresis. The samples, in some aspects, contain lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and/or platelets, and in some aspects contains cells other than red blood cells and platelets.

[00422] In some embodiments, the blood cells collected from the subject are washed, e.g., to remove the plasma fraction and to place the cells in an appropriate buffer or media for subsequent processing steps. In some embodiments, the cells are washed with phosphate buffered saline (PBS). In some embodiments, the wash solution lacks calcium and/or magnesium and/or many or all divalent cations. In some aspects, a washing step is accomplished a semi-automated "flow-through" centrifuge (for example, the Cobe 2991 cell processor, Baxter) according to the manufacturer's instructions. In some aspects, a washing step is accomplished by tangential flow filtration (TFF) according to the manufacturer's instructions. In some embodiments, the cells are resuspended in a variety of biocompatible buffers after washing, such as, for example, Ca++/Mg++ free PBS. In certain embodiments, components of a blood cell sample are removed and the cells directly resuspended in culture media.

[00423] In some embodiments, the methods include density-based cell separation methods, such as the preparation of white blood cells from peripheral blood by lysing the red blood cells and centrifugation through a Percoll or Ficoll gradient.

[00424] In some embodiments, the isolation methods include the separation of different cell types based on the expression or presence in the cell of one or more specific molecules, such as surface markers, e.g., surface proteins, intracellular markers, or nucleic acid. In some embodiments, any known method for separation based on such markers may be used. In some embodiments, the separation is affinity- or immunoaffinity-based separation. For example, the isolation in some aspects includes separation of cells and cell populations based on the cells' expression or expression level of one or more markers, typically cell surface markers, for example, by incubation with an antibody or binding partner that specifically binds to such markers, followed generally by washing steps and separation of cells having bound the antibody or binding partner, from those cells having not bound to the antibody or binding partner.

[00425] Such separation steps can be based on positive selection, in which the cells having bound the reagents are retained for further use, and/or negative selection, in which the cells

having not bound to the antibody or binding partner are retained. In some examples, both fractions are retained for further use. In some aspects, negative selection can be particularly useful where no antibody is available that specifically identifies a cell type in a heterogeneous population, such that separation is best carried out based on markers expressed by cells other than the desired population.

[00426] The separation need not result in 100% enrichment or removal of a particular cell population or cells expressing a particular marker. For example, positive selection of or enrichment for cells of a particular type, such as those expressing a marker, refers to increasing the number or percentage of such cells, but need not result in a complete absence of cells not expressing the marker. Likewise, negative selection, removal, or depletion of cells of a particular type, such as those expressing a marker, refers to decreasing the number or percentage of such cells, but need not result in a complete removal of all such cells.

[00427] In some examples, multiple rounds of separation steps are carried out, where the positively or negatively selected fraction from one step is subjected to another separation step, such as a subsequent positive or negative selection. In some examples, a single separation step can deplete cells expressing multiple markers simultaneously, such as by incubating cells with a plurality of antibodies or binding partners, each specific for a marker targeted for negative selection. Likewise, multiple cell types can simultaneously be positively selected by incubating cells with a plurality of antibodies or binding partners expressed on the various cell types.

[00428] For example, in some aspects, specific subpopulations of T cells, such as cells positive or expressing high levels of one or more surface markers, e.g., CD28+, CD62L+, CCR7+, CD27+, CD127+, CD4+, CD8+, CD45RA+, and/or CD45RO+ T cells, are isolated by positive or negative selection techniques.

[00429] For example, CD3+, CD28+ T cells can be positively selected using CD3/CD28 conjugated magnetic beads (e.g., DYNABEADS.RTM. M-450 CD3/CD28 T Cell Expander).

[00430] In some embodiments, isolation is carried out by enrichment for a particular cell population by positive selection, or depletion of a particular cell population, by negative selection. In some embodiments, positive or negative selection is accomplished by incubating cells with one or more antibodies or other binding agent that specifically bind to one or more surface markers expressed or expressed (marker+) at a relatively higher level (marker^{high}) on the positively or negatively selected cells, respectively.

[00431] In some embodiments, T cells are separated from a PBMC sample by negative selection of markers expressed on non-T cells, such as B cells, monocytes, or other white blood cells, such as CD14. In some aspects, a CD4+ or CD8+ selection step is used to separate CD4+ helper and CD8+ cytotoxic T cells. Such CD4+ and CD8+ populations can be further sorted into sub-populations by positive or negative selection for markers expressed or expressed to a relatively higher degree on one or more naive, memory, and/or effector T cell subpopulations.

[00432] In some embodiments, CD8+ cells are further enriched for or depleted of naive, central memory, effector memory, and/or central memory stem cells, such as by positive or negative selection based on surface antigens associated with the respective subpopulation. In some embodiments, enrichment for central memory T (TCM) cells is carried out to increase efficacy, such as to improve long-term survival, expansion, and/or engraftment following administration, which in some aspects is particularly robust in such sub-populations. See Terakura et al. (2012) Blood. 1:72-82; Wang et al. (2012) J Immunother. 35(9):689-701. In some embodiments, combining TCM-enriched CD8+ T cells and CD4+ T cells further enhances efficacy.

[00433] In embodiments, memory T cells are present in both CD62L+ and CD62L- subsets of CD8+ peripheral blood lymphocytes. PBMC can be enriched for or depleted of CD62L-CD8+ and/or CD62L+CD8+ fractions, such as using anti-CD8 and anti-CD62L antibodies.

[00434] In some embodiments, the enrichment for central memory T (TCM) cells is based on positive or high surface expression of CD45RO, CD62L, CCR7, CD28, CD3, and/or CD 127; in some aspects, it is based on negative selection for cells expressing or highly expressing CD45RA and/or granzyme B. In some aspects, isolation of a CD8+ population enriched for TCM cells is carried out by depletion of cells expressing CD4, CD14, CD45RA, and positive selection or enrichment for cells expressing CD62L. In one aspect, enrichment for central memory T (TCM) cells is carried out starting with a negative fraction of cells selected based on CD4 expression, which is subjected to a negative selection based on expression of CD14 and CD45RA, and a positive selection based on CD62L. Such selections in some aspects are carried out simultaneously and in other aspects are carried out sequentially, in either order. In some aspects, the same CD4 expression-based selection step used in preparing the CD8+ cell population or subpopulation, also is used to generate the CD4+ cell population or sub-population, such that both the positive and negative fractions from the CD4-based separation are retained and used in

subsequent steps of the methods, optionally following one or more further positive or negative selection steps.

[00435] In a particular example, a sample of PBMCs or other white blood cell sample is subjected to selection of CD4+ cells, where both the negative and positive fractions are retained. The negative fraction then is subjected to negative selection based on expression of CD14 and CD45RA or ROR1, and positive selection based on a marker characteristic of central memory T cells, such as CD62L or CCR7, where the positive and negative selections are carried out in either order.

[00436] CD4+ T helper cells are sorted into naive, central memory, and effector cells by identifying cell populations that have cell surface antigens. CD4+ lymphocytes can be obtained by standard methods. In some embodiments, naive CD4+ T lymphocytes are CD45RO-, CD45RA+, CD62L+, CD4+ T cells. In some embodiments, central memory CD4+ cells are CD62L+ and CD45RO+. In some embodiments, effector CD4+ cells are CD62L- and CD45RO-.

[00437] In one example, to enrich for CD4+ cells by negative selection, a monoclonal antibody cocktail typically includes antibodies to CD14, CD20, CD11b, CD16, HLA-DR, and CD8. In some embodiments, the antibody or binding partner is bound to a solid support or matrix, such as a magnetic bead or paramagnetic bead, to allow for separation of cells for positive and/or negative selection. For example, in some embodiments, the cells and cell populations are separated or isolated using immune-magnetic (or affinity-magnetic) separation techniques (reviewed in Methods in Molecular Medicine, vol. 58: Metastasis Research Protocols, Vol. 2: Cell Behavior In Vitro and In Vivo, p 17-25 Edited by: S. A. Brooks and U. Schumacher Humana Press Inc., Totowa, N.J.).

[00438] In some aspects, the sample or composition of cells to be separated is incubated with small, magnetizable or magnetically responsive material, such as magnetically responsive particles or microparticles, such as paramagnetic beads (e.g., such as Dynabeads or MACS beads). The magnetically responsive material, e.g., particle, generally is directly or indirectly attached to a binding partner, e.g., an antibody, that specifically binds to a molecule, e.g., surface marker, present on the cell, cells, or population of cells that it is desired to separate, e.g., that it is desired to negatively or positively select.

[00439] In some embodiments, the magnetic particle or bead comprises a magnetically responsive material bound to a specific binding member, such as an antibody or other binding

partner. There are many well-known magnetically responsive materials used in magnetic separation methods. Suitable magnetic particles include those described in Molday, U.S. Pat. No. 4,452,773, and in European Patent Specification EP 452342 B, which are hereby incorporated by reference. Colloidal sized particles, such as those described in Owen U.S. Pat. No. 4,795,698, and Liberti et al., U.S. Pat. No. 5,200,084 are other examples.

[00440] The incubation generally is carried out under conditions whereby the antibodies or binding partners, or molecules, such as secondary antibodies or other reagents, which specifically bind to such antibodies or binding partners, which are attached to the magnetic particle or bead, specifically bind to cell surface molecules if present on cells within the sample.

[00441] In some aspects, the sample is placed in a magnetic field, and those cells having magnetically responsive or magnetizable particles attached thereto will be attracted to the magnet and separated from the unlabeled cells. For positive selection, cells that are attracted to the magnet are retained; for negative selection, cells that are not attracted (unlabeled cells) are retained. In some aspects, a combination of positive and negative selection is performed during the same selection step, where the positive and negative fractions are retained and further processed or subject to further separation steps.

[00442] In certain embodiments, the magnetically responsive particles are coated in primary antibodies or other binding partners, secondary antibodies, lectins, enzymes, or streptavidin. In certain embodiments, the magnetic particles are attached to cells via a coating of primary antibodies specific for one or more markers. In certain embodiments, the cells, rather than the beads, are labeled with a primary antibody or binding partner, and then cell-type specific secondary antibody- or other binding partner (e.g., streptavidin)-coated magnetic particles, are added. In certain embodiments, streptavidin-coated magnetic particles are used in conjunction with biotinylated primary or secondary antibodies.

[00443] In some embodiments, the magnetically responsive particles are left attached to the cells that are to be subsequently incubated, cultured and/or engineered; in some aspects, the particles are left attached to the cells for administration to a patient. In some embodiments, the magnetizable or magnetically responsive particles are removed from the cells. Methods for removing magnetizable particles from cells are known and include, e.g., the use of competing non-labeled antibodies, magnetizable particles or antibodies conjugated to cleavable linkers, etc. In some embodiments, the magnetizable particles are biodegradable.

[00444] In some embodiments, the affinity-based selection is via magnetic-activated cell sorting (MACS) (Miltenyi Biotech, Auburn, Calif.). Magnetic Activated Cell Sorting (MACS) systems are capable of high-purity selection of cells having magnetized particles attached thereto. In certain embodiments, MACS operates in a mode wherein the non-target and target species are sequentially eluted after the application of the external magnetic field. That is, the cells attached to magnetized particles are held in place while the unattached species are eluted. Then, after this first elution step is completed, the species that were trapped in the magnetic field and were prevented from being eluted are freed in some manner such that they can be eluted and recovered. In certain embodiments, the non-target cells are labelled and depleted from the heterogeneous population of cells.

[00445] In certain embodiments, the isolation or separation is carried out using a system, device, or apparatus that carries out one or more of the isolation, cell preparation, separation, processing, incubation, culture, and/or formulation steps of the methods. In some aspects, the system is used to carry out each of these steps in a closed or sterile environment, for example, to minimize error, user handling and/or contamination. In one example, the system is a system as described in International Patent Application, Publication Number WO2009/072003, or US 20110003380 A1.

[00446] In some embodiments, the system or apparatus carries out one or more, e.g., all, of the isolation, processing, engineering, and formulation steps in an integrated or self-contained system, and/or in an automated or programmable fashion. In some aspects, the system or apparatus includes a computer and/or computer program in communication with the system or apparatus, which allows a user to program, control, assess the outcome of, and/or adjust various aspects of the processing, isolation, engineering, and formulation steps.

[00447] In some aspects, the separation and/or other steps is carried out using CliniMACS system (Miltenyi Biotic), for example, for automated separation of cells on a clinical-scale level in a closed and sterile system. Components can include an integrated microcomputer, magnetic separation unit, peristaltic pump, and various pinch valves. The integrated computer in some aspects controls all components of the instrument and directs the system to perform repeated procedures in a standardized sequence. The magnetic separation unit in some aspects includes a movable permanent magnet and a holder for the selection column. The peristaltic pump controls the flow rate throughout the tubing set and, together with the pinch valves, ensures the controlled flow of buffer through the system and continual suspension of cells.

[00448] The CliniMACS system in some aspects uses antibody-coupled magnetizable particles that are supplied in a sterile, non-pyrogenic solution. In some embodiments, after labelling of cells with magnetic particles the cells are washed to remove excess particles. A cell preparation bag is then connected to the tubing set, which in turn is connected to a bag containing buffer and a cell collection bag. The tubing set consists of pre-assembled sterile tubing, including a pre-column and a separation column, and are for single use only. After initiation of the separation program, the system automatically applies the cell sample onto the separation column. Labelled cells are retained within the column, while unlabeled cells are removed by a series of washing steps. In some embodiments, the cell populations for use with the methods described herein are unlabeled and are not retained in the column. In some embodiments, the cell populations for use with the methods described herein are labeled and are retained in the column. In some embodiments, the cell populations for use with the methods described herein are eluted from the column after removal of the magnetic field, and are collected within the cell collection bag.

[00449] In certain embodiments, separation and/or other steps are carried out using the CliniMACS Prodigy system (Miltenyi Biotec). The CliniMACS Prodigy system in some aspects is equipped with a cell processing unity that permits automated washing and fractionation of cells by centrifugation. The CliniMACS Prodigy system can also include an onboard camera and image recognition software that determines the optimal cell fractionation endpoint by discerning the macroscopic layers of the source cell product. For example, peripheral blood may be automatically separated into erythrocytes, white blood cells and plasma layers. The CliniMACS Prodigy system can also include an integrated cell cultivation chamber which accomplishes cell culture protocols such as, e.g., cell differentiation and expansion, antigen loading, and long-term cell culture. Input ports can allow for the sterile removal and replenishment of media and cells can be monitored using an integrated microscope. *See, e.g.,* Klebanoff et al. (2012) J Immunother. 35(9): 651-660, Terakura et al. (2012) Blood. 1:72-82, and Wang et al. (2012) J Immunother. 35(9):689-701.

[00450] In some embodiments, a cell population described herein is collected and enriched (or depleted) via flow cytometry, in which cells stained for multiple cell surface markers are carried in a fluidic stream. In some embodiments, a cell population described herein is collected and enriched (or depleted) via preparative scale (FACS)-sorting. In certain embodiments, a cell population described herein is collected and enriched (or depleted) by use of

microelectromechanical systems (MEMS) chips in combination with a FACS-based detection system (see, e.g., WO 2010/033140, Cho et al. (2010) Lab Chip 10, 1567-1573; and Godin et al. (2008) J Biophoton. 1(5):355-376. In both cases, cells can be labeled with multiple markers, allowing for the isolation of well-defined T cell subsets at high purity.

[00451] In some embodiments, the antibodies or binding partners are labeled with one or more detectable marker, to facilitate separation for positive and/or negative selection. For example, separation may be based on binding to fluorescently labeled antibodies. In some examples, separation of cells based on binding of antibodies or other binding partners specific for one or more cell surface markers are carried in a fluidic stream, such as by fluorescence-activated cell sorting (FACS), including preparative scale (FACS) and/or microelectromechanical systems (MEMS) chips, e.g., in combination with a flow-cytometric detection system. Such methods allow for positive and negative selection based on multiple markers simultaneously.

[00452] In some embodiments, the preparation methods include steps for freezing, e.g., cryopreserving, the cells, either before or after isolation, incubation, and/or engineering. In some embodiments, the freeze and subsequent thaw step removes granulocytes and, to some extent, monocytes in the cell population. In some embodiments, the cells are suspended in a freezing solution, e.g., following a washing step to remove plasma and platelets. Any of a variety of known freezing solutions and parameters in some aspects may be used. One example involves using PBS containing 20% DMSO and 8% human serum albumin (HSA), or other suitable cell freezing media. This can then be diluted 1:1 with media so that the final concentration of DMSO and HSA are 10% and 4%, respectively. Other examples include Cryostor®, CTL-Cryo™ ABC freezing media, and the like. The cells are then frozen to -80 degrees C at a rate of 1degree per minute and stored in the vapor phase of a liquid nitrogen storage tank.

[00453] In some embodiments, the provided methods include cultivation, incubation, culture, and/or genetic engineering steps. For example, in some embodiments, provided are methods for incubating and/or engineering the depleted cell populations and culture-initiating compositions.

[00454] Thus, in some embodiments, the cell populations are incubated in a culture-initiating composition. The incubation and/or engineering may be carried out in a culture vessel, such as a unit, chamber, well, column, tube, tubing set, valve, vial, culture dish, bag, or other container for culture or cultivating cells.

[00455] In some embodiments, the cells are incubated and/or cultured prior to or in connection with genetic engineering. The incubation steps can include culture, cultivation, stimulation, activation, and/or propagation. In some embodiments, the compositions or cells are incubated in the presence of stimulating conditions or a stimulatory agent. Such conditions include those designed to induce proliferation, expansion, activation, and/or survival of cells in the population, to mimic antigen exposure, and/or to prime the cells for genetic engineering, such as for the introduction of a recombinant antigen receptor.

[00456] The conditions can include one or more of particular media, temperature, oxygen content, carbon dioxide content, time, agents, e.g., nutrients, amino acids, antibiotics, ions, and/or stimulatory factors, such as cytokines, chemokines, antigens, binding partners, fusion proteins, recombinant soluble receptors, and any other agents designed to activate the cells.

[00457] In some embodiments, the stimulating conditions or agents include one or more agent, e.g., ligand, which is capable of activating an intracellular signaling domain of a TCR complex. In some aspects, the agent turns on or initiates TCR/CD3 intracellular signaling cascade in a T cell. Such agents can include antibodies, such as those specific for a TCR component and/or costimulatory receptor, e.g., anti-CD3, anti-CD28, for example, bound to solid support such as a bead, and/or one or more cytokines. Optionally, the expansion method may further comprise the step of adding anti-CD3 and/or anti CD28 antibody to the culture medium (e.g., at a concentration of at least about 0.5 ng/ml). In some embodiments, the stimulating agents include IL-2 and/or IL-15, for example, an IL-2 concentration of at least about 10 units/mL.

[00458] In some aspects, incubation is carried out in accordance with techniques such as those described in U.S. Pat. No. 6,040,177 to Riddell et al., Klebanoff et al. (2012) J Immunother. 35(9): 651-660, Terakura et al. (2012) Blood. 1:72-82, and/or Wang et al. (2012) J Immunother. 35(9):689-701.

[00459] In some embodiments, the T cells are expanded by adding to the culture-initiating composition feeder cells, such as non-dividing peripheral blood mononuclear cells (PBMC), (e.g., such that the resulting population of cells contains at least about 5, 10, 20, or 40 or more PBMC feeder cells for each T lymphocyte in the initial population to be expanded); and incubating the culture (e.g. for a time sufficient to expand the numbers of T cells). In some aspects, the non-dividing feeder cells can comprise gamma-irradiated PBMC feeder cells. In some embodiments, the PBMC are irradiated with gamma rays in the range of about 3000 to

3600 rads to prevent cell division. In some embodiments, the PBMC feeder cells are inactivated with Mytomicin C. In some aspects, the feeder cells are added to culture medium prior to the addition of the populations of T cells.

[00460] In some embodiments, the stimulating conditions include temperature suitable for the growth of human T lymphocytes, for example, at least about 25 degrees Celsius, generally at least about 30 degrees, and generally at or about 37 degrees Celsius. Optionally, the incubation may further comprise adding non-dividing EBV-transformed lymphoblastoid cells (LCL) as feeder cells. LCL can be irradiated with gamma rays in the range of about 6000 to 10,000 rads. The LCL feeder cells in some aspects is provided in any suitable amount, such as a ratio of LCL feeder cells to initial T lymphocytes of at least about 10:1.

[00461] In embodiments, antigen-specific T cells, such as antigen-specific CD4+ and/or CD8+ T cells, are obtained by stimulating naive or antigen specific T lymphocytes with antigen. For example, antigen-specific T cell lines or clones can be generated to cytomegalovirus antigens by isolating T cells from infected subjects and stimulating the cells in vitro with the same antigen.

Assays

[00462] A variety of assays known in the art may be used to identify and characterize an HLA-PEPTIDE ABP provided herein.

Binding, Competition, and Epitope Mapping Assays

[00463] Specific antigen-binding activity of an ABP provided herein may be evaluated by any suitable method, including using SPR, BLI, RIA and MSD-SET, as described elsewhere in this disclosure. Additionally, antigen-binding activity may be evaluated by ELISA assays, using flow cytometry, and/or Western blot assays.

[00464] Assays for measuring competition between two ABPs, or an ABP and another molecule (e.g., one or more ligands of HLA-PEPTIDE such as a TCR) are described elsewhere in this disclosure and, for example, in Harlow and Lane, *ABPs: A Laboratory Manual* ch.14, 1988, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y, incorporated by reference in its entirety.

[00465] Assays for mapping the epitopes to which an ABP provided herein bind are described, for example, in Morris "Epitope Mapping Protocols," in *Methods in Molecular Biology* vol. 66, 1996, Humana Press, Totowa, N.J., incorporated by reference in its entirety. In some

embodiments, the epitope is determined by peptide competition. In some embodiments, the epitope is determined by mass spectrometry. In some embodiments, the epitope is determined by mutagenesis. In some embodiments, the epitope is determined by crystallography.

Assays for Effector Functions

[00466] Effector function following treatment with an ABP and/or cell provided herein may be evaluated using a variety of *in vitro* and *in vivo* assays known in the art, including those described in Ravetch and Kinet, *Annu. Rev. Immunol.*, 1991, 9:457-492; U.S. Pat. Nos. 5,500,362, 5,821,337; Hellstrom et al., *Proc. Nat'l Acad. Sci. USA*, 1986, 83:7059-7063; Hellstrom et al., *Proc. Nat'l Acad. Sci. USA*, 1985, 82:1499-1502; Bruggemann et al., *J. Exp. Med.*, 1987, 166:1351-1361; Clynes et al., *Proc. Nat'l Acad. Sci. USA*, 1998, 95:652-656; WO 2006/029879; WO 2005/100402; Gazzano-Santoro et al., *J. Immunol. Methods*, 1996, 202:163-171; Cragg et al., *Blood*, 2003, 101:1045-1052; Cragg et al. *Blood*, 2004, 103:2738-2743; and Petkova et al., *Int'l. Immunol.*, 2006, 18:1759-1769; each of which is incorporated by reference in its entirety.

Pharmaceutical Compositions

[00467] An ABP, cell, or HLA-PEPTIDE target provided herein can be formulated in any appropriate pharmaceutical composition and administered by any suitable route of administration. Suitable routes of administration include, but are not limited to, the intra-arterial, intradermal, intramuscular, intraperitoneal, intravenous, nasal, parenteral, pulmonary, and subcutaneous routes.

[00468] The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the *Handbook of Pharmaceutical Excipients*, Rowe et al. (Eds.) 6th Ed. (2009), incorporated by reference in its entirety.

[00469] In some embodiments, the pharmaceutical composition comprises an anti-foaming agent. Any suitable anti-foaming agent may be used. In some aspects, the anti-foaming agent is selected from an alcohol, an ether, an oil, a wax, a silicone, a surfactant, and combinations thereof. In some aspects, the anti-foaming agent is selected from a mineral oil, a vegetable oil,

ethylene *bis* stearamide, a paraffin wax, an ester wax, a fatty alcohol wax, a long chain fatty alcohol, a fatty acid soap, a fatty acid ester, a silicon glycol, a fluorosilicone, a polyethylene glycol-polypropylene glycol copolymer, polydimethylsiloxane-silicon dioxide, ether, octyl alcohol, capryl alcohol, sorbitan trioleate, ethyl alcohol, 2-ethyl-hexanol, dimethicone, oleyl alcohol, simethicone, and combinations thereof.

[00470] In some embodiments, the pharmaceutical composition comprises a co-solvent. Illustrative examples of co-solvents include ethanol, poly(ethylene) glycol, butylene glycol, dimethylacetamide, glycerin, propylene glycol, and combinations thereof.

[00471] In some embodiments, the pharmaceutical composition comprises a buffer. Illustrative examples of buffers include acetate, borate, carbonate, lactate, malate, phosphate, citrate, hydroxide, diethanolamine, monoethanolamine, glycine, methionine, guar gum, monosodium glutamate, and combinations thereof.

[00472] In some embodiments, the pharmaceutical composition comprises a carrier or filler. Illustrative examples of carriers or fillers include lactose, maltodextrin, mannitol, sorbitol, chitosan, stearic acid, xanthan gum, guar gum, and combinations thereof.

[00473] In some embodiments, the pharmaceutical composition comprises a surfactant. Illustrative examples of surfactants include *d*-alpha tocopherol, benzalkonium chloride, benzethonium chloride, cetrimide, cetylpyridinium chloride, docusate sodium, glyceryl behenate, glyceryl monooleate, lauric acid, macrogol 15 hydroxystearate, myristyl alcohol, phospholipids, polyoxyethylene alkyl ethers, polyoxyethylene sorbitan fatty acid esters, polyoxyethylene stearates, polyoxylglycerides, sodium lauryl sulfate, sorbitan esters, vitamin E polyethylene(glycol) succinate, and combinations thereof.

[00474] In some embodiments, the pharmaceutical composition comprises an anti-caking agent. Illustrative examples of anti-caking agents include calcium phosphate (tribasic), hydroxymethyl cellulose, hydroxypropyl cellulose, magnesium oxide, and combinations thereof.

[00475] Other excipients that may be used with the pharmaceutical compositions include, for example, albumin, antioxidants, antibacterial agents, antifungal agents, bioabsorbable polymers, chelating agents, controlled release agents, diluents, dispersing agents, dissolution enhancers, emulsifying agents, gelling agents, ointment bases, penetration enhancers, preservatives, solubilizing agents, solvents, stabilizing agents, sugars, and combinations thereof. Specific examples of each of these agents are described, for example, in the *Handbook of Pharmaceutical*

Excipients, Rowe et al. (Eds.) 6th Ed. (2009), The Pharmaceutical Press, incorporated by reference in its entirety.

[00476] In some embodiments, the pharmaceutical composition comprises a solvent. In some aspects, the solvent is saline solution, such as a sterile isotonic saline solution or dextrose solution. In some aspects, the solvent is water for injection.

[00477] In some embodiments, the pharmaceutical compositions are in a particulate form, such as a microparticle or a nanoparticle. Microparticles and nanoparticles may be formed from any suitable material, such as a polymer or a lipid. In some aspects, the microparticles or nanoparticles are micelles, liposomes, or polymersomes.

[00478] Further provided herein are anhydrous pharmaceutical compositions and dosage forms comprising an ABP, since water can facilitate the degradation of some ABPs.

[00479] Anhydrous pharmaceutical compositions and dosage forms provided herein can be prepared using anhydrous or low moisture containing ingredients and low moisture or low humidity conditions. Pharmaceutical compositions and dosage forms that comprise lactose and at least one active ingredient that comprises a primary or secondary amine can be anhydrous if substantial contact with moisture and/or humidity during manufacturing, packaging, and/or storage is expected.

[00480] An anhydrous pharmaceutical composition should be prepared and stored such that its anhydrous nature is maintained. Accordingly, anhydrous compositions can be packaged using materials known to prevent exposure to water such that they can be included in suitable formulary kits. Examples of suitable packaging include, but are not limited to, hermetically sealed foils, plastics, unit dose containers (*e.g.*, vials), blister packs, and strip packs.

[00481] In certain embodiments, an ABP and/or cell provided herein is formulated as parenteral dosage forms. Parenteral dosage forms can be administered to subjects by various routes including, but not limited to, subcutaneous, intravenous (including infusions and bolus injections), intramuscular, and intra-arterial. Because their administration typically bypasses subjects' natural defenses against contaminants, parenteral dosage forms are typically, sterile or capable of being sterilized prior to administration to a subject. Examples of parenteral dosage forms include, but are not limited to, solutions ready for injection, dry (e.g., lyophilized) products ready to be dissolved or suspended in a pharmaceutically acceptable vehicle for injection, suspensions ready for injection, and emulsions.

[00482] Suitable vehicles that can be used to provide parenteral dosage forms are well known to those skilled in the art. Examples include, but are not limited to: Water for Injection USP; aqueous vehicles such as, but not limited to, Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, and Lactated Ringer's Injection; water miscible vehicles such as, but not limited to, ethyl alcohol, polyethylene glycol, and polypropylene glycol; and non-aqueous vehicles such as, but not limited to, corn oil, cottonseed oil, peanut oil, sesame oil, ethyl oleate, isopropyl myristate, and benzyl benzoate.

[00483] Excipients that increase the solubility of one or more of the ABPs and/or cells disclosed herein can also be incorporated into the parenteral dosage forms.

[00484] In some embodiments, the parenteral dosage form is lyophilized. Exemplary lyophilized formulations are described, for example, in U.S. Pat. Nos. 6,267,958 and 6,171,586; and WO 2006/044908; each of which is incorporated by reference in its entirety.

[00485] In human therapeutics, the doctor will determine the posology which he considers most appropriate according to a preventive or curative treatment and according to the age, weight, condition and other factors specific to the subject to be treated.

[00486] In certain embodiments, a composition provided herein is a pharmaceutical composition or a single unit dosage form. Pharmaceutical compositions and single unit dosage forms provided herein comprise a prophylactically or therapeutically effective amount of one or more prophylactic or therapeutic ABP.

[00487] The amount of the ABP, cell, or composition which will be effective in the prevention or treatment of a disorder or one or more symptoms thereof will vary with the nature and severity of the disease or condition, and the route by which the ABP and/or cell is administered. The frequency and dosage will also vary according to factors specific for each subject depending on the specific therapy (*e.g.*, therapeutic or prophylactic agents) administered, the severity of the disorder, disease, or condition, the route of administration, as well as age, body, weight, response, and the past medical history of the subject. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

[00488] Different therapeutically effective amounts may be applicable for different diseases and conditions, as will be readily known by those of ordinary skill in the art. Similarly, amounts sufficient to prevent, manage, treat or ameliorate such disorders, but insufficient to cause, or sufficient to reduce, adverse effects associated with the ABPs and/or cells provided herein are also encompassed by the dosage amounts and dose frequency schedules provided herein. Further,

when a subject is administered multiple dosages of a composition provided herein, not all of the dosages need be the same. For example, the dosage administered to the subject may be increased to improve the prophylactic or therapeutic effect of the composition or it may be decreased to reduce one or more side effects that a particular subject is experiencing.

[00489] In certain embodiments, treatment or prevention can be initiated with one or more loading doses of an ABP or composition provided herein followed by one or more maintenance doses.

[00490] In certain embodiments, a dose of an ABP, cell, or composition provided herein can be administered to achieve a steady-state concentration of the ABP and/or cell in blood or serum of the subject. The steady-state concentration can be determined by measurement according to techniques available to those of skill or can be based on the physical characteristics of the subject such as height, weight and age.

[00491] As discussed in more detail elsewhere in this disclosure, an ABP and/or cell provided herein may optionally be administered with one or more additional agents useful to prevent or treat a disease or disorder. The effective amount of such additional agents may depend on the amount of ABP present in the formulation, the type of disorder or treatment, and the other factors known in the art or described herein.

Therapeutic Applications

[00492] For therapeutic applications, ABPs and/or cells are administered to a mammal, generally a human, in a pharmaceutically acceptable dosage form such as those known in the art and those discussed above. For example, ABPs and/or cells may be administered to a human intravenously as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intra-cerebrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, or intratumoral routes. The ABPs also are suitably administered by peritumoral, intralesional, or perilesional routes, to exert local as well as systemic therapeutic effects. The intraperitoneal route may be particularly useful, for example, in the treatment of ovarian tumors.

[00493] The ABPs and/or cells provided herein can be useful for the treatment of any disease or condition involving HLA-PEPTIDE. In some embodiments, the disease or condition is a disease or condition that can benefit from treatment with an anti-HLA-PEPTIDE ABP and/or cell. In some embodiments, the disease or condition is a tumor. In some embodiments, the disease or condition is a cell proliferative disorder. In some embodiments, the disease or condition is a cancer.

[00494] In some embodiments, the ABPs and/or cells provided herein are provided for use as a medicament. In some embodiments, the ABPs and/or cells provided herein are provided for use in the manufacture or preparation of a medicament. In some embodiments, the medicament is for the treatment of a disease or condition that can benefit from an anti-HLA-PEPTIDE ABP and/or cell. In some embodiments, the disease or condition is a tumor. In some embodiments, the disease or condition is a cell proliferative disorder. In some embodiments, the disease or condition is a cancer.

[00495] In some embodiments, provided herein is a method of treating a disease or condition in a subject in need thereof by administering an effective amount of an ABP and/or cell provided herein to the subject. In some aspects, the disease or condition is a cancer.

[00496] In some embodiments, provided herein is a method of treating a disease or condition in a subject in need thereof by administering an effective amount of an ABP and/or cell provided herein to the subject, wherein the disease or condition is a cancer, and the cancer is selected from a solid tumor and a hematological tumor.

[00497] In some embodiments, provided herein is a method of modulating an immune response in a subject in need thereof, comprising administering to the subject an effective amount of an ABP and/or cell or a pharmaceutical composition disclosed herein.

Combination Therapies

[00498] In some embodiments, an ABP and/or cell provided herein is administered with at least one additional therapeutic agent. Any suitable additional therapeutic agent may be administered with an ABP and/or cell provided herein. An additional therapeutic agent can be fused to an ABP. In some aspects, the additional therapeutic agent is selected from radiation, a cytotoxic agent, a toxin, a chemotherapeutic agent, a cytostatic agent, an anti-hormonal agent, an EGFR inhibitor, an immunomodulatory agent, an anti-angiogenic agent, and combinations thereof. In some embodiments, the additional therapeutic agent is an ABP.

Diagnostic Methods

[00499] Also provided are methods for predicting and/or detecting the presence of a given HLA-PEPTIDE on a cell from a subject. Such methods may be used, for example, to predict and evaluate responsiveness to treatment with an ABP and/or cell provided herein.

[00500] In some embodiments, a blood or tumor sample is obtained from a subject and the fraction of cells expressing HLA-PEPTIDE is determined. In some aspects, the relative amount

of HLA-PEPTIDE expressed by such cells is determined. The fraction of cells expressing HLA-PEPTIDE and the relative amount of HLA-PEPTIDE expressed by such cells can be determined by any suitable method. In some embodiments, flow cytometry is used to make such measurements. In some embodiments, fluorescence assisted cell sorting (FACS) is used to make such measurement. *See* Li et al., *J. Autoimmunity*, 2003, 21:83-92 for methods of evaluating expression of HLA-PEPTIDE in peripheral blood.

[00501] In some embodiments, detecting the presence of a given HLA-PEPTIDE on a cell from a subject is performed using immunoprecipitation and mass spectrometry. This can be performed by obtaining a tumor sample (e.g., a frozen tumor sample) such as a primary tumor specimen and applying immunoprecipitation to isolate one or more peptides. The HLA alleles of the tumor sample can be determined experimentally or obtained from a third party source. The one or more peptides can be subjected to MS to determine their sequence(s). The spectra from the MS can then be searched against a database. An example is provided in the Examples section below.

[00502] In some embodiments, predicting the presence of a given HLA-PEPTIDE on a cell from a subject is performed using a computer-based model applied to the peptide sequence and/or RNA measurements of one or more genes comprising that peptide sequence (e.g., RNA seq or RT-PCR, or nanostring) from a tumor sample. The model used can be as described in international patent application no. PCT/US2016/067159, herein incorporated by reference, in its entirety, for all purposes.

Kits

[00503] Also provided are kits comprising an ABP and/or cell provided herein. The kits may be used for the treatment, prevention, and/or diagnosis of a disease or disorder, as described herein.

[00504] In some embodiments, the kit comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, and IV solution bags. The containers may be formed from a variety of materials, such as glass or plastic. The container holds a composition that is by itself, or when combined with another composition, effective for treating, preventing and/or diagnosing a disease or disorder. The container may have a sterile access port. For example, if the container is an intravenous solution bag or a vial, it may have a port that can be pierced by a needle. At least one active agent in the

composition is an ABP provided herein. The label or package insert indicates that the composition is used for treating the selected condition.

[00505] In some embodiments, the kit comprises (a) a first container with a first composition contained therein, wherein the first composition comprises an ABP and/or cell provided herein; and (b) a second container with a second composition contained therein, wherein the second composition comprises a further therapeutic agent. The kit in this embodiment can further comprise a package insert indicating that the compositions can be used to treat a particular condition, e.g., cancer.

[00506] Alternatively, or additionally, the kit may further comprise a second (or third) container comprising a pharmaceutically-acceptable excipient. In some aspects, the excipient is a buffer. The kit may further include other materials desirable from a commercial and user standpoint, including filters, needles, and syringes.

EXAMPLES

[00507] Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

[00508] The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T.E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990); Carey and Sundberg *Advanced Organic Chemistry 3rd Ed.* (Plenum Press) Vols A and B(1992).

Example 1: Identification of Predicted HLA-PEPTIDE Complexes

[00509] We identified cancer specific HLA-peptide targets using three computational steps: First, we identified genes that are not generally expressed in most normal tissues using data

available through the Genotype-Tissue Expression (GTEx) Project [1]. We then identified which of those genes are aberrantly expressed in cancer samples using data from The Cancer Genome Atlas (TCGA) Research Network: http://cancergenome.nih.gov/. In these genes, we identified which peptides are likely to be presented as cell surface antigens by MHC Class I proteins using a deep learning model trained on HLA presented peptides sequenced by MS/MS, as described in international patent application no. PCT/US2016/067159, herein incorporated by reference, in its entirety, for all purposes.

[00510] To identify genes that are not usually expressed in normal tissues, we obtained aggregated gene expression data from the Genotype-Tissue Expression (GTEx) Project (version V6p). This dataset comprised 8,555 post-mortem samples from over 50 tissue types. Expression was measured using RNA-Seq and computationally processed according to the GTEx standard pipeline (https://www.gtexportal.org/home/documentationPage). For the purposes of this analysis, genes were considered not expressed in normal tissues if they were found not to be expressed in any tissues in GTEx or were only expressed in one or more of testis, minor salivary gland, and the endocervix (i.e., immune privileged or non-essential tissues). We also restricted our search to only include protein coding genes. Because GTEx and TCGA use different annotations of the human genome in their computational analyses, we excluded genes which we could not map between the two datasets using standard techniques such as ENCODE mappings.

[00511] We sought to define criteria to excluded genes that were expressed in normal tissue that was strict to ensure tumor specificity, but would not exclude non-zero measurements arising from sporadic, low level transcription or potential artifacts such as read misalignment. Therefore, we designated a gene to be not normally expressed in a non-immune privileged or essential tissue if its median expression across GTEx samples was less than 0.5 RPKM (Reads Per Kilobase of transcript per Million mapped reads), and it was never expressed with greater than 10 RPKM, and it was expressed at 5 RPKM in no more than two samples across all essential tissue samples. To exclude genes which were potentially expressed but could not be measured by RNA-Seq using the GTEX analysis pipeline, we also excluded genes which were measured at 0 RPKM in all samples. These criteria left us with a set of protein coding genes that did not appear to be expressed in most normal tissues.

[00512] We next sought to identify which of these genes are aberrantly expressed in tumors. We examined 11,093 samples available from TCGA (Data Release 6.0). We considered a gene expressed if it was observed at expression of at least 5 FPKM (Fragments Per Kilobase of

transcript per Million mapped reads) in at least 5 samples. Because one fragment usually consists of two mapped reads, 5 FPKM equals approximately 10 RPKM.

[00513] While the GTEx data spans a broad range of tissue types, it does not include all cell types that are present in the human body. We therefore further examined the list for the gene's biological function category using the DAVID v 6.8 [2] and used this analysis, along with literature review, to filter the gene list further. We removed genes likely to be expressed in immune cells (e.g., interferon family genes), eye-related genes (e.g., retina in the FANTOM5 dataset http://www.proteinatlas.org), genes expressed in the mouth and nose (e.g. olfactory genes and taste receptors), and genes related to the circadian cycle. We also excluded genes that are part of large gene families, including histone genes, because their expression is difficult to accurately assess with RNA Sequencing due to sequence homology.

[00514] We then examined the distribution of the expression of the remaining genes across the TCGA samples. When we examined the known Cancer Testis Antigens (CTAs), e.g., the MAGE family of genes, we observed that the expression of these genes in log space was generally characterized by a bimodal distribution across samples in the TCGA. This distribution included a left mode around a lower expression value and a right mode (or thick tail) at a higher expression level. This expression pattern is consistent with a biological model in which some minimal expression is detected at baseline in all samples and higher expression of the gene is observed in a subset of tumors experiencing epigenetic dysregulation. We reviewed the distribution of expression of each gene across TCGA samples and discarded those where we observed only a unimodal distribution with no significant right-hand tail, as this distribution may (as a non-limiting example) more likely characterize genes that have a low baseline of expression in normal tissues.

[00515] This left us with a remaining gene list of >630 genes that was highly enriched for genes involved in testis-specific biological processes and development. Because many of these genes produce different isoforms, these genes mapped to >1,200 proteins using the UNIPROT mapping service. In addition to the genes that met our strict computational criteria, we added several genes that have previously been identified in the scientific literature as cancer testes antigens.

[00516] To identify the peptides that are likely to be presented as cell surface antigens by MHC Class I proteins, we used a sliding window to parse each of these proteins into its constituent 8-11 amino acid sequences. We processed these peptides and their flanking sequences

with the HLA peptide presentation deep learning model to calculate the likelihood of presentation of each peptide at expression levels between five TPM, which approximately corresponds to one transcript per cell [3], to 200 TPM (i.e., a high level of expression). We considered a peptide a putative HLA-PEPTIDE target if its probability of presentation calculated by our model was greater than 0.1 in 10 or more patients in the TCGA dataset with expression 5 TPM or greater.

[00517] The results are shown in Table A. From this example, there are >1,800 HLA-PEPTIDE targets across ~400 genes and 25 analyzed HLA alleles. For clarity, each HLA-PEPTIDE was assigned a target number in Table A. For example, HLA-PEPTIDE target 1 is HLA-A*01:01_EVDPIGHLY, HLA-PEPTIDE target 2 is HLA-A*29:02_FVQENYLEY, and so forth.

[00518] Collectively, this list of HLA-PEPTIDE targets is expected to be a significant contribution to the state of knowledge of cancer specific targets. In summary, the example provides a large set of tumor-specific HLA-PEPTIDEs that can be pursued as candidate targets for ABP research and development.

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Example 2: Initial Validation of Predicted HLA-PEPTIDE Complexes

[00523] As an initial assessment to validate the predicted HLA-PEPTIDE targets arising from the above described approach, we evaluated public databases and selected literature for reports of these targets as having been previously identified by various assay techniques, including HLA binding affinity measurements, HLA peptide mass-spectrometry, as well as measures of T cell responses. Two comprehensive databases containing assay result annotations for HLA-PEPTIDE pairs were used: IEDB (Vita et al., 2015) and Tantigen (Olsen et al., 2017). We determined that 19 (15 unique across genes) of the computationally predicted targets were previously reported in

the databases, many in genes (e.g., cancer testis antigens) that have long been the subject of study in cancer immunology. *See* Table B.

Table B

Protein Name	HLA-PEPTIDE	Found in IEDB or Tantigen	IEDB Status	Tantigen Status
MAGA3	HLA-A*01:01_EVDPIGHLY	TRUE	Found	Found
MAGA3	HLA-A*29:02_FVQENYLEY	TRUE	Found	Not found
MAGA3	HLA-A*29:02_LVHFLLLKY	TRUE	Found	Not found
MAGA3	HLA-B*44:03_MEVDPIGHLY	TRUE	Not found	Found
MAGA6	HLA-A*29:02_FVQENYLEY	TRUE	Found	Not found
MAGA6	HLA-A*29:02_LVHFLLLKY	TRUE	Found	Not found
MAGA4	HLA-A*01:01_EVDPASNTY	TRUE	Not found	Found
MAGA1	HLA-A*02:01_KVLEYVIKV	TRUE	Found	Found
MAGAC	HLA-A*29:02_LVHFLLLKY	TRUE	Found	Not found
MAGAC	HLA-A*29:02_LVQENYLEY	TRUE	Found	Not found
SSX1	HLA-C*04:01_AFDDIATYF	TRUE	Found	Not found
MAGA4	HLA-A*29:02_WVQENYLEY	TRUE	Found	Not found
MAGB2	HLA-A*02:01_GVYDGEEHSV	TRUE	Found	Not found
MAGA1	HLA-A*03:01_SLFRAVITK	TRUE	Found	Found
MAGA4	HLA-A*11:01_ALAETSYVK	TRUE	Found	Not found
SAGE1	HLA-A*24:02_LYATVIHDI	TRUE	Not found	Found
PASD1	HLA-A*02:01_QLLDGFMITL	TRUE	Found	Not found
MAGA8	HLA-A*29:02_WVQENYLEY	TRUE	Found	Not found
MAGAC	HLA-A*29:02_STLPTTINY	TRUE	Found	Not found

[00524] Additional limited literature review was carried out for peptides not found in the above public databases. The following peptides were identified, as shown in Table C:

Table C

HLA allele/peptide complex	Protein Name	HLA/peptide known status IEDB or Tantig 2017	HLA/peptide known status in literature (preliminary) if not in IEDB or Tantigen
HLA-A*01:01_NTDNNLAVY	KKLC1	Not known	WO 2017/089756 A1 (Stevanović et al., 2017)
HLA-B*35:01_YPAPLESLDY	PRA10	Not known	WO2008118017 A2
HLA-A*11:01_ATLENLLSH	PRAM4	Not known	WO2008118017 A2
HLA-B*51:01_DALLAQKV	PRA12	Not known	WO2008118017 A2
HLA-B*44:03_SESDLKHLSW	PRA12	Not known	WO2008118017 A2
HLA-A*11:01_ATLENLLSH	PRAM9	Not known	WO2008118017 A2
HLA-A*02:07_TLDEYLTYL	PRAM9	Not known	WO2008118017 A2

[00525] One notable example from Table C was KKLC1 HLA-A*01:01_NTDNNLAVY. Kita-kyushu lung cancer antigen-1 (KK-LC-1; CT83) is a cancer testis antigen (CTA) that has been shown to be widely expressed in many different cancer types. It was originally discovered

based on a cloned CTL to KK-LC-1 peptide 76-84 – RQKRILVNL (Fukuyama et al., 2006). More recently Stevanović et al., 2017 revealed another peptide from KK-LC-1 recognized by a CTL in a patient with cervical cancer, the predicted peptide KK-LC-1 52-60 NTDNNLAVY. The corresponding TCR for this CTL is now listed on the NIH website https://www.ott.nih.gov/technology/e-153-2016/ and the peptide is listed in WO 2017/089756 A1, herein incorporated by reference, in its entirety, for all purposes.

[00526] This example highlights the expected value of predicted HLA-PEPTIDE targets in Table A: Although no information on which CTA HLA-PEPTIDE targets were previously known was incorporated in the prediction, the analysis yielded many targets that were described in the literature, indicating that many of the novel targets can likewise be validated experimentally and ultimately serve as targets for one or more ABPs.

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Example 3: Identification of Predicted HLA-PEPTIDE Complexes

[00532] Next, HLA-peptide targets from proteins of seven genes were identified: AFP, KKLC-1, MAGE-A4, MAGE-A10, MART-1, NY-ESO-1, and WT1.

[00533] To identify peptides that are likely to be presented as cell surface antigens by MHC Class I proteins, a sliding window was used to parse each of these proteins into its constituent 8-11 amino acid sequences. These peptides and their flanking sequences were then processed with

the HLA peptide presentation deep learning model (*see* PCT/US2016/067159 and Example 1 above) to calculate the likelihood of presentation of each peptide at an expression level of 100 TPM (high expression) for each of 64 Class I HLA types. Potential modeling artifacts were removed that could give stronger scores to certain HLAs due to training data biases by quantile normalizing model scores for each HLA so that each HLA present scores from the same distribution. In the normalization, the seven target genes as well as 50 randomly selected genes were included to control for HLA allele sequence preferences. A gene was considered likely to be presented if the model normalized score was higher than 0.00075, which was chosen based on the presentation scores of peptides known to be presented in the literature.

[00534] The results are shown in Table A (cont.). Target numbers were assigned to each HLA-PEPTIDE target as described in Example 1.

Example 4: Validation of Predicted HLA-PEPTIDE Complexes

[00535] The presence of peptides from the HLA-PEPTIDE complexes of Table A were determined using mass spectrometry (MS) on tumor samples known to be positive for each given HLA allele from the respective HLA-PEPTIDE complex.

[00536] Isolation of HLA-peptide molecules was performed using classic immunoprecipitation (IP) methods after lysis and solubilization of the tissue sample (1-4). Fresh frozen tissue was first frozen in liquid nitrogen and pulverized (CryoPrep; Covaris, Woburn, MA). Lysis buffer (1% CHAPS, 20mM Tris-HCl, 150mM NaCl, protease and phosphatase inhibitors, pH=8) was added to solubilize the tissue and $1/10^{th}$ of the sample was aliquoted for proteomics and genomic sequencing efforts. The remainder of the sample was spun at 4C for 2 hrs to pellet debris. The clarified lysate was used for the HLA specific IP.

[00537] Immunoprecipitation was performed using antibodies coupled to beads where the antibody was specific for HLA molecules. For a pan-Class I HLA immunoprecipitation, the antibody W6/32 (5) was used, for Class II HLA – DR, antibody L243 (6) was used. Antibody was covalently attached to NHS-sepharose beads during overnight incubation. After covalent attachment, the beads were washed and aliquoted for IP. Additional methods for IP can be used including but not limited to Protein A/G capture of antibody, magnetic bead isolation, or other methods commonly used for immunoprecipitation.

[00538] The lysate was added to the antibody beads and rotated at 4C overnight for the immunoprecipitation. After immunoprecipitation, the beads were removed from the lysate and the lysate was stored for additional experiments, including additional IPs. The IP beads are

washed to remove non-specific binding and the HLA/peptide complex was eluted from the beads with 2N acetic acid. The protein components were removed from the peptides using a molecular weight spin column. The resultant peptides were taken to dryness by SpeedVac evaporation and can be stored at -20C prior to MS analysis.

[00539] Dried peptides were reconstituted in HPLC buffer A and loaded onto a C-18 microcapillary HPLC column for gradient elution in to the mass spectrometer. A gradient of 0-40%B (solvent A – 0.1% formic acid, solvent B- 0.1% formic acid in 80% acetonitrile) in 180 minutes was used to elute the peptides into the Fusion Lumos mass spectrometer (Thermo). MS1 spectra of peptide mass/charge (m/z) were collected in the Orbitrap detector with 120,000 resolution followed by 20 MS2 scans. Selection of MS2 ions was performed using data dependent acquisition mode and dynamic exclusion of 30 sec after MS2 selection of an ion. Automatic gain control (AGC) for MS1 scans was set to 4x105 and for MS2 scans was set to 1x104. For sequencing HLA peptides, +1, +2 and +3 charge states can be selected for MS2 fragmentation. This was commonly referred to as Targeted Mass Spectrometry and was performed in either a qualitative manner or can be quantitative. Quantitation methods require each peptide to be quantitated to be synthesized using heavy labeled amino acids. (Doerr 2013)

[00540] MS2 spectra from each analysis were searched against a protein database using Comet (7-8) and the peptide identification was scored using Percolator (9-11) or using the integrated de novo sequencing and database search algorithm of PEAKS. .

[00541] The presence of peptides from HLA-PEPTIDE complexes was determined using mass spectrometry (MS) on various tumor samples known to be positive for each given HLA allele from the respective HLA-PEPTIDE complex.. Representative spectra data forfor selected HLA-restricted peptides is shown in FIGS. 6 and 7. Each spectra contains the peptide fragmentation information as well as information related to the patient sample, including HLA types.

[00542] The spontaneous modification of amino acids can occur to many amino acids. Cysteine is especially susceptible to this modification and can be oxidized or modified with a free cysteine. Additionally N-terminal glutamine amino acids can be converted to pyro-glutamic acid. Since each of these modifications results in a change in mass, they can be definitively assigned in the MS2 spectra. To use these peptides in preparation of ABPs the peptide may need to contain the same modification as seen in the mass spectrometer. These modifications can be created using simple laboratory and peptide synthesis methods (Lee et al.; Ref 14).

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[00558] 2017) or other method to analyze predicted fragment ions.

[00559] The presence of multiple peptides from the predicted HLA-PEPTIDE complexes is determined using mass spectrometry (MS) on various tumor samples known to be positive for each given HLA allele from the respective HLA-PEPTIDE complex.

[00560] The spontaneous modification of amino acids can occur to many amino acids. Cysteine is especially susceptible to this modification and can be oxidized or modified with a free cysteine. Additionally N-terminal glutamine amino acids can be converted to pyro-glutamic acid. Since each of these modifications results in a change in mass, they can be definitively assigned in the MS2 spectra. To use these peptides in preparation of ABPs the peptide may need to contain the same modification as seen in the mass spectrometer. These modifications can be created using simple laboratory and peptide synthesis methods (Lee et al.; Ref 14).

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Example 6: Identification of Antibodies or Antigen-Binding Fragments Thereof that Bind HLA-PEPTIDE Complexes

[00576] Overview

[00577] The following exemplification demonstrates that antibodies (Abs) can be identified that recognize tumor-specific HLA-restricted peptides. The overall epitope that is recognized by such Abs generally comprises a composite surface of both the peptide as well as the HLA protein presenting that particular peptide. Abs that recognize HLA complexes in a peptide-specific manner are often referred to as T cell receptor (TCR)-like Abs or TCR-mimetic Abs. The HLA-PEPTIDE target antigens that were selected for antibody discovery are HLA-A*01:01_NTDNNLAVY (Target X in Table A, designated as "G2") and HLA-A*02:01_ LLASSILCA (Target X in Table A, designated as "G7"). Cell surface presentation of these HLA-PEPTIDE antigens was confirmed by mass spectrometry analysis of HLA complexes obtained from tumor samples, as described in Example 4.

[00578] Generation of HLA-PEPTIDE target complexes and counterscreen peptide-HLA complexes, and stability analysis

[00579] The HLA-PEPTIDE targets G2 and G7, as well as counterscreen negative control peptide-HLAs, were produced recombinantly using conditional ligands for HLA molecules using established methods. In all, 18 counterscreen HLA-peptides were generated for each of the G2 and G7 targets.

[00580] *Overall design of phage library screening*

[00581] The highly diverse SuperHuman 2.0 synthetic naïve scFv library from Distributed Bio Inc (7.6e10 total diversity on ultra-stable and diverse VH/VL scaffolds) was used for phage display. The phage library was initially depleted with 18 pooled negative pHLA

complexes (the "complete pool") followed by three to four rounds of bead-based phage panning withwith the target pHLA complex using established protocols to identify scFv binders to HLA-PEPTIDE targets G2 and G7, respectively. The phage titer was determined at every round of panning to establish removal of non-binding phage. Phage ELISA results are shown in FIGS. 14A and 14B. There was an enrichment of bound phage in later rounds of panning for each of the G2 and G7 targetsThe output phage supernatant was also tested for target binding by ELISA .

[00582] The design of target screen 1 for the G2 target is shown in FIG. 8. Similarly, the design of target screen 2 for the G7 target is shown in FIG. 11. Briefly, for each target, three "minipool" counterscreen peptides were selected for their ability to bind the same HLA allele as the target and also to have significantly different ABP-facing features such as charge, bulk, aromatic, or hydrophobic residues. See FIG. 9A for G2 and FIG. 13A for G7. In addition, additional counterscreen peptide-HLA complexes, featuring distinct restricted peptide sequences and different HLA alleles were generated. The 15 additional counterscreen HLA-peptides plus the three "minipool" HLA-peptides formed a "complete pool" of 18 total counterscreen HLA-peptide complexes.

[00583] *Generation of peptide-HLA complexes*

[00584] α-, and β2 microglobulin chain of various human leukocyte antigens (HLA) were expressed separately in BL21 competent *E. Coli* cells (New England Biolabs) using established procedures (Garboczi, Hung, & Wiley, 1992). Following auto-induction, cells were lysed via sonication in Bugbuster® plus benzonase protein extraction reagent (Novagen). The resulting inclusion bodies were washed and sonicated in wash buffer with and without 0.5% Triton X-100 (50 mM Tris, 100 mM NaCl, 1 mM EDTA). After the final centrifugation, inclusion pellets were dissolved in urea solution (8 M urea, 25 mM MES, 10 mM EDTA, 0.1 mM DTT, pH 6.0). Bradford assay (Biorad) was used to quantify the concentration and the inclusion bodies were stored at -80°C.

[00585] HLA complexes were obtained by refolding of recombinantly produced subunits and a synthetically obtained peptide using established procedures.(Garboczi et al., 1992). Briefly, the purified α and β2 microglobulin chains were refolded in refold buffer (100 mM Tris pH 8.0, 400 mM L-Arginine HCl, 2 mM EDTA, 50 mM oxidized glutathione, 5 mM reduced glutathione, protease inhibitor tablet) with the restricted peptide of choice. In some experiments, the restricted peptide of choice was a conditional ligand peptide, which is

cleavable upon exposure to a conditional stimulus. In some experiments, the restricted peptide of choice was the G2 or G7 target peptide, or counterscreen peptide. The refold solution was concentrated with a Vivaflow 50 or 50R crossflow cassette (Sartorius Stedim). Three rounds of dialyses in 20 mM Tris pH 8.0 were performed for at least 8 hours each. For the antibody screening and functional assays, the refolded HLA was enzymatically biotinylated using BirA biotin ligase (Avidity). Refolded protein complexes were purified using a HiPrep (16/60 Sephacryl S200) size exclusion column attached to an Akta FPLC system. Biotinylation was confirmed in a streptavidin gel-shift assay under non-reducing conditions by incubating the refolded protein with an excess of streptavidin at room temperature for 15 minutes prior to SDS-PAGE. The resulting peptide-HLA complexes were aliquoted and stored at -80°C.

[00586] *Stability analysis of the peptide-HLA complexes*

[00587] HLA-peptide stability was assessed by conditional ligand peptide exchange and stability ELISA assay. Briefly, conditional ligand-HLA complexes were subjected to ± conditional stimulus in the presence or absence of the counterscreen or test peptides. Exposure to the conditional stimulus cleaves the conditional ligand from the HLA complex, resulting in dissociation of the HLA complex. If the counterscreen or test peptide stably binds the α1/α2 groove of the HLA complex, it "rescues" the HLA complex from disassociation.

[00588] The HLA stability ELISA was performed using established procedures. (Chew et al., 2011; Rodenko et al., 2006) A 384-well clear flat bottom polystyrene microplate (Corning) was precoated with 50 µl of streptavidin (Invitrogen) at 2 µg mL^{-1} in PBS. Following 2 h of incubation at 37 °C, the wells were washed with 0.05% Tween 20 in PBS (four times, 50 µL) wash buffer, treated with 50 µl of blocking buffer (2% BSA in PBS), and incubated 30 min at room temperature. Subsequently, 25 µl of peptide-exchanged samples that were 300× diluted with 20 mM Tris HCl/50mM NaCl were added in quadruplicate. The samples were incubated for 15 min at RT, washed with 0.05% Tween wash buffer (4 × 50 µL), treated for 15 min with 25 µL of HRP-conjugated anti-β2m (1 µg mL^{-1} in PBS) at RT, washed with 0.05% Tween wash buffer (4 × 50 µL), and developed for 10–15 min with 25 µL of ABTS-solution (Invitrogen), and the reactions were stopped by the addition of 12.5 µL of stop buffer (0.01% sodium azide in 0.1 M citric acid). Absorbance was subsequently measured at 415 nm using a spectrophotometer (SpectraMax i3x; Molecular Devices).

[00589] Results for the G2 counterscreen "minipool" and G2 target are shown in FIG. 9B. All three counterscreen peptides and the G2 peptide rescued the HLA complex from dissociation.

[00590] Results for the additional G2 "complete" pool counterscreen peptides are shown in FIG. 10, demonstrating that they also form stable HLA-peptide complexes.

[00591] Results for the G7 counterscreen "minipool" and G7 target are shown in FIG. 13B. All three counterscreen peptides and the G7 peptide rescued the HLA complex from dissociation.

[00592] Results for the additional G7 "complete" pool counterscreen peptides are shown in FIG. 12, demonstrating that they also form stable HLA-peptide complexes.

[00593] *Phage Library Screening*

[00594] Phage library screening was carried out according to the overall screening design described above. Three to four rounds of bead-based panning were performed to identify scFv binders to each peptide-HLA complex. For each round of panning, an aliquot of starting phage was set aside for input titering and the remaining phage was depleted three times against Dynabead M-280 streptavidin beads (Life Technologies) followed by a depletion against Streptavidin beads pre-bound with 100 pmoles of pooled negative peptide-HLA complexes. For the first round of panning, 100 pmoles of peptide-HLA complex bound to streptavidin beads was incubated with depleted phage for 2 hours at room temperature with rotation. Three five-minute washes with 0.5% BSA in 1X PBST (PBS + 0.05% Tween-20) followed by three five-minute washes with 0.5% BSA in 1X PBS were utilized to remove any unbound phage to the peptide-HLA complex bound beads. To elute the bound phage from the washed beads, 1 ml 0.1M TEA was added and incubated for 10 minutes at room temperature with rotation. The eluted phage was collected from the beads and neutralized with 0.5 ml 1M Tris-HCl pH 7.5. The neutralized phage was then used to infect log growth TG-1 cells (OD_{600} = 0.5) and after an hour of infection at 37°C, cells were plated onto 2YT media with 100 μg/ml carbenicillin and 2% glucose (2YTCG) agar plates for output titer and bacterial growth for subsequent panning rounds. For subsequent rounds of panning, selection antigen concentrations were lowered while washes increased by amount and length of wash times at show in Table 1.

[00595] Table 1: Phage library screening strategy

Round	Antigen concentration	Washes
R1	100 pmol	3X PBST + 3X PBS (5 min washes)

R2	25 pmol	5 PBST (2x 30 sec, 3x 5 min) + 5 PBS (2x 30 sec, 3x 5 min)
R3	10 pmol	8 PBST (4x 30 sec, 4x 5 min) + 8 PBS (4x 30 sec, 4x 5 min)
R4	5 pmol, 10 pmol	30 min PBST + 30 min PBS

[00596] Individual scFvs were cloned from phage and sequenced by DNA Sanger sequencing ("Sequence Unique Binders"). The indivual scFvs were also expressed in E. coli and periplasmic extracts (PPE) from E. coli containing the individual crude scFvs were subjected to scFv ELISA

[00597] scFv periplasmic extract (PPE) ELISA

[00598] The individual scFv cloned from phage obtained in the final round of panning, and expressed in E. coli, was subjected to scFv PPE ELISA as follows.

[00599] 96-well and/or 384-well streptavidin coated plates (Pierce) were coated with 2 ug/ml peptide-HLA complex in HLA buffer and incubated overnight at 4 °C. Plates were washed three times between each step with PBST (PBS + 0.05%). The antigen coated plates were blocked with 3% BSA in PBS (blocking buffer) for 1 hour at room temperature. After washing, scFv PPEs were added to the plates and incubated at room temperature for 1 hour. Following washing, mouse anti-v5 antibody (Invitrogen) in blocking buffer was added to detect scFv and incubated at room temperature for 1 hour. After washing, HRP-goat anti-mouse antibody (Jackson ImmunoResearch) was added and incubated at room temperature for 1 hour. The plates were then washed three times with PBST and 3 times with PBS before HRP activity was detected with TMB 1-component Microwell Peroxidase Substrate (Seracare) and neutralized with 2N sulfuric acid.

[00600] For negative peptide-HLA complex counter-screening, scFv PPE ELISAs were performed as described above, except for the coating antigen. HLA mini-pools consisted of 2 ug/ml of each of the three negative peptide-HLA complexes pooled together and coated onto streptavidin plates for comparison binding to their particular peptide-HLA complex. HLA big pools consisted of 2 ug/ml of each of all 18 negative peptide-HLA complexes pooled together and coated onto streptavidin plates for comparison binding to their particular peptide-HLA complex.

[00601] Those scFvs that showed selectivity for target pHLA compared to negative control pHLA by scFv-ELISA as crude PPE, were separately expressed and purified. The purified scFvs were titratated by scFv ELISA for confirmation of binding only target pHLA compared to negative control pHLA ("Selective Binders").

[00602] Clones were formatted into IgG, Fab, or scFv for further biochemical and functional analysis. ScFv clones selected for Fab production to be used for crystallization with their corresponding pHLA complexes were selected based on several parameters: sequence diversity, binding affinity, selectivity, and CDR3 diversity. The clustal software was used to produce a dendrogram and assess the sequence diversity of the Fab clones. The canonical 3D structures of the scFv sequences, based on the VH type, were also considered when possible. Binding affinity, as determined by the equilibrium dissociation constant (KD), was measured using an Octet HTX (ForteBio). Selectivity for the specific peptide-HLA complexes was determined with an ELISA titration of the purified scFvs and compared to negative peptides or streptavidin alone. Cutoff values for the KD and selectivity were determined for each target set based on the range of values obtained for the Fabs within each set. Final clones were then selected to obtain the highest diversity in sequence families and CDR3.

[00603] Table 2 shows the hit rate for the screening campaign described above.

Table 2: hit rate for screening campaigns

Group	**G2**	**G7**
Gene target	CT83	CT83
HLA	A*01:01	A*02:01
Restricted peptide	NTDNNLAVY	LLASSILCA
# Sequence Unique Binders	74	8
# Selective Binders	27	6
# selected for IgG	20	8
# selected for Fab	6	3
# selected for scFv	20	7

[00604] Table 3 shows the VH and VL sequences of the G2 scFv Selective Binders, selective for HLA-PEPTIDE Target HLA-A*01:01_ NTDNNLAVY

[00605] Table 4 shows the CDR sequences for the G2 Selective Binders, selective for HLA-PEPTIDE Target HLA-A*01:01_ NTDNNLAVY. CDRs were determined according to the Kabat numbering system._

[00606] Table 5 shows the VH and VL sequences of the G7 scFv Selective Binders, selective for HLA-PEPTIDE Target HLA-A*02:01_ LLASSILCA.

[00607] Table 6 shows the CDR sequences for the G7 Selective Binders, selective for HLA-PEPTIDE Target HLA-A*02:01_ LLASSILCA. CDRs were determined according to the Kabat numbering system.

Example 7: Reformatting of antibodies into Fab / scFv / IgG clones

[00608] Selected clones were reformatted into Fab, scFv, or IgG formats as follows.

[00609] Construction and production of Fab protein fragments

[00610] The constructs of selected G2, and G7 Fabs were cloned into a vector optimized for mammalian expression. Each DNA construct was scaled up for transfection and sequences were confirmed. A 100 mL transient production was completed in HEK293 cells (Tuna293™ Process) for each. The proteins were purified by anti-CH1 purification subsequently purified by SEC-polishing via HiLoad 16/600 Superdex 200. The mobile phase used for SEC-polishing was 20 mM Tris, 50 mM NaCl, pH 7. Final confirmatory CE-SDS analysis was performed.

[00611] Construction and production of scFv protein fragments

[00612] The expression plasmid was transformed into BL21(DE3) strain and co-expressed with a periplasmid chaperone in a 400 mL E. coli culture. The cell pellet was reconstituted: 10 ml/1g biomass with (25mM HEPES, pH7.4, 0.3M NaCl, 10mM MgCl2, 10%glycerol, 0.75% CHAPS, 1mM DTT) plus lysozyme, and benzonase and Lake Pharma protease inhibitor cocktail. The cell suspension was incubated on a shaking platform at RT for 30 minutes. Lysates were clarified by centrifugation at 4C, 13,000 x rpm for 15 min. The clarified lysate was loaded onto 5ml of Ni NTA resin pre-equilibrated in IMAC Buffer A (20mM Tris-HCl, Ph7.5; 300mM NaCl /10% Glycerol/1 mM DTT). The resin was washed with 10CVs of Buffer A (or until a stable baseline was reached), followed by 10 CVs of 8% IMAC Buffer B (20mM Tris-HCl, Ph7.5; 300mM NaCl /10% Glycerol/1mM DTT/250mM Imidazole). The target protein was eluted in a 20CV gradient to 100% IMAC Buffer B. The column was washed with 5CVs of 100% IMAC B to ensure complete protein removal. Elution fractions were analyzed by SDS-PAGE and Western blot (anti-His) and pooled accordingly. The pool was dialyzed to versus final formulation buffer (20mM Tris-HCl, Ph7.5; 300mM NaCl / 10% glycerol/ 1mM DTT), concentrated to a final protein concentration >0.3 mg/ml, aliquoted into 1 mL vials, and flash frozen in liquid nitrogen. Final QC steps included SDS-PAGE and measuring A280.

[00613] Construction and production of IgG proteins

[00614] The expression constructs of the G series antibodies were cloned into a vector optimized for mammalian expression. Each DNA construct was scaled up for transfection and sequences were confirmed. A 10 mL transient production was completed in HEK293 cells

(Tuna293™ Process) for each. The proteins were purified by Protein A purification and final CE-SDS analysis was performed.

Example 8: Affinity of Fab clones for the HLA-PEPTIDE target

[00615] Affinity measurements were performed on the Octet Qke (ForteBio). Biotinylated pHLA complexes in 1X kinetics buffer were loaded onto streptavidin sensors at concentrations that gave the optimal nm shift response (approximately 0.6 nm) for each Fab at the highest concentration used. The pHLA complexes were loaded for 300 seconds and the ligand-loaded tips were subsequently equilibrated in the kinetics buffer for 120 seconds. The ligand-loaded biosensors were then dipped for 200 seconds in the Fab solution titrated into 2-fold dilutions. Starting Fab concentrations ranged from 100 nM to 2 uM, then optimized based on the K_D values of the Fab. The dissociation step in the kinetics buffer was measured for 200 seconds. Data was analyzed using the ForteBio data analysis software using a 1:1 binding model.

[00616] FIG. 15A and 15B show BLI results for G2 target Fab clone G-2P1H11 and for G7 target Fab clone G7R4-B5-P2E9, respectively.

[00617] Results are shown in the Table below.

[00618] Table 7: Optimized Octet BLI affinity measurements of Fabs binding to their target peptide-HLA complex

Target	Fab clone	KD (M)	Kon (1/Ms)	Kdis (1/s)	Full R^2
G2	G2-P1B06	4.44E-08	1.06E+06	3.23E-02	0.991
G2	G2-P2A03	1.09E-07	3.32E+05	3.60E-02	0.998
G2	G2-P1B12	2.28E-08	3.66E+05	7.28E-03	0.980
G2	G2-P2A11	2.81E-08	6.33E+05	1.72E-02	0.992
G2	G2-P1H01	1.55E-08	9.52E+05	1.48E-02	0.984
G2	G2-P1H11	4.99E-08	5.81E+05	2.80E-02	0.994
G7	2-G7R4-P2C2	5.31E-07	1.04E+05	5.43E-02	0.986
G7	3-G7R4-P1A3	5.32E-07	1.97E+05	9.94E-02	0.988
G7	4-G7R4-B5-P2E9	1.18E-08	1.85E+05	2.12E-03	0.992

Example 9: positional scanning of G2 and G7 restricted peptide sequences.

[00619] Positional scanning of the G2 and G7 restricted peptides was carried out to determine the amino acid residues which act as contact points for selected Fab clones.

[00620] Briefly, positional scanning libraries of variant G2 and G7 restricted peptides were generated with amino acid substitutions at a single position in the G2 or G7 peptide sequence,

scanning across all positions. The amino acid substitutions at a given position were either alanine (conservative substitution), arginine (positively charged), or aspartate (negatively charged). A map of the amino acid substitutions for the positional scanning experiment is shown in FIG. 16. Asterisks denote lack of amino acid substitution.

[00621] Peptide-HLA complexes comprising the positional scanning library members and the HLA subtype allele were generated as described in Example 6. To determine whether the variant G2 and G7 peptides could complex with the desired HLA alleles, stability analyses of the resulting complexes were carried out using conditional ligand peptide exchange and ELISA as described in Example 6. Next, binding affinity of the positional variant-HLA complexes to the Fab clones was assessed by BLI, as described in Example 8.

[00622] A stability heat map for the G2 positional variant-HLAs is shown in FIG. 17A. [Red] denotes very low stability, [gray] denotes low stability, and [blue] denotes high stability. FIG. 17A shows that the C-terminal amino acid residue (position 9) and the second and third N-terminal residues (positions 2 and 3) were critical residues for anchoring the peptide to the HLA thereby stabilizing the ternary complex.

[00623] An affinity heat map for Fab clone G2-P1H11 is shown in FIG. 17B. The degree of binding indicated on the heatmap is based on the nm shift on the BLI biosensor due to Fab binding to the pHLA. As stated above, [Red] denotes no binding affinity (-0.02 to 0.18 nm shift), [gray] denotes weak binding affinity (0.19-0.25 nm shift), and [blue] denotes high binding affinity (0.26-0.32 nm shift). As expected, positional mutations which resulted in unstable complexes (at positions 2, 3, and 9) also resulted in no Fab binding. FIG. 17B shows that introduced substitutions at positions 3-8 resulted in failure of the Fab clone to bind the HLA-peptide complex. These results suggest that the majority of the residues which are not involved in binding the HLA molecule, and are residues that likely protrude from the HLA protein, are important for peptide-specificity of Fab clone G2-P1H11.

[00624] A stability heat map for the G7 positional variants is shown in FIG. 18A. Positions 1, 2, 6, and 9 appear to be important for stabilizing the HLA complex.

[00625] An affinity heat map for Fab clone G7R4-B5-P2E9 is shown in FIG. 18B. As stated above, [Red] denotes no binding affinity (-0.02 to 0.18 nm shift), [gray] denotes weak binding affinity (0.19-0.25 nm shift), and [blue] denotes high binding affinity (0.26-0.72 nm shift). indicating that positions 1-5 are important for peptide-specificity of the Fab clone.

Example 10: Generated antibodies successfully bind cells presenting the HLA-PEPTIDE target.

[00626] IgGs from scFv clones G2-P1H11 and G7-Ep were created as described in Example 7.

[00627] The ability of IgGs to bind to K562 cells pulsed with the target restricted peptide was assessed by flow cytometry.

[00628] *Retroviral production*

[00629] Phoenix-AMPHO cells (ATCC®, CRL-3213™) were plated at $5x10^5$ cells/well in a 6 well plate and incubated overnight at 37°C.

[00630] Phoenix-AMPHO cells were transfected with retroviral vectors containing expression cassettes for the desired HLA subtypes as follows. 10μg plasmid, 10μL Lipofectamine LTX PLUS (Fisher Scientific, cat # 15338100) reagent and 100μL Opti-MEM (Gibco™, cat # 31985062) were incubated at room temperature for 15 minutes. Simultaneously, 8μL Lipofectamine was incubated with 92μL Opti-MEM at room temperature for 15 minutes. These two reactions were combined and incubated again for 15 minutes at room temperature after which 800μL Opti-MEM was added. The culture media was aspirated from the Phoenix cells and they were washed with 5 mL pre-warmed Opti-MEM. The Opti-MEM was aspirated from the cells and the lipofectamine mixture was added. The cells were incubated for 3 hours at 37°C and 3 mL complete culture medium was added. The plate was then incubated overnight at 37°C. The media was replaced with Phoenix culture medium and the plate incubated an additional 2 days at 37°C.

[00631] The media was collected and filtered through a 45μm filter into a clean 6 well dish. 20μL Plus reagent was added to each virus suspension and incubated at room temperature for 15 minutes followed by the addition of 8μL/well of Lipofectamine and another 15 minute room temperature incubation.

[00632] *Generation of K562 cells expressing the HLA-PEPTIDE targets and cell binding with exemplary IgG clones*

[00633] K562 cells, which lack endogenous MHC, were transduced with retrovirus for introduction of the HLA subtype for G2 or G7, respectively. HLA-transduced K562 cells were pulsed the night before with 50 μM of target or negative control peptide (Genscript) in IDMEM containing 1% FBS in 6 well plates and incubated under standard tissue culture conditions. Cells were harvested, washed in PBS, and stained with eBioscience Fixable

Viability Dye eFluor 450 for 15 minutes at room temperature. Following another wash in PBS + 1% FBS, cells were resuspended with test IgGs (G2-P1H11 or G7R4-B5-P2E9) at varying concentrations. Cells were incubated with the antibodies for 1 hour at 4°C. After another wash, PE-congugated goat anti- human IgG secondary antibody (Jackson ImmunoResearch) was added at 1:200 for 30 minutes at 4°C. After washing in PBS + 1% FBS, cells were resuspended in PBS + 1% FBS and analyzed by flow cytometry. Flow cytometric analysis was performed on the Attune NxT Flow Cytometer (ThermoFisher) using the Attune NxT Software. Data was analyzed using FlowJo.

[00634] Results are shown in FIGS. 19 and 20. Both G2-P1H11 and G7R4-B5-P2E9 selectively bound HLA-transduced K562 cells pulsed with the target peptide, as compared to HLA-transduced cells pulsed with the negative control peptides.

[00635] *In vivo* proof-of-concept

[00636] Lead antibody or CAR-T constructs are evaluated in vivo to demonstrate directed tumor killing in humanized mouse tumor models. Lead antibody or CAR-T constructs are evaluated in xenograft tumor models engrafted with human tumors and PBMCs. Anti-tumor activity is measured and compared to control constructs to demonstrate target-specific tumor killing.

Example 11: scFv-pHLA structures by Hydrogen/Deuterium Exchange and mass spectrometry

Hydrogen/Deuterium Exchange

[00637] 20 μM of HLA-peptide was incubated with a 3-fold molar excess of scFv or Fab formatted ABPs for 20 min at room temperature (20-25°C) to generate complexes for the exchange experiments. For the Apo control, the HLA-peptide was incubated with an equal volume of 50 mM NaCl, 20 mM Tris pH 8.0, without the ABP. All subsequent reaction steps were performed at 4°C by an automated HDX PAL system controlled by Chronos 4.8.0 software (Leap Technologies, Morrisville, NC). Deuterium exchange was carried out in duplicate for time periods ranging from 30 s to 3 hrs. 5 μl of protein complexes were diluted 10-fold into H2O (for the 0 min. control time-point) or D2O for the indicated time-points prior to quenching in 0.8 M guanidine hydrochloride, 0.4% acetic acid (v/v), and 75 mM tris(2-carboxyethyl) phosphine for 3 min. ~ 50 pmol of quenched protein complexes were

transferred onto an immobilized Protein XIII/Pepsin column (NovaBioAssays, Woburn, MA) for integrated on-line protein digestion.

Liquid Chromatography, Mass Spectrometry, and HDX analysis

[00638] Chromatographic separation of peptides was carried out using an UltiMate 3000 Basic Manual UHPLC System (ThermoFisher Scientific, Waltham, MA), which contained a trap C18 column (5 μM particle size and 2.1 mm diameter) and an analytical C18 column (1.9 μM particle size and 1 mm diameter). Samples were desalted with 10% acetonitrile, 0.5% formic acid at a 40 μl/min flow rate for 2 min and peptides were eluted at a 40 μl/min flow rate with an increasing concentration of 95% acetonitrile, 0.5% formic acid. Mass spectrometry was performed with an Orbitrap Fusion Lumos mass spectrometer (ThermoFisher, Waltham, MA) with the ESI source set at a positive ion voltage of 3700 V. Prior to performing hydrogen-deuterium exchange experiments, peptide fragments of each HLA-peptide complex were analyzed by data-dependent LC/MS/MS and the data searched using PEAKS Studio (Bioinformatics Solutions Inc., Waterloo, ON, Canada) with a peptide precursor mass tolerance of 10 ppm and fragment ion mass tolerance of 0.1 Da. The sequences of the HLA, β2M, and the peptide were searched, and false detection rates identified using a decoy-database strategy. Peptides from the hydrogen-deuterium experiments were detected by LC/MS and analyzed by HDX Workbench (Omics Informatics, Honolulu, HI) with a retention time window size of 0.22 min and a 7.0 ppm error. In the deuterium (D) exchange samples the peptide was then identified in the elution time window and the difference in mass was determined. Mass increases by 1 for each D exchanged in the peptide backbone since D has a molecular weight of 1 more than H. The difference in mass and the intensity of the isotopic ions produced values of %D for each peptide. Differences in deuterium uptake were mapped to relevant protein crystallographic structures using Pymol (Schrödinger, Cambridge, MA). The decrease in D exchange between the Apo control and ABP was calculated and plotted by amino acid. Statistical analysis and graphical representations were performed using GraphPad Prism 7.0 (La Jolla, CA).

[00639] An example of the data from scFv G2-P1G07 plotted on a crystal structure PDB 5bs0 is shown in FIG. 21. The crystal structure can be found at URL https://www.rcsb.org/structure/5bs0 (Raman et al). Areas not covered with MS data are shown in black and those with the greatest decrease in D exchange (indicating a binding site for the ABP) is circled. For clarity, only the binding groove and helices are shown.

[00640] An exemplary heatmap for scFv clone G2-P1G07 visualized in its entirety using a consolidated perturbation view is shown in FIG. 22.

[00641] To better compare the data across the ABPs tested for a given HLA-PEPTIDE target, data for each ABP was exported, and a heat map was generated in Excel. Resulting heat maps are shown in FIG. 23 showing a heat map across the α1 helix (top) and across the α2 helix (bottom). FIG. 24 shows a heat map for all ABPs tested for A*0101_NTDNNLAVY, across restricted peptide residues 1-9. These results indicate that residues 6-9 of the restricted peptide, and HLA residues 157-160 are important contact points of the A*0101_NTDNNLAVY HLA-PEPTIDE target complex for binding to its specific ABP. All clone entries in the HDX heat maps are scFv formats unless otherwise noted.

Example 12: Isolation of TCRs that specifially bind HLA-PEPTIDE targets

[00642] FIG. 25 depicts an experimental workflow by which TCRs which specifically bind HLA-PEPTIDE targets were isolated. Briefly, naïve CD8+ T cells that bind to the HLA-PEPTIDE target were isolated by flow cytometry and polyclonally expanded. Following expansion, specificity of cells for HLA-PEPTIDE target complex was tested by flow cytometry. If a large fraction (>75%) of an expanded population was specific for the HLA-PEPTIDE target, the population as a whole was sequenced as a whole to identify TCRs. Alternatively, cells that specifically bound the HLA-PEPTIDE target were resorted, and only cells isolated after resort were sequenced. TCR sequences were cloned into expression vectors and introduced into recipient T cells as recombinant TCRs. Expression of the evaluated TCR and binding of cognate HLA-PEPTIDE target complex by the TCR-recombinant T cells was assessed.

Identified HLA-PEPTIDE targets were readily recognized by CD8+ T cells

[00643] Peripheral Blood Mononuclear Cells (PBMCs) from healthy donors were magnetically enriched for naïve CD8+ T cells as follows. PBMCs were obtained by processing leukapheresis samples from healthy donors. Frozen PBMCs were thawed and incubated with cocktail of biotinylated CD45RO, CD14, CD15, CD16, CD19, CD25, CD34, CD36, CD57, CD123, anti-HLA-DR, CD235a (Glycophorin A), CD244, and CD4 antibodies and were subsequently magnetically labeled with anti-biotin microbeads for removal from PBMC population. Enriched naïve CD8 T cells were labelled with tetramers comprising of target peptide and appropriate HLA molecule, stained with live/dead and lineage markers and

sorted by flow cytometry according to the gating procedure depicted in FIG. 26. Cells that bound the HLA-PEPTIDE tetramers were isolated. Following polyclonal expansion, specificity of expanded CD8+ T cells was reassessed by labeling with the HLA-PEPTIDE or no tetramer control. Flow cytometry results for exemplary HLA-PEPTIDE targets B*44:02_GEMSSNSTAL and A*01:01_EVDPIGHLY are shown in FIG 27. Flow cytometry results for the HLA-PETPIDE target A*03:01_GVHGGILNK is shown in FIG. 28.

[00644] The number of isolated CD8+ T cells per HLA-PEPTIDE target per donor and distribution of isolated CD8+ T cells frequency per HLA-PEPTIDE target across all donors tested is shown in Figure 29: 29A (number of isolated CD8+ T cells) and 29B (frequency). Total number of isolated naïve CD8+ T cells per target ranged from 23-4181 antigen specific cells, which is in line with precursor frequencies of T cells specific for known immunogenic viral antigens. These cells present the source of natural TCRs for sequencing and further characterization.

[00645] The number of isolated target-specific T cells per target summarized across all tested donors is shown in Table 8.

[00646] Table 8: number of isolated target-specific T cells per target summarized across all donors

Target	Gene	Cumulative Number of TCR Source Cells Per Target
EVDPIGHLY (HLA-A*0101)	MAGEA3	5242
EVDPIGHVY (HLA-A*0101	MAGEA6	1296
GEMSSNSTAL (HLA-B*4402)	CT 83	48
GVHGGILNK (HLA-A*0301)	PFN3	219
GVYDGEEHSV (HLA-A*0201)	MAGEB2	17
LLASSILCA (HLA-A*0201)	CT 83	1665
LVIDTVTEV (HLA-A*0201)	SPERT	16
NTDNNLAVY (HLA-A*0101)	CT 83	575

[00647] These data demonstrate that identified HLA-PEPTIDE targets are biologically relevant, as natural CD8+ T cells exist in HLA matched human blood which bind/recognize target peptides in the context of predicted associated MHC molecule.

CD8+ T cells yielded a diverse repertoire of unique TCRs which bound the HLA-PEPTIDE targets

[00648] *Criteria for sequencing of T-cells*

[00649] If a large fraction (>75%) of an expanded population was specific for the HLA-PEPTIDE target, the population as a whole was sequenced as a whole to identify TCRs. Then, selected TCR sequences from the population were cloned into expression vectors and transfected into recipient T-cells for confirmation of specificity. Alternatively, cells that specifically bound the HLA-PEPTIDE target were resorted, and only cells isolated after resort were sequenced.

[00650] *Sequencing protocol*

[00651] T cells isolated and expanded as described in Figure 26 were sequenced using 10x Genomics single cell resolution paired immune TCR profiling approach. Specifically, two-to-eight thousand live T cells were partitioned into single cell emulsions for subsequent single cell cDNA generation and full-length TCR profiling (5' UTR through constant region – ensuring alpha and beta pairing). One approach utilizes a molecularly barcoded template switching oligo at the 5'end of the transcript, a second approach utilizes a molecularly barcoded constant region oligo at the 3' end, and a third approach couples an RNA polymerase promoter to either the 5' or 3' end of a TCR. All of these approaches enable the identification and deconvolution of alpha and beta TCR pairs at the single-cell level. The resulting barcoded cDNA transcripts underwent an optimized enzymatic and library construction workflow to reduce bias and ensure accurate representation of clonotypes within the pool of cells. Libraries were sequenced on Illumina's MiSeq or HiSeq4000 instruments (paired-end 150 cycles) for a target sequencing depth of about five to fifty thousand reads per cell.

[00652] Sequencing reads were processed through the 10X provided software Cell Ranger. Sequencing reads were tagged with a Chromium cellular barcodes and UMIs, which were used to assemble the V(D)J transcripts cell by cell. The assembled contigs for each cell were then annotated by mapping the assembled contigs to V(D)J reference sequences from Ensembl version 87 (http://www.ensembl.org/).

[00653] Clonotypes were defined as alpha, beta chain pairs of unique CDR3 amino acid sequences. Clonotypes were filtered for single alpha and single beta chain pairs present at frequency above 2 cells to yield the final list of clonotypes per target peptide in a specific donor. FIG. 30A depicts the number of unique TCR clonotypes per HLA-PEPTIDE target for each tested donor. FIG. 30B depicts the total number of unique clonotypes per HLA-PEPTIDE target, summed across all donors tested.

[00654] *TCR sequences of unique clonotypes from resorted cells*

[00655] Annotated variable, diversity, joining, and constant regions of TCR clonotypes specific for A*0101_EVDPHIGHLY, from resorted cells, are shown below in Table 9.

Table 9: annotated TCR sequences of unique TCRs specific for A*0101_EVDPHIGHLY, sequenced from resorted cells

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR101	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR102	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR103	EVDPIGHLY	A0101	TRAV21	TRAJ4	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR104	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR105	EVDPIGHLY	A0101	TRAV1-1	TRAJ4	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR106	EVDPIGHLY	A0101	TRAV12-1	TRAJ17	TRAC	TRBV6-1	TRBD2	TRBJ2-1	TRBC2
TCR107	EVDPIGHLY	A0101	TRAV4	TRAJ47	TRAC	TRBV20-1	TRBD2	TRBJ2-3	TRBC2
TCR108	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV5-4	None	TRBJ2-1	TRBC1
TCR109	EVDPIGHLY	A0101	TRAV12-1	TRAJ11	TRAC	TRBV11-3	TRBD1	TRBJ1-1	TRBC1
TCR110	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV5-1	TRBD1	TRBJ1-1	TRBC1
TCR111	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-1	TRBD1	TRBJ2-3	TRBC2
TCR112	EVDPIGHLY	A0101	TRAV34	TRAJ40	TRAC	TRBV9	TRBD2	TRBJ2-7	TRBC2
TCR113	EVDPIGHLY	A0101	TRAV29DV5	TRAJ29	TRAC	TRBV7-9	TRBD1	TRBJ2-3	TRBC2
TCR114	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR115	EVDPIGHLY	A0101	TRAV4	TRAJ47	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR116	EVDPIGHLY	A0101	TRAV21	TRAJ54	TRAC	TRBV5-1	TRBD1	TRBJ2-1	TRBC2
TCR117	EVDPIGHLY	A0101	TRAV21	TRAJ42	TRAC	TRBV7-9	TRBD1	TRBJ2-7	TRBC2
TCR118	EVDPIGHLY	A0101	TRAV21	TRAJ4	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR119	EVDPIGHLY	A0101	TRAV21	TRAJ40	TRAC	TRBV29-1	None	TRBJ2-2	TRBC2
TCR120	EVDPIGHLY	A0101	TRAV29DV5	TRAJ49	None	TRBV10-2	TRBD1	TRBJ2-7	TRBC2
TCR121	EVDPIGHLY	A0101	TRAV21	TRAJ40	TRAC	TRBV27	TRBD2	TRBJ2-2	TRBC2
TCR122	EVDPIGHLY	A0101	TRAV21	TRAJ11	TRAC	TRBV5-4	None	TRBJ2-2	TRBC1
TCR123	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV20-1	TRBD2	TRBJ2-3	TRBC2
TCR124	EVDPIGHLY	A0101	TRAV26-2	TRAJ49	TRAC	TRBV19	None	TRBJ1-5	TRBC1
TCR125	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV6-1	TRBD2	TRBJ2-1	TRBC2
TCR126	EVDPIGHLY	A0101	TRAV17	TRAJ34	TRAC	TRBV11-1	TRBD1	TRBJ1-2	TRBC1
TCR127	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR128	EVDPIGHLY	A0101	TRAV21	TRAJ26	TRAC	TRBV5-6	TRBD1	TRBJ2-7	TRBC2
TCR129	EVDPIGHLY	A0101	TRAV29DV5	TRAJ4	TRAC	TRBV27	TRBD1	TRBJ1-5	TRBC1
TCR130	EVDPIGHLY	A0101	TRAV4	TRAJ47	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR131	EVDPIGHLY	A0101	TRAV13-1	TRAJ49	TRAC	TRBV27	TRBD1	TRBJ2-7	TRBC2
TCR132	EVDPIGHLY	A0101	TRAV12-1	TRAJ10	TRAC	TRBV25-1	TRBD1	TRBJ2-7	TRBC2
TCR133	EVDPIGHLY	A0101	TRAV29DV5	TRAJ39	TRAC	TRBV7-9	None	TRBJ2-7	TRBC2
TCR134	EVDPIGHLY	A0101	TRAV21	TRAJ47	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR135	EVDPIGHLY	A0101	TRAV39	TRAJ41	TRAC	TRBV13	None	TRBJ1-4	TRBC1
TCR136	EVDPIGHLY	A0101	TRAV17	TRAJ53	TRAC	TRBV29-1	TRBD1	TRBJ2-1	TRBC2
TCR137	EVDPIGHLY	A0101	TRAV26-1	TRAJ42	TRAC	TRBV19	TRBD1	TRBJ2-3	TRBC2
TCR138	EVDPIGHLY	A0101	TRAV8-6	TRAJ50	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR139	EVDPIGHLY	A0101	TRAV19	TRAJ10	TRAC	TRBV7-9	None	TRBJ2-7	TRBC2
TCR140	EVDPIGHLY	A0101	TRAV8-4	TRAJ42	TRAC	TRBV3-1	TRBD2	TRBJ2-1	TRBC2
TCR141	EVDPIGHLY	A0101	TRAV12-1	TRAJ47	TRAC	TRBV5-8	TRBD1	TRBJ1-1	TRBC1
TCR142	EVDPIGHLY	A0101	TRAV29DV5	TRAJ42	TRAC	TRBV10-3	None	TRBJ2-7	TRBC2
TCR143	EVDPIGHLY	A0101	TRAV13-2	TRAJ20	TRAC	TRBV27	TRBD2	TRBJ1-1	TRBC1
TCR144	EVDPIGHLY	A0101	TRAV10	TRAJ9	TRAC	TRBV3-1	TRBD1	TRBJ1-3	TRBC1
TCR145	EVDPIGHLY	A0101	TRAV19	TRAJ27	TRAC	TRBV27	TRBD1	TRBJ2-7	TRBC2
TCR146	EVDPIGHLY	A0101	TRAV9-2	TRAJ20	TRAC	TRBV12-4	TRBD1	TRBJ2-1	TRBC2
TCR147	EVDPIGHLY	A0101	TRAV12-2	TRAJ20	TRAC	TRBV7-6	TRBD2	TRBJ2-1	TRBC2
TCR148	EVDPIGHLY	A0101	TRAV12-1	TRAJ17	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR149	EVDPIGHLY	A0101	TRAV30	TRAJ58	TRAC	TRBV19	None	TRBJ2-7	TRBC2
TCR150	EVDPIGHLY	A0101	TRAV8-1	TRAJ43	TRAC	TRBV7-8	TRBD2	TRBJ2-1	TRBC2

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR151	EVDPIGHLY	A0101	TRAV13-1	TRAJ9	TRAC	TRBV9	TRBD1	TRBJ2-5	TRBC2
TCR152	EVDPIGHLY	A0101	TRAV12-1	TRAJ29	TRAC	TRBV6-1	TRBD1	TRBJ1-2	TRBC1
TCR153	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV20-1	TRBD2	TRBJ2-3	TRBC2
TCR154	EVDPIGHLY	A0101	TRAV21	TRAJ43	TRAC	TRBV7-3	None	TRBJ2-2	TRBC2
TCR155	EVDPIGHLY	A0101	TRAV21	TRAJ4	TRAC	TRBV5-1	TRBD1	TRBJ2-1	TRBC2
TCR156	EVDPIGHLY	A0101	TRAV26-2	TRAJ32	TRAC	TRBV24-1	TRBD1	TRBJ2-2	TRBC2
TCR157	EVDPIGHLY	A0101	TRAV21	TRAJ4	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR158	EVDPIGHLY	A0101	TRAV19	TRAJ15	TRAC	TRBV7-8	TRBD1	TRBJ2-7	TRBC2
TCR159	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV6-1	TRBD2	TRBJ2-1	TRBC2
TCR160	EVDPIGHLY	A0101	TRAV12-2	TRAJ13	TRAC	TRBV25-1	None	TRBJ2-7	TRBC2
TCR161	EVDPIGHLY	A0101	TRAV29DV5	TRAJ54	TRAC	TRBV7-8	None	TRBJ2-1	TRBC2
TCR162	EVDPIGHLY	A0101	TRAV19	TRAJ53	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR163	EVDPIGHLY	A0101	TRAV23DV6	TRAJ36	TRAC	TRBV9	TRBD2	TRBJ1-2	TRBC1
TCR164	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR165	EVDPIGHLY	A0101	TRAV8-6	TRAJ32	TRAC	TRBV19	TRBD1	TRBJ1-1	TRBC1
TCR166	EVDPIGHLY	A0101	TRAV1-1	TRAJ13	TRAC	TRBV14	TRBD1	TRBJ2-1	TRBC2
TCR167	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR168	EVDPIGHLY	A0101	TRAV21	TRAJ44	TRAC	TRBV9	None	TRBJ2-7	TRBC2
TCR169	EVDPIGHLY	A0101	TRAV29DV5	TRAJ3	TRAC	TRBV3-1	TRBD2	TRBJ2-5	TRBC2
TCR170	EVDPIGHLY	A0101	TRAV17	TRAJ39	TRAC	TRBV7-2	None	TRBJ1-2	TRBC1
TCR171	EVDPIGHLY	A0101	TRAV26-2	TRAJ12	TRAC	TRBV7-9	TRBD1	TRBJ1-2	TRBC1
TCR172	EVDPIGHLY	A0101	TRAV29DV5	TRAJ22	TRAC	TRBV11-3	TRBD1	TRBJ2-7	TRBC2
TCR173	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV12-4	TRBD2	TRBJ2-3	TRBC2
TCR174	EVDPIGHLY	A0101	TRAV12-3	TRAJ3	TRAC	TRBV27	TRBD1	TRBJ2-7	TRBC2
TCR175	EVDPIGHLY	A0101	TRAV27	TRAJ33	TRAC	TRBV6-5	TRBD2	TRBJ2-2	TRBC2
TCR176	EVDPIGHLY	A0101	TRAV13-1	TRAJ22	TRAC	TRBV12-4	TRBD1	TRBJ2-3	TRBC2
TCR177	EVDPIGHLY	A0101	TRAV26-1	TRAJ34	TRAC	TRBV27	None	TRBJ1-2	TRBC1
TCR178	EVDPIGHLY	A0101	TRAV10	TRAJ4	TRAC	TRBV7-9	TRBD1	TRBJ2-4	TRBC2
TCR179	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR180	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR181	EVDPIGHLY	A0101	TRAV21	TRAJ26	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR182	EVDPIGHLY	A0101	TRAV12-2	TRAJ20	TRAC	TRBV18	TRBD1	TRBJ2-7	TRBC2
TCR183	EVDPIGHLY	A0101	TRAV9-2	TRAJ23	TRAC	TRBV11-3	TRBD1	TRBJ1-1	TRBC1
TCR184	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV6-1	TRBD2	TRBJ2-1	TRBC2
TCR185	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV7-8	TRBD1	TRBJ2-2	TRBC2
TCR186	EVDPIGHLY	A0101	TRAV9-2	TRAJ23	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR187	EVDPIGHLY	A0101	TRAV24	TRAJ45	TRAC	TRBV5-4	TRBD1	TRBJ1-4	TRBC1
TCR188	EVDPIGHLY	A0101	TRAV13-1	TRAJ3	TRAC	TRBV27	TRBD2	TRBJ1-1	TRBC1
TCR189	EVDPIGHLY	A0101	TRAV20	TRAJ20	TRAC	TRBV7-2	TRBD1	TRBJ2-7	TRBC2
TCR190	EVDPIGHLY	A0101	TRAV8-4	TRAJ42	TRAC	TRBV9	TRBD1	TRBJ2-1	TRBC2
TCR191	EVDPIGHLY	A0101	TRAV1-2	TRAJ31	TRAC	TRBV7-9	TRBD1	TRBJ1-5	TRBC1
TCR192	EVDPIGHLY	A0101	TRAV12-1	TRAJ13	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR193	EVDPIGHLY	A0101	TRAV12-1	TRAJ4	TRAC	TRBV28	TRBD2	TRBJ2-7	TRBC2
TCR194	EVDPIGHLY	A0101	TRAV21	TRAJ4	TRAC	TRBV27	TRBD2	TRBJ2-2	TRBC2
TCR195	EVDPIGHLY	A0101	TRAV3	TRAJ9	TRAC	TRBV7-9	TRBD1	TRBJ2-7	TRBC2
TCR196	EVDPIGHLY	A0101	TRAV26-1	TRAJ42	TRAC	TRBV19	None	TRBJ2-2	TRBC2
TCR197	EVDPIGHLY	A0101	TRAV21	TRAJ47	TRAC	TRBV19	None	TRBJ1-1	TRBC1
TCR198	EVDPIGHLY	A0101	TRAV26-1	TRAJ34	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR199	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR200	EVDPIGHLY	A0101	TRAV12-1	TRAJ11	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR201	EVDPIGHLY	A0101	TRAV17	TRAJ34	TRAC	TRBV6-1	TRBD2	TRBJ2-1	TRBC2
TCR202	EVDPIGHLY	A0101	TRAV13-2	TRAJ47	TRAC	TRBV19	TRBD2	TRBJ2-1	TRBC2
TCR203	EVDPIGHLY	A0101	TRAV29DV5	TRAJ28	TRAC	TRBV27	TRBD2	TRBJ2-4	TRBC2
TCR204	EVDPIGHLY	A0101	TRAV13-2	TRAJ17	TRAC	TRBV27	TRBD2	TRBJ1-5	TRBC1
TCR205	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ57	TRAC	TRBV5-4	TRBD1	TRBJ1-2	TRBC1
TCR206	EVDPIGHLY	A0101	TRAV17	TRAJ32	TRAC	TRBV7-8	TRBD2	TRBJ2-1	TRBC2
TCR207	EVDPIGHLY	A0101	TRAV21	TRAJ39	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR208	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV7-9	TRBD1	TRBJ2-3	TRBC2
TCR209	EVDPIGHLY	A0101	TRAV1-1	TRAJ4	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR210	EVDPIGHLY	A0101	TRAV12-1	TRAJ9	TRAC	TRBV2	TRBD1	TRBJ2-7	TRBC2
TCR211	EVDPIGHLY	A0101	TRAV19	TRAJ32	TRAC	TRBV9	TRBD1	TRBJ1-2	TRBC1
TCR212	EVDPIGHLY	A0101	TRAV8-3	TRAJ6	TRAC	TRBV9	TRBD2	TRBJ2-1	TRBC2
TCR213	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV7-9	None	TRBJ2-7	TRBC2
TCR214	EVDPIGHLY	A0101	TRAV5	TRAJ37	TRAC	TRBV5-6	TRBD2	TRBJ1-1	TRBC1
TCR215	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR216	EVDPIGHLY	A0101	TRAV29DV5	TRAJ3	TRAC	TRBV20-1	TRBD1	TRBJ2-7	TRBC2
TCR217	EVDPIGHLY	A0101	TRAV1-1	TRAJ4	TRAC	TRBV20-1	TRBD2	TRBJ1-2	TRBC1
TCR218	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV10-3	None	TRBJ1-1	TRBC1
TCR219	EVDPIGHLY	A0101	TRAV19	TRAJ23	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR220	EVDPIGHLY	A0101	TRAV12-2	TRAJ20	TRAC	TRBV11-2	TRBD2	TRBJ2-2	TRBC2
TCR221	EVDPIGHLY	A0101	TRAV1-2	TRAJ15	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR222	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV5-4	None	TRBJ1-6	TRBC1
TCR223	EVDPIGHLY	A0101	TRAV8-6	TRAJ12	TRAC	TRBV7-9	TRBD1	TRBJ2-2	TRBC2
TCR224	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV11-2	TRBD2	TRBJ1-2	TRBC1
TCR225	EVDPIGHLY	A0101	TRAV21	TRAJ41	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR226	EVDPIGHLY	A0101	TRAV25	TRAJ28	TRAC	TRBV7-2	TRBD2	TRBJ2-6	TRBC2
TCR227	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV10-3	TRBD1	TRBJ1-3	TRBC1

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR228	EVDPIGHLY	A0101	TRAV21	TRAJ49	TRAC	TRBV5-1	TRBD1	TRBJ2-5	TRBC2
TCR229	EVDPIGHLY	A0101	TRAV1-1	TRAJ34	TRAC	TRBV6-6	None	TRBJ1-5	TRBC1
TCR230	EVDPIGHLY	A0101	TRAV24	TRAJ6	TRAC	TRBV7-2	TRBD1	TRBJ2-1	TRBC2
TCR231	EVDPIGHLY	A0101	TRAV1-1	TRAJ15	TRAC	TRBV6-6	None	TRBJ1-5	TRBC1
TCR232	EVDPIGHLY	A0101	TRAV21	TRAJ15	TRAC	TRBV29-1	None	TRBJ1-1	TRBC1
TCR233	EVDPIGHLY	A0101	TRAV21	TRAJ43	TRAC	TRBV12-4	None	TRBJ1-5	TRBC1
TCR234	EVDPIGHLY	A0101	TRAV21	TRAJ30	TRAC	TRBV9	TRBD1	TRBJ1-4	TRBC1
TCR235	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV5-1	TRBD1	TRBJ2-7	TRBC2
TCR236	EVDPIGHLY	A0101	TRAV26-1	TRAJ45	TRAC	TRBV19	TRBD2	TRBJ2-1	TRBC2
TCR237	EVDPIGHLY	A0101	TRAV21	TRAJ43	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR238	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR239	EVDPIGHLY	A0101	TRAV29DV5	TRAJ28	TRAC	TRBV4-1	TRBD1	TRBJ1-4	TRBC1
TCR240	EVDPIGHLY	A0101	TRAV26-2	TRAJ44	TRAC	TRBV27	None	TRBJ2-1	TRBC2
TCR241	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV9	TRBD1	TRBJ1-5	TRBC1
TCR242	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV9	TRBD1	TRBJ1-2	TRBC1
TCR243	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR244	EVDPIGHLY	A0101	TRAV8-3	TRAJ15	TRAC	TRBV4-1	None	TRBJ2-1	TRBC2
TCR245	EVDPIGHLY	A0101	TRAV21	TRAJ43	TRAC	TRBV24-1	TRBD1	TRBJ2-3	TRBC2
TCR246	EVDPIGHLY	A0101	TRAV29DV5	TRAJ40	TRAC	TRBV7-9	TRBD1	TRBJ1-6	TRBC1
TCR247	EVDPIGHLY	A0101	TRAV30	TRAJ32	TRAC	TRBV28	TRBD1	TRBJ1-1	TRBC1
TCR248	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ26	TRAC	TRBV7-9	TRBD2	TRBJ2-5	TRBC2
TCR249	EVDPIGHLY	A0101	TRAV12-1	TRAJ6	TRAC	TRBV20-1	TRBD1	TRBJ1-3	TRBC1
TCR250	EVDPIGHLY	A0101	TRAV21	TRAJ47	TRAC	TRBV5-1	None	TRBJ1-1	TRBC1
TCR251	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ45	TRAC	TRBV29-1	TRBD1	TRBJ2-7	TRBC2
TCR252	EVDPIGHLY	A0101	TRAV21	TRAJ15	TRAC	TRBV7-2	None	TRBJ1-1	TRBC1
TCR253	EVDPIGHLY	A0101	TRAV12-2	TRAJ29	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR254	EVDPIGHLY	A0101	TRAV3	TRAJ6	TRAC	TRBV28	TRBD1	TRBJ2-7	TRBC2
TCR255	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV10-3	TRBD1	TRBJ1-3	TRBC1
TCR256	EVDPIGHLY	A0101	TRAV1-2	TRAJ15	TRAC	TRBV7-9	TRBD1	TRBJ2-2	TRBC2
TCR257	EVDPIGHLY	A0101	TRAV8-6	TRAJ40	TRAC	TRBV15	None	TRBJ2-5	TRBC2
TCR258	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ57	TRAC	TRBV13	TRBD1	TRBJ1-4	TRBC1
TCR259	EVDPIGHLY	A0101	TRAV8-6	TRAJ10	TRAC	TRBV7-9	None	TRBJ1-1	TRBC1
TCR260	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV5-4	TRBD1	TRBJ1-5	TRBC1
TCR261	EVDPIGHLY	A0101	TRAV13-1	TRAJ28	TRAC	TRBV7-8	TRBD1	TRBJ1-5	TRBC1
TCR262	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR263	EVDPIGHLY	A0101	TRAV1-2	TRAJ15	TRAC	TRBV2	TRBD2	TRBJ2-1	TRBC2
TCR264	EVDPIGHLY	A0101	TRAV35	TRAJ26	TRAC	TRBV27	TRBD1	TRBJ1-1	TRBC1
TCR265	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ43	TRAC	TRBV5-1	TRBD2	TRBJ2-5	TRBC2
TCR266	EVDPIGHLY	A0101	TRAV5	TRAJ32	TRAC	TRBV19	TRBD2	TRBJ2-7	TRBC2
TCR267	EVDPIGHLY	A0101	TRAV13-1	TRAJ21	TRAC	TRBV5-1	TRBD2	TRBJ2-7	TRBC2
TCR268	EVDPIGHLY	A0101	TRAV12-2	TRAJ45	TRAC	TRBV12-4	TRBD1	TRBJ2-1	TRBC2
TCR269	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV12-5	None	TRBJ2-2	TRBC2
TCR270	EVDPIGHLY	A0101	TRAV24	TRAJ52	TRAC	TRBV27	None	TRBJ2-1	TRBC2
TCR271	EVDPIGHLY	A0101	TRAV21	TRAJ52	TRAC	TRBV19	TRBD1	TRBJ1-1	TRBC1
TCR272	EVDPIGHLY	A0101	TRAV36DV7	TRAJ44	TRAC	TRBV7-9	TRBD1	TRBJ2-2	TRBC2
TCR273	EVDPIGHLY	A0101	TRAV3	TRAJ29	TRAC	TRBV11-2	TRBD1	TRBJ2-5	TRBC2
TCR274	EVDPIGHLY	A0101	TRAV1-1	TRAJ15	TRAC	TRBV13	TRBD1	TRBJ1-2	TRBC1
TCR275	EVDPIGHLY	A0101	TRAV29DV5	TRAJ52	TRAC	TRBV11-3	TRBD1	TRBJ2-3	TRBC2
TCR276	EVDPIGHLY	A0101	TRAV12-1	TRAJ6	TRAC	TRBV19	TRBD1	TRBJ1-1	TRBC1
TCR277	EVDPIGHLY	A0101	TRAV19	TRAJ13	TRAC	TRBV27	TRBD2	TRBJ2-7	TRBC2
TCR278	EVDPIGHLY	A0101	TRAV17	TRAJ43	TRAC	TRBV12-3	None	TRBJ1-4	TRBC1
TCR279	EVDPIGHLY	A0101	TRAV12-3	TRAJ20	TRAC	TRBV12-4	None	TRBJ2-1	TRBC2
TCR280	EVDPIGHLY	A0101	TRAV21	TRAJ52	TRAC	TRBV4-1	TRBD2	TRBJ2-7	TRBC2
TCR281	EVDPIGHLY	A0101	TRAV21	TRAJ23	TRAC	TRBV19	TRBD1	TRBJ2-7	TRBC2
TCR282	EVDPIGHLY	A0101	TRAV1-1	TRAJ30	TRAC	TRBV13	TRBD1	TRBJ1-2	TRBC1
TCR283	EVDPIGHLY	A0101	TRAV12-2	TRAJ43	TRAC	TRBV12-4	TRBD2	TRBJ2-7	TRBC2
TCR284	EVDPIGHLY	A0101	TRAV24	TRAJ10	TRAC	TRBV5-1	TRBD1	TRBJ1-2	TRBC1
TCR285	EVDPIGHLY	A0101	TRAV5	TRAJ9	TRAC	TRBV4-1	TRBD2	TRBJ1-1	TRBC1
TCR286	EVDPIGHLY	A0101	TRAV21	TRAJ40	TRAC	TRBV7-8	None	TRBJ1-1	TRBC1
TCR287	EVDPIGHLY	A0101	TRAV13-1	TRAJ45	TRAC	TRBV9	TRBD1	TRBJ1-6	TRBC1
TCR288	EVDPIGHLY	A0101	TRAV12-1	TRAJ26	TRAC	TRBV4-1	TRBD1	TRBJ2-7	TRBC2
TCR289	EVDPIGHLY	A0101	TRAV26-2	TRAJ45	TRAC	TRBV19	None	TRBJ1-2	TRBC1
TCR290	EVDPIGHLY	A0101	TRAV22	TRAJ23	TRAC	TRBV5-4	TRBD1	TRBJ1-1	TRBC1
TCR291	EVDPIGHLY	A0101	TRAV19	TRAJ42	TRAC	TRBV28	None	TRBJ2-7	TRBC2
TCR292	EVDPIGHLY	A0101	TRAV17	TRAJ52	TRAC	TRBV7-8	TRBD1	TRBJ1-2	TRBC1
TCR293	EVDPIGHLY	A0101	TRAV12-1	TRAJ39	TRAC	TRBV3-1	TRBD1	TRBJ2-3	TRBC2
TCR294	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV5-1	TRBD1	TRBJ2-7	TRBC2
TCR295	EVDPIGHLY	A0101	TRAV1-1	TRAJ5	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR296	EVDPIGHLY	A0101	TRAV23DV6	TRAJ13	TRAC	TRBV6-5	TRBD1	TRBJ2-1	TRBC2
TCR297	EVDPIGHLY	A0101	TRAV8-6	TRAJ12	TRAC	TRBV24-1	TRBD2	TRBJ2-1	TRBC2
TCR298	EVDPIGHLY	A0101	TRAV1-2	TRAJ28	TRAC	TRBV27	None	TRBJ2-3	TRBC2
TCR299	EVDPIGHLY	A0101	TRAV29DV5	TRAJ34	TRAC	TRBV4-1	TRBD2	TRBJ2-3	TRBC2
TCR300	EVDPIGHLY	A0101	TRAV12-1	TRAJ21	TRAC	TRBV28	TRBD1	TRBJ1-5	TRBC1
TCR301	EVDPIGHLY	A0101	TRAV9-2	TRAJ29	TRAC	TRBV5-8	TRBD2	TRBJ1-1	TRBC1
TCR302	EVDPIGHLY	A0101	TRAV27	TRAJ40	TRAC	TRBV7-6	None	TRBJ2-7	TRBC2
TCR303	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV7-8	TRBD1	TRBJ1-2	TRBC1
TCR304	EVDPIGHLY	A0101	TRAV21	TRAJ30	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR305	EVDPIGHLY	A0101	TRAV19	TRAJ30	TRAC	TRBV20-1	None	TRBJ2-1	TRBC2
TCR306	EVDPIGHLY	A0101	TRAV1-1	TRAJ26	TRAC	TRBV12-5	TRBD2	TRBJ2-1	TRBC2
TCR307	EVDPIGHLY	A0101	TRAV1-2	TRAJ33	TRAC	TRBV9	TRBD2	TRBJ2-3	TRBC2
TCR308	EVDPIGHLY	A0101	TRAV26-1	TRAJ50	TRAC	TRBV27	TRBD1	TRBJ2-3	TRBC2
TCR309	EVDPIGHLY	A0101	TRAV40	TRAJ41	TRAC	TRBV6-5	TRBD2	TRBJ1-2	TRBC1
TCR310	EVDPIGHLY	A0101	TRAV12-2	TRAJ31	TRAC	TRBV7-9	TRBD1	TRBJ1-5	TRBC1
TCR311	EVDPIGHLY	A0101	TRAV5	TRAJ43	TRAC	TRBV5-1	TRBD1	TRBJ2-3	TRBC2
TCR312	EVDPIGHLY	A0101	TRAV24	TRAJ52	TRAC	TRBV5-1	None	TRBJ1-1	TRBC1
TCR313	EVDPIGHLY	A0101	TRAV1-2	TRAJ11	TRAC	TRBV7-6	TRBD1	TRBJ1-3	TRBC1
TCR314	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-1	TRBD1	TRBJ2-7	TRBC2
TCR315	EVDPIGHLY	A0101	TRAV21	TRAJ39	TRAC	TRBV10-3	None	TRBJ2-1	TRBC2
TCR316	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV14	TRBD1	TRBJ1-2	TRBC1
TCR317	EVDPIGHLY	A0101	TRAV29DV5	TRAJ48	TRAC	TRBV7-9	TRBD1	TRBJ1-2	TRBC1
TCR318	EVDPIGHLY	A0101	TRAV13-1	TRAJ22	TRAC	TRBV29-1	None	TRBJ1-1	TRBC1
TCR319	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV10-3	None	TRBJ2-1	TRBC2
TCR320	EVDPIGHLY	A0101	TRAV39	TRAJ49	TRAC	TRBV24-1	TRBD1	TRBJ1-4	TRBC1
TCR321	EVDPIGHLY	A0101	TRAV13-1	TRAJ23	TRAC	TRBV27	TRBD1	TRBJ1-2	TRBC1
TCR322	EVDPIGHLY	A0101	TRAV21	TRAJ9	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR323	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV9	None	TRBJ1-1	TRBC1
TCR324	EVDPIGHLY	A0101	TRAV19	TRAJ28	TRAC	TRBV19	TRBD1	TRBJ1-4	TRBC1
TCR325	EVDPIGHLY	A0101	TRAV10	TRAJ8	TRAC	TRBV5-1	TRBD1	TRBJ2-7	TRBC2
TCR326	EVDPIGHLY	A0101	TRAV21	TRAJ48	TRAC	TRBV27	TRBD2	TRBJ2-2	TRBC2
TCR327	EVDPIGHLY	A0101	TRAV12-2	TRAJ4	TRAC	TRBV7-2	TRBD2	TRBJ2-1	TRBC2
TCR328	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV5-1	None	TRBJ1-1	TRBC1
TCR329	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV9	None	TRBJ1-1	TRBC1
TCR330	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV6-6	TRBD1	TRBJ1-5	TRBC1
TCR331	EVDPIGHLY	A0101	TRAV21	TRAJ29	TRAC	TRBV5-1	TRBD2	TRBJ2-5	TRBC2
TCR332	EVDPIGHLY	A0101	TRAV41	TRAJ41	TRAC	TRBV7-9	TRBD1	TRBJ1-2	None
TCR333	EVDPIGHLY	A0101	TRAV21	TRAJ33	None	TRBV5-1	None	TRBJ1-1	TRBC1
TCR334	EVDPIGHLY	A0101	TRAV17	TRAJ39	TRAC	TRBV27	TRBD2	TRBJ2-1	TRBC2
TCR335	EVDPIGHLY	A0101	TRAV13-2	TRAJ13	TRAC	TRBV9	None	TRBJ1-3	TRBC1
TCR336	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-1	TRBD2	TRBJ2-5	TRBC2
TCR337	EVDPIGHLY	A0101	TRAV17	TRAJ57	TRAC	TRBV9	TRBD2	TRBJ1-1	TRBC1
TCR338	EVDPIGHLY	A0101	TRAV5	TRAJ44	TRAC	TRBV7-9	TRBD1	TRBJ1-1	TRBC1
TCR339	EVDPIGHLY	A0101	TRAV3	TRAJ39	TRAC	TRBV27	TRBD1	TRBJ1-5	TRBC1
TCR340	EVDPIGHLY	A0101	TRAV1-2	TRAJ4	TRAC	TRBV11-1	TRBD2	TRBJ2-1	TRBC2
TCR341	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ40	TRAC	TRBV7-8	TRBD1	TRBJ2-7	TRBC2
TCR342	EVDPIGHLY	A0101	TRAV8-3	TRAJ41	TRAC	TRBV7-9	None	TRBJ1-1	TRBC1
TCR343	EVDPIGHLY	A0101	TRAV5	TRAJ4	TRAC	TRBV11-2	None	TRBJ2-1	TRBC2
TCR344	EVDPIGHLY	A0101	TRAV24	TRAJ49	TRAC	TRBV6-5	TRBD1	TRBJ1-1	TRBC1
TCR345	EVDPIGHLY	A0101	TRAV4	TRAJ45	TRAC	TRBV24-1	TRBD2	TRBJ1-1	TRBC1
TCR346	EVDPIGHLY	A0101	TRAV29DV5	TRAJ48	TRAC	TRBV20-1	TRBD2	TRBJ2-7	TRBC2
TCR347	EVDPIGHLY	A0101	TRAV26-2	TRAJ44	TRAC	TRBV6-1	None	TRBJ2-7	TRBC2
TCR348	EVDPIGHLY	A0101	TRAV21	TRAJ27	TRAC	TRBV7-9	None	TRBJ1-6	TRBC1
TCR349	EVDPIGHLY	A0101	TRAV26-1	TRAJ49	TRAC	TRBV7-9	None	TRBJ2-7	TRBC2
TCR350	EVDPIGHLY	A0101	TRAV12-1	TRAJ5	TRAC	TRBV7-8	TRBD1	TRBJ2-1	TRBC2
TCR351	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR352	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV27	TRBD1	TRBJ2-4	TRBC2
TCR353	EVDPIGHLY	A0101	TRAV39	TRAJ42	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR354	EVDPIGHLY	A0101	TRAV1-2	TRAJ39	TRAC	TRBV27	TRBD2	TRBJ1-4	TRBC1
TCR355	EVDPIGHLY	A0101	TRAV1-1	TRAJ34	TRAC	TRBV9	TRBD1	TRBJ2-3	TRBC2
TCR356	EVDPIGHLY	A0101	TRAV25	TRAJ34	TRAC	TRBV29-1	TRBD1	TRBJ1-2	TRBC1
TCR357	EVDPIGHLY	A0101	TRAV39	TRAJ39	TRAC	TRBV30	TRBD1	TRBJ2-1	TRBC2
TCR358	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV20-1	TRBD2	TRBJ1-1	TRBC1
TCR359	EVDPIGHLY	A0101	TRAV8-6	TRAJ30	TRAC	TRBV9	TRBD2	TRBJ2-2	TRBC2
TCR360	EVDPIGHLY	A0101	TRAV21	TRAJ18	TRAC	TRBV27	TRBD1	TRBJ1-2	TRBC1
TCR361	EVDPIGHLY	A0101	TRAV12-3	TRAJ23	TRAC	TRBV11-3	TRBD1	TRBJ2-2	TRBC2
TCR362	EVDPIGHLY	A0101	TRAV12-1	TRAJ47	TRAC	TRBV5-6	None	TRBJ1-2	TRBC1
TCR363	EVDPIGHLY	A0101	TRAV22	TRAJ31	TRAC	TRBV5-6	None	TRBJ2-7	TRBC2
TCR364	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV14	TRBD1	TRBJ1-2	TRBC1
TCR365	EVDPIGHLY	A0101	TRAV1-2	TRAJ31	TRAC	TRBV2	TRBD2	TRBJ2-7	TRBC2
TCR366	EVDPIGHLY	A0101	TRAV1-2	TRAJ5	TRAC	TRBV20-1	TRBD2	TRBJ2-7	TRBC2
TCR367	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-1	TRBD1	TRBJ1-2	TRBC1
TCR368	EVDPIGHLY	A0101	TRAV16	TRAJ28	TRAC	TRBV7-9	TRBD1	TRBJ2-1	TRBC2
TCR369	EVDPIGHLY	A0101	TRAV13-1	TRAJ12	TRAC	TRBV20-1	TRBD2	TRBJ1-1	TRBC1
TCR370	EVDPIGHLY	A0101	TRAV17	TRAJ52	TRAC	TRBV29-1	TRBD2	TRBJ2-1	TRBC2
TCR371	EVDPIGHLY	A0101	TRAV36DV7	TRAJ49	TRAC	TRBV15	TRBD2	TRBJ2-3	TRBC2
TCR372	EVDPIGHLY	A0101	TRAV12-3	TRAJ58	TRAC	TRBV12-4	TRBD2	TRBJ2-1	TRBC2
TCR373	EVDPIGHLY	A0101	TRAV16	TRAJ18	TRAC	TRBV27	TRBD1	TRBJ2-7	TRBC2
TCR374	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV27	TRBD2	TRBJ2-2	TRBC2
TCR375	EVDPIGHLY	A0101	TRAV12-2	TRAJ48	TRAC	TRBV27	None	TRBJ2-6	TRBC2
TCR376	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV2	TRBD1	TRBJ1-2	TRBC1
TCR377	EVDPIGHLY	A0101	TRAV29DV5	TRAJ37	TRAC	TRBV5-4	TRBD2	TRBJ2-7	TRBC2
TCR378	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV24-1	TRBD1	TRBJ1-4	TRBC1
TCR379	EVDPIGHLY	A0101	TRAV12-2	TRAJ6	TRAC	TRBV15	TRBD1	TRBJ2-2	TRBC2
TCR380	EVDPIGHLY	A0101	TRAV12-1	TRAJ42	TRAC	TRBV27	TRBD1	TRBJ1-5	TRBC1
TCR381	EVDPIGHLY	A0101	TRAV1-1	TRAJ23	TRAC	TRBV25-1	TRBD1	TRBJ2-7	TRBC2

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR382	EVDPIGHLY	A0101	TRAV38-1	TRAJ28	TRAC	TRBV5-1	TRBD1	TRBJ2-1	TRBC2
TCR383	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV2	TRBD1	TRBJ1-1	TRBC1
TCR384	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV5-1	TRBD1	TRBJ2-7	TRBC2
TCR385	EVDPIGHLY	A0101	TRAV8-6	TRAJ42	TRAC	TRBV27	None	TRBJ1-1	TRBC1
TCR386	EVDPIGHLY	A0101	TRAV40	TRAJ32	TRAC	TRBV7-6	None	TRBJ2-2	TRBC2
TCR387	EVDPIGHLY	A0101	TRAV5	TRAJ5	TRAC	TRBV20-1	TRBD1	TRBJ2-5	TRBC2
TCR388	EVDPIGHLY	A0101	TRAV12-1	TRAJ40	TRAC	TRBV4-1	None	TRBJ2-5	TRBC2
TCR389	EVDPIGHLY	A0101	TRAV13-2	TRAJ53	TRAC	TRBV5-1	None	TRBJ1-1	TRBC1
TCR390	EVDPIGHLY	A0101	TRAV12-2	TRAJ48	TRAC	TRBV5-6	TRBD1	TRBJ2-2	TRBC2
TCR391	EVDPIGHLY	A0101	TRAV12-3	TRAJ15	TRAC	TRBV20-1	None	TRBJ2-7	TRBC2
TCR392	EVDPIGHLY	A0101	TRAV12-3	TRAJ23	TRAC	TRBV13	TRBD1	TRBJ2-3	TRBC2
TCR393	EVDPIGHLY	A0101	TRAV13-2	TRAJ9	TRAC	TRBV7-3	None	TRBJ1-6	TRBC1
TCR394	EVDPIGHLY	A0101	TRAV21	TRAJ45	TRAC	TRBV5-1	None	TRBJ1-1	TRBC1
TCR395	EVDPIGHLY	A0101	TRAV25	TRAJ31	TRAC	TRBV29-1	TRBD1	TRBJ1-2	TRBC1
TCR396	EVDPIGHLY	A0101	TRAV34	TRAJ37	TRAC	TRBV28	None	TRBJ1-1	TRBC1
TCR397	EVDPIGHLY	A0101	TRAV1-2	TRAJ9	TRAC	TRBV9	TRBD1	TRBJ2-6	TRBC2
TCR398	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR399	EVDPIGHLY	A0101	TRAV12-1	TRAJ34	TRAC	TRBV6-1	None	TRBJ2-7	TRBC2
TCR400	EVDPIGHLY	A0101	TRAV12-1	TRAJ26	TRAC	TRBV11-3	TRBD1	TRBJ1-1	TRBC1
TCR401	EVDPIGHLY	A0101	TRAV17	TRAJ36	TRAC	TRBV5-4	None	TRBJ2-1	TRBC2
TCR402	EVDPIGHLY	A0101	TRAV21	TRAJ49	TRAC	TRBV4-1	TRBD1	TRBJ1-1	TRBC1
TCR403	EVDPIGHLY	A0101	TRAV12-1	TRAJ13	TRAC	TRBV9	TRBD2	TRBJ2-7	TRBC2
TCR404	EVDPIGHLY	A0101	TRAV24	TRAJ7	TRAC	TRBV7-9	TRBD1	TRBJ2-1	TRBC2
TCR405	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV9	TRBD2	TRBJ1-1	TRBC1
TCR406	EVDPIGHLY	A0101	TRAV13-2	TRAJ49	TRAC	TRBV6-1	TRBD1	TRBJ2-5	TRBC2
TCR407	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-5	TRBD1	TRBJ1-2	TRBC1
TCR408	EVDPIGHLY	A0101	TRAV12-1	TRAJ39	TRAC	TRBV4-2	TRBD2	TRBJ2-7	TRBC2
TCR409	EVDPIGHLY	A0101	TRAV26-2	TRAJ30	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR410	EVDPIGHLY	A0101	TRAV20	TRAJ45	TRAC	TRBV5-4	TRBD1	TRBJ2-7	TRBC2
TCR411	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV7-8	TRBD2	TRBJ1-2	TRBC1
TCR412	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ48	TRAC	TRBV2	TRBD1	TRBJ1-5	TRBC1
TCR413	EVDPIGHLY	A0101	TRAV25	TRAJ15	TRAC	TRBV9	TRBD1	TRBJ2-1	TRBC2
TCR414	EVDPIGHLY	A0101	TRAV21	TRAJ49	TRAC	TRBV5-4	None	TRBJ2-7	TRBC2
TCR415	EVDPIGHLY	A0101	TRAV21	TRAJ12	TRAC	TRBV27	TRBD1	TRBJ2-2	TRBC2
TCR416	EVDPIGHLY	A0101	TRAV38-2DV8	TRAJ54	TRAC	TRBV24-1	None	TRBJ2-2	TRBC2
TCR417	EVDPIGHLY	A0101	TRAV17	TRAJ52	TRAC	TRBV27	None	TRBJ2-1	TRBC2
TCR418	EVDPIGHLY	A0101	TRAV21	TRAJ28	TRAC	TRBV9	TRBD2	TRBJ2-7	TRBC2
TCR419	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV4-1	TRBD1	TRBJ1-1	TRBC1
TCR420	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV5-4	None	TRBJ1-2	TRBC1
TCR421	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV5-1	TRBD1	TRBJ2-3	TRBC2
TCR422	EVDPIGHLY	A0101	TRAV12-1	TRAJ43	TRAC	TRBV6-5	TRBD1	TRBJ2-7	TRBC2
TCR423	EVDPIGHLY	A0101	TRAV21	TRAJ41	TRAC	TRBV9	None	TRBJ2-2	TRBC2
TCR424	EVDPIGHLY	A0101	TRAV19	TRAJ40	TRAC	TRBV20-1	None	TRBJ2-7	TRBC2
TCR425	EVDPIGHLY	A0101	TRAV12-2	TRAJ52	TRAC	TRBV6-1	TRBD2	TRBJ2-7	TRBC1
TCR426	EVDPIGHLY	A0101	TRAV26-1	TRAJ57	TRAC	TRBV2	None	TRBJ2-7	TRBC2
TCR427	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV12-4	TRBD1	TRBJ1-6	TRBC1
TCR428	EVDPIGHLY	A0101	TRAV8-4	TRAJ34	TRAC	TRBV7-9	None	TRBJ2-7	TRBC2
TCR429	EVDPIGHLY	A0101	TRAV19	TRAJ32	TRAC	TRBV7-9	None	TRBJ1-2	TRBC1
TCR430	EVDPIGHLY	A0101	TRAV21	TRAJ6	TRAC	TRBV3-1	TRBD2	TRBJ1-4	TRBC1
TCR431	EVDPIGHLY	A0101	TRAV13-2	TRAJ29	TRAC	TRBV5-1	None	TRBJ2-2	TRBC2
TCR432	EVDPIGHLY	A0101	TRAV14DV4	TRAJ26	TRAC	TRBV7-9	TRBD1	TRBJ2-5	TRBC2
TCR433	EVDPIGHLY	A0101	TRAV35	TRAJ44	TRAC	TRBV27	TRBD1	TRBJ2-1	TRBC2
TCR434	EVDPIGHLY	A0101	TRAV21	TRAJ24	TRAC	TRBV27	TRBD1	TRBJ1-6	TRBC1
TCR435	EVDPIGHLY	A0101	TRAV25	TRAJ21	TRAC	TRBV28	TRBD1	TRBJ2-7	TRBC2
TCR436	EVDPIGHLY	A0101	TRAV3	TRAJ36	TRAC	TRBV28	None	TRBJ1-5	TRBC1
TCR437	EVDPIGHLY	A0101	TRAV26-2	TRAJ52	TRAC	TRBV5-6	TRBD2	TRBJ2-1	TRBC2
TCR438	EVDPIGHLY	A0101	TRAV8-6	TRAJ40	TRAC	TRBV9	TRBD1	TRBJ2-7	TRBC2
TCR439	EVDPIGHLY	A0101	TRAV21	TRAJ42	TRAC	TRBV28	TRBD1	TRBJ2-7	TRBC2
TCR440	EVDPIGHLY	A0101	TRAV12-1	TRAJ32	TRAC	TRBV20-1	TRBD1	TRBJ1-1	TRBC1
TCR441	EVDPIGHLY	A0101	TRAV24	TRAJ24	TRAC	TRBV28	TRBD2	TRBJ2-5	TRBC2
TCR442	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV9	TRBD2	TRBJ1-1	TRBC1
TCR443	EVDPIGHLY	A0101	TRAV12-1	TRAJ26	TRAC	TRBV2	None	TRBJ1-6	TRBC1
TCR444	EVDPIGHLY	A0101	TRAV21	TRAJ31	TRAC	TRBV29-1	TRBD1	TRBJ1-1	TRBC1
TCR445	EVDPIGHLY	A0101	TRAV39	TRAJ33	TRAC	TRBV6-1	None	TRBJ1-5	TRBC1
TCR446	EVDPIGHLY	A0101	TRAV3	TRAJ38	TRAC	TRBV27	TRBD2	TRBJ2-7	TRBC2
TCR447	EVDPIGHLY	A0101	TRAV10	TRAJ33	TRAC	TRBV30	TRBD2	TRBJ2-1	TRBC2
TCR448	EVDPIGHLY	A0101	TRAV21	TRAJ20	TRAC	TRBV2	TRBD1	TRBJ2-1	TRBC2
TCR449	EVDPIGHLY	A0101	TRAV13-1	TRAJ20	TRAC	TRBV5-1	TRBD1	TRBJ1-1	TRBC1
TCR450	EVDPIGHLY	A0101	TRAV27	TRAJ45	TRAC	TRBV27	TRBD1	TRBJ1-6	TRBC1
TCR451	EVDPIGHLY	A0101	TRAV21	TRAJ18	TRAC	TRBV9	TRBD1	TRBJ2-1	TRBC2
TCR452	EVDPIGHLY	A0101	TRAV26-2	TRAJ28	TRAC	TRBV27	None	TRBJ1-5	TRBC1
TCR453	EVDPIGHLY	A0101	TRAV12-1	TRAJ34	TRAC	TRBV9	TRBD2	TRBJ2-7	TRBC2
TCR454	EVDPIGHLY	A0101	TRAV13-2	TRAJ40	TRAC	TRBV4-1	None	TRBJ1-3	TRBC1
TCR455	EVDPIGHLY	A0101	TRAV12-1	TRAJ34	TRAC	TRBV4-2	TRBD2	TRBJ2-7	TRBC2
TCR456	EVDPIGHLY	A0101	TRAV13-2	TRAJ46	TRAC	TRBV7-9	TRBD1	TRBJ2-1	TRBC2
TCR457	EVDPIGHLY	A0101	TRAV21	TRAJ36	TRAC	TRBV9	TRBD2	TRBJ2-7	TRBC2
TCR458	EVDPIGHLY	A0101	TRAV1-2	TRAJ20	TRAC	TRBV11-3	TRBD1	TRBJ2-3	TRBC2

TCR ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR459	EVDPIGHLY	A0101	TRAV3	TRAJ6	TRAC	TRBV12-4	TRBD1	TRBJ2-2	TRBC2
TCR460	EVDPIGHLY	A0101	TRAV25	TRAJ32	TRAC	TRBV19	TRBD1	TRBJ1-1	TRBC1
TCR461	EVDPIGHLY	A0101	TRAV21	TRAJ33	TRAC	TRBV9	TRBD1	TRBJ1-1	TRBC1
TCR462	EVDPIGHLY	A0101	TRAV19	TRAJ53	TRAC	TRBV7-7	TRBD1	TRBJ2-1	TRBC2
TCR463	EVDPIGHLY	A0101	TRAV12-1	TRAJ20	TRAC	TRBV10-3	TRBD2	TRBJ2-3	TRBC2
TCR464	EVDPIGHLY	A0101	TRAV12-1	TRAJ34	TRAC	TRBV6-5	TRBD1	TRBJ2-7	TRBC2
TCR465	EVDPIGHLY	A0101	TRAV26-2	TRAJ43	TRAC	TRBV25-1	TRBD1	TRBJ1-2	TRBC1
TCR466	EVDPIGHLY	A0101	TRAV8-6	TRAJ20	TRAC	TRBV7-9	TRBD1	TRBJ2-2	TRBC2
TCR467	EVDPIGHLY	A0101	TRAV3	TRAJ18	TRAC	TRBV20-1	TRBD2	TRBJ2-1	TRBC2
TCR468	EVDPIGHLY	A0101	TRAV21	TRAJ40	TRAC	TRBV11-3	TRBD1	TRBJ1-2	TRBC1
TCR469	EVDPIGHLY	A0101	TRAV2	TRAJ10	TRAC	TRBV6-5	TRBD2	TRBJ2-7	TRBC2

[00656] V(D)J and CDR3 sequences of α and β chains of the TCR clonotypes specific for A*0101_EVDPHIGHLY are shown in Table 10.

[00657] Annotated variable, diversity, joining, and constant regions of TCR clonotypes that demonstrated confirmed specificity in recipient T-cells is shown in Table 11, below.

Table 11: annotated TCR sequences from unique TCRs with confirmed specificity in recipient T cells.

TCR Clonotype ID #	PEPTIDE	HLA	TRAV	TRAJ	TRAC	TRBV	TRBD	TRBJ	TRBC
TCR2	EVDPIGHLY	A0101	TRAV24	TRAJ31	TRAC	TRBV3-1	TRBD1	TRBJ2-1	TRBC2
TCR4	EVDPIGHLY	A0101	TRAV3	TRAJ6	TRAC	TRBV19	None	TRBJ2-1	TRBC1
TCR53	EVDPIGHLY	A0101	TRAV21	TRAJ26	TRAC	TRBV27	TRBD1	TRBJ1-6	TRBC1
TCR54	EVDPIGHLY	A0101	TRAV20	TRAJ15	TRAC	TRBV27	None	TRBJ2-3	TRBC2
TCR19	LLASSILCA	A0201	TRAV19	TRAJ4	TRAC	TRBV6-5	TRBD2	TRBJ2-7	TRBC1
TCR21	LLASSILCA	A0201	TRAV5	TRAJ13	TRAC	TRBV7-9	TRBD1	TRBJ2-7	TRBC2
TCR22	LLASSILCA	A0201	TRAV3	TRAJ39	TRAC	TRBV7-9	None	TRBJ2-2	TRBC2
TCR18	LLASSILCA	A0201	TRAV38-2DV8	TRAJ21	TRAC	TRBV9	TRBD1	TRBJ2-1	TRBC2
TCR23	LLASSILCA	A0201	TRAV4	TRAJ9	TRAC	TRBV27	None	TRBJ1-5	TRBC1
TCR26	GVYDGEEHSV	A0201	TRAV13-1	TRAJ11	TRAC	TRBV6-3	None	TRBJ2-1	TRBC2
TCR28	GVYDGEEHSV	A0201	TRAV14DV4	TRAJ54	TRAC	TRBV4-3	TRBD1	TRBJ2-4	TRBC2
TCR29	GEMSSNSTAL	B4402	TRAV19	TRAJ39	TRAC	TRBV7-6	TRBD1	TRBJ1-1	TRBC1
TCR30	GEMSSNSTAL	B4402	TRAV36DV7	TRAJ34	TRAC	TRBV7-6	TRBD2	TRBJ2-2	TRBC2
TCR32	GEMSSNSTAL	B4402	TRAV24	TRAJ15	TRAC	TRBV7-6	TRBD2	TRBJ2-1	TRBC2
TCR33	GEMSSNSTAL	B4402	TRAV8-4	TRAJ12	TRAC	TRBV12-4	TRBD2	TRBJ2-3	TRBC2

[00658] V(D)J and CDR3 sequences of α and β chains of TCR clonotypes that demonstrated confirmed specificity in recipient T-cells is shown in Table 12.

[00659] A table of the annotated reference α variable (TRAV), α joining (TRAJ), α constant (TRAC), β variable (TRBV), β diversity (TRBD), β joining (TRBJ), and β constant

(TRBC) sequences and their corresponding Ensembl transcript (ENST) reference number is shown in Table 13. For any of the TCRs disclosed, amino acid sequences that are at least 95%, at least 96%, at least 97%, and least 98%, at least 99%, or more than 99% identical to the the annotated reference sequences as disclosed in Tables 9 and 11 are encompassed in the invention.

Table 13: Annotated reference genes for alpha and beta TCR regions

Gene	Ensemble Transcript ID
TRAC	ENST00000636588, ENST00000637010, ENST00000611116, ENST00000636320, ENST00000616778
TRAJ1	ENST00000390536
TRAJ10	ENST00000390527
TRAJ11	ENST00000390526
TRAJ12	ENST00000390525
TRAJ13	ENST00000390524
TRAJ14	ENST00000390523
TRAJ15	TENX_TRAJ15 (10X internal ref #)
TRAJ16	ENST00000390521
TRAJ17	ENST00000390520
TRAJ18	ENST00000390519
TRAJ19	ENST00000390518
TRAJ2	ENST00000390535
TRAJ20	ENST00000390517
TRAJ21	ENST00000390516
TRAJ22	ENST00000390515
TRAJ23	ENST00000390514
TRAJ24	ENST00000390513
TRAJ25	ENST00000390512
TRAJ26	ENST00000390511
TRAJ27	ENST00000390510
TRAJ28	ENST00000390509
TRAJ29	ENST00000390508
TRAJ3	ENST00000390534
TRAJ30	ENST00000390507
TRAJ31	ENST00000390506
TRAJ32	ENST00000390505
TRAJ33	ENST00000390504
TRAJ34	ENST00000390503
TRAJ35	ENST00000390502
TRAJ36	ENST00000614481
TRAJ37	ENST00000612375
TRAJ38	ENST00000390499
TRAJ39	ENST00000390498
TRAJ4	ENST00000390533
TRAJ40	ENST00000390497
TRAJ41	ENST00000390496
TRAJ42	ENST00000390495
TRAJ43	ENST00000390494
TRAJ44	ENST00000390493
TRAJ45	ENST00000390492
TRAJ46	ENST00000390491
TRAJ47	ENST00000390490
TRAJ48	ENST00000390489
TRAJ49	ENST00000390488
TRAJ5	ENST00000390532
TRAJ50	ENST00000390487
TRAJ52	ENST00000390486
TRAJ53	ENST00000390485
TRAJ54	ENST00000390484
TRAJ56	ENST00000390483
TRAJ57	ENST00000390482
TRAJ58	ENST00000390481

Gene	Ensemble Transcript ID
TRAJ59	ENST00000390480
TRAJ6	ENST00000390531
TRAJ61	ENST00000390479
TRAJ7	ENST00000390530
TRAJ8	ENST00000390529
TRAJ9	ENST00000390528
TRAV1-1	ENST00000542354
TRAV1-2	ENST00000390423
TRAV10	ENST00000390432
TRAV12-1	ENST00000390433
TRAV12-2	ENST00000390437
TRAV12-3	ENST00000390442
TRAV13-1	ENST00000390436
TRAV13-2	ENST00000390439
TRAV14DV4	ENST00000390440
TRAV16	ENST00000390444
TRAV17	ENST00000390445
TRAV18	ENST00000390446
TRAV19	ENST00000390447
TRAV2	ENST00000390424
TRAV20	ENST00000390448
TRAV21	ENST00000390449
TRAV22	ENST00000390450
TRAV23DV6	ENST00000390451
TRAV24	ENST00000390453
TRAV25	ENST00000390454
TRAV26-1	ENST00000390455
TRAV26-2	ENST00000390460
TRAV27	ENST00000390457
TRAV29DV5	ENST00000390458
TRAV3	ENST00000390425
TRAV30	ENST00000557168
TRAV34	ENST00000390461
TRAV35	TENX_TRAV35 (10X internal ref #)
TRAV36DV7	ENST00000390463
TRAV38-1	ENST00000390464
TRAV38-2DV8	ENST00000390465
TRAV39	ENST00000390466
TRAV4	ENST00000390426
TRAV40	ENST00000390467
TRAV41	ENST00000390468
TRAV5	ENST00000390427
TRAV6	ENST00000390428
TRAV7	ENST00000390429
TRAV8-1	ENST00000390430
TRAV8-2	ENST00000390434
TRAV8-3	ENST00000390435
TRAV8-4	ENST00000390438
TRAV8-6	ENST00000390443
TRAV8-7	ENST00000390456
TRAV9-1	ENST00000390431
TRAV9-2	ENST00000390441
TRBC1	ENST00000632136, ENST00000633705
TRBC2	ENST00000636844, ENST00000614992, ENST00000622053, ENST00000613720, ENST00000466254, ENST00000637077, ENST00000610416, ENST00000620987
TRBD1	ENST00000631435
TRBD2	TENX_TRBD2 (10X internal ref #)
TRBJ1-1	ENST00000632951
TRBJ1-2	ENST00000631745
TRBJ1-3	ENST00000633936
TRBJ1-4	ENST00000632041
TRBJ1-5	ENST00000634000
TRBJ1-6	ENST00000633713, ENST00000632228
TRBJ2-1	ENST00000631600
TRBJ2-2	ENST00000633188

Gene	Ensemble Transcript ID
TRBJ2-2P	ENST00000633209
TRBJ2-3	ENST00000631840
TRBJ2-4	ENST00000390416
TRBJ2-5	ENST00000634149
TRBJ2-6	ENST00000632996
TRBJ2-7	ENST00000390419, ENST00000633660
TRBV10-1	ENST00000390364
TRBV10-2	ENST00000426318, ENST00000633575
TRBV10-3	ENST00000611462, ENST00000631471
TRBV11-1	ENST00000390367
TRBV11-2	TENX_TRBV11_2 (10X internal ref #)
TRBV11-3	ENST00000634111
TRBV12-3	ENST00000633292
TRBV12-4	ENST00000631824, ENST00000617347
TRBV12-5	ENST00000632829, ENST00000621184
TRBV13	ENST00000633796
TRBV14	ENST00000617639
TRBV15	ENST00000631835
TRBV16	ENST00000633244
TRBV17	ENST00000619103, ENST00000631663
TRBV18	ENST00000611520, ENST00000631559
TRBV19	ENST00000390393, ENST00000632638
TRBV2	ENST00000632828, ENST00000455382
TRBV20-1	ENST00000390394, ENST00000633466
TRBV21-1	TENX_TRBV21 (10X internal ref #)
TRBV23-1	ENST00000390396
TRBV24-1	ENST00000633092, ENST00000390397
TRBV25-1	ENST00000390398, ENST00000610439
TRBV27	ENST00000633283
TRBV28	ENST00000390400
TRBV29-1	ENST00000422143
TRBV3-1	ENST00000390387
TRBV30	ENST00000631690, ENST00000417977
TRBV4-1	ENST00000632713, ENST00000390357
TRBV4-2	ENST00000390392
TRBV4-3	ENST00000631427
TRBV5-1	ENST00000633384
TRBV5-3	ENST00000390362, ENST00000634123
TRBV5-4	ENST00000633696, ENST00000454561
TRBV5-5	ENST00000632187, ENST00000390372
TRBV5-6	ENST00000390375
TRBV5-7	ENST00000633790
TRBV5-8	ENST00000631639
TRBV6-1	ENST00000631557
TRBV6-2	ENST00000632016
TRBV6-3	ENST00000632148
TRBV6-4	ENST00000390360, ENST00000633472
TRBV6-5	ENST00000633072
TRBV6-6	ENST00000633963, ENST00000390371
TRBV6-7	ENST00000631511, ENST00000390373
TRBV6-8	ENST00000632425, ENST00000390376
TRBV6-9	ENST00000634093
TRBV7-1	ENST00000632308
TRBV7-2	ENST00000634605
TRBV7-3	ENST00000390361, ENST00000631882
TRBV7-4	ENST00000633313, ENST00000390369
TRBV7-6	ENST00000390374, ENST00000633265
TRBV7-7	ENST00000631548
TRBV7-8	ENST00000632560
TRBV7-9	ENST00000612787, ENST00000632021
TRBV9	ENST00000633328, ENST00000390363

Example 13: T cell line transiently transfected with identified TCRs specifically bind to their target HLA-PEPTIDE complex, but not to negative control peptide-HLAs.

[00660] Jurkat TIB-152 T cell line cultures were co-transfected with a plasmid expressing human CD8 and a plasmid expressing TCR α and β chains with a GFP reporter gene using Nucleofector 4D electroporator. Plasmids used for transfection are described in FIGS. 4 and 5. 24-48 hours post transfection, Jurkat T cells were analyzed for expression of the TCR of interest. Cells were assessed for binding to HLA-PEPTIDE complexes and a control infectious-disease-based peptide tetramer using flow cytometry. Total population was gated on live single GFP-expressing cells before evaluating binding of HLA-PEPTIDE target tetramer. FIG. 31 shows examples of Jurkat cells expressing A*0201_LLASSILCA-, A*0201_GVYDGEEHSV-, B*4402_GEMSSNSTAL-, and A*0101_EVDPIGHLY-specific TCRs binding to their respective HLA-PEPTIDE targets but not to the control peptide tetramer.

Example 14: TCRs cloned into a viral vector are stably expressed in primary human CD8+ T cells and bind cognate peptide target-MHC complexes

[00661] Lentiviral vectors were generated for TCR specific for the HLA-PEPTIDE target HLA-A*0201_LLASSILCA. As a model vector system, we used commercially available 3rd generation lentivirus base expression vector system from System Biosciences, Palo Alto, CA. See FIG. 33.

[00662] Primary human CD8+ T cells were isolated and transduced with the recombinant TCR lentivirus at multiplicity of infection (MOI~10). T cells were expanded using rapid expansion protocol for 1-2 weeks before assessment of TCR expression on CD8 T cells by tetramer staining.

[00663] FIG. 32 depicts the gating strategy and flow data demonstrating that transduced human CD8+ cells bind to the HLA-PEPTIDE target.

Example 15: Identification of MHC/peptide target-reactive TCRs

[00664] T cells are isolated from blood, lymph nodes, or tumors of patients. Patients are HLA-matched to SAT, and are selected based on expression of target-harboring protein. T cells are then enriched for SAT-specific T cells, e.g., by sorting SAT-MHC tetramer binding cells or by

sorting activated cells stimulated in an *in vitro* co-culture of T cells and SAT-pulsed antigen presenting cells.

[00665] SAT-relevant alpha-beta TCR dimers are identified by single cell sequencing of TCRs of SAT-specific T cells. Alternatively, bulk TCR sequencing of SAT-specific T cells is performed and alpha-beta pairs with a high probability of matching are determined using a TCR pairing method.

[00666] Alternatively or in addition, SAT-specific T cells can be obtained through *in vitro* priming of naïve T cells from healthy donors. T cells obtained from PBMCs, lymph nodes, or cord blood are repeatedly stimulated by SAT-pulsed antigen presenting cells to prime differentiation of antigen-experienced T cells. TCRs are then identified similarly as described above for SAT-specific T cells from patients.

Example 16: Production of engineered TCR T cells

[00667] TCR alpha and beta chain sequences are cloned into appropriate constructs. TCR-autologous or heterologous bulk T cells are transduced with the constructs to produce engineered TCR T cells. These T cells are expanded in the presence of anti-CD3 antibodies and IL-2 cytokine for use in subsequent experiments. In certain instances, native TCR is deleted or the inserted TCR is modified to increase proper multimerization.

[00668] *In vitro* verification of TCR specificity

[00669] First, T cells bearing engineered TCRs are screened for target recognition using antigen presenting cells expressing the appropriate MHC and pulsed with appropriate target(s).

[00670] TCRs identified in the first round of screening are then tested for recognition of natural target. Lead TCRs are nominated based on specific recognition of HLA-matched primary tumors and tumor cell lines expressing SAT-harboring protein.

[00671] To assure specificity, lead TCRs are de-selected based on off-target recognition. They are screened against a panel of HLA matched and mismatched cell lines, covering multiple tissues and organ types, and with HLA-matched and mismatched antigen presenting cells pulsed with a panel of infectious disease antigens. TCRs with specific and non-specific off-target recognition of self-antigens or common non-self-antigens are de-selected.

Example 17: Identification of monoclonal antibodies (mAbs) that target MHC class I molecules presenting tumor antigens using rabbit B cell cloning technologies

[00672] Potent and selective mAbs targeting human class I MHC molecules presenting tumor antigens of interest are identified. Soluble human pMHC molecules presenting human tumor antigens are utilized for multiple mouse or rabbit immunizations followed by screening of B cells derived from the immunized animals to identify B cells that express mAbs that bind to target class I MHC molecules. Sequences encoding the mAbs identified from the mouse or rabbit screens will be cloned from the isolated B cells. The recovered mAbs are then evaluated against a panel of irrelevant pMHCs to identify lead mAbs that bind selectively to the target pMHCs. Lead mAbs will be fully characterized to determine target binding affinity and selectivity. Lead mAbs that demonstrate potent and selective binding are humanized to generate full-length human IgG monoclonal antibody (mAb) constructs. In addition, the lead mAbs are incorporated into bi-specific mAb constructs and chimeric antigen receptor (CAR) constructs that can be used to generate CAR T-cells. Full-length bi-specifics or scFV-based bi-specifics can be constructed.

[00673] Demonstrate targeting of human tumor cells *in vitro*

[00674] Immunohistochemistry techniques are utilized to demonstrate specific binding of lead antibodies to human tumor cells expressing target pMHC molecules. T-cell lines transfected with CAR-T constructs are incubated with human tumor cells to demonstrate killing of tumor cells *in vitro*. Alternatively, tumor cells expressing the target are incubated with bi-specific constructs (encoding the ABP and an effector domain) and PBMCs or T cells.

[00675] *In vivo* proof-of-concept

[00676] Lead antibody or CAR-T constructs are evaluated *in vivo* to demonstrate directed tumor killing in humanized mouse tumor models. Lead antibody or CAR-T constructs are evaluated in xenograft tumor models engrafted with human PBMCs. Anti-tumor activity is measured and compared to control constructs to demonstrate target-dependent tumor killing.

[00677] Potent and selective ABPs that selectively target human class I MHC molecules presenting tumor antigens will be identified using phage display or B cell cloning technologies. The utility of the ABPs will be demonstrated by showing that the ABPs mediated tumor cell killing *in vitro* and *in vivo* when incorporated into antibody or CAR-T cell constructs.

[00678] While the invention has been particularly shown and described with reference to a preferred embodiment and various alternate embodiments, it will be understood by persons skilled in the relevant art that various changes in form and details can be made therein without departing from the spirit and scope of the invention.

[00679] All references, issued patents and patent applications cited within the body of the instant specification are hereby incorporated by reference in their entirety, for all purposes.

SEQUENCES

Table 3: VH and VL sequences for G2 scFv Selective Binders, selective for HLA-PEPTIDE Target HLA-A*01:01_NTDNNLAVY (SEQ ID NO: 23).

Target group	Clone name	VH (SEQ ID NO)	VL (SEQ ID NO)
G2	G2-P2E07	2781	2816
G2	G2-P2E03	2782	2817
G2	G2-P2A11	2783	2818
G2	G2-P2C06	2784	2819
G2	G2-P1G01	2785	2820
G2	G2-P1C02	2786	2821
G2	G2-P1H01	2787	2822
G2	G2-P1B12	2788	2823
G2	G2-P1B06	2789	2824
G2	G2-P2H10	2790	2825
G2	G2-P1H10	2791	2826
G2	G2-P2C11	2792	2827
G2	G2-P1C09	2793	2828
G2	G2-P1A10	2794	2829
G2	G2-P1B10	2795	2830
G2	G2-P1D07	2796	2831
G2	G2-P1E05	2797	2832
G2	G2-P1D03	2798	2833
G2	G2-P1G12	2799	2834
G2	G2-P2H11	2800	2835
G2	G2-P1C03	2801	2836
G2	G2-P1G07	2802	2837
G2	G2-P1F12	2803	2838
G2	G2-P1G03	2804	2839
G2	G2-P2B08	2805	2840
G2	G2-P2A10	2806	2841
G2	G2-P2D04	2807	2842
G2	G2-P1C06	2808	2843
G2	G2-P2A09	2809	2844
G2	G2-P1B08	2810	2845
G2	G2-P1E03	2811	2846
G2	G2-P2A03	2812	2847
G2	G2-P2F01	2813	2848
G2	G2-P1H11	2814	2849
G2	G2-P1D06	2815	2850

Table 4: CDR sequences for G2 selective binders, selective for HLA-PEPTIDE Target HLA-A*01:01_NTDNNLAVY (SEQ ID NO: 23) (determined according to Kabat numbering)

Target group	Clone name	CDR-H1 (SEQ ID NO)	CDR-H2 (SEQ ID NO)	CDR-H3 (SEQ ID NO)	CDR-L1 (SEQ ID NO)	CDR-L2 (SEQ ID NO)	CDR-L3 (SEQ ID NO)
G2	G2-P2E07	2851	2880	2902	2934	2955	2971
G2	G2-P2E03	2852	2881	2903	2935	2956	2972
G2	G2-P2A11	2853	2882	2903	2936	2957	2973
G2	G2-P2C06	2854	2882	2904	2937	2958	2974
G2	G2-P1G01	2855	2883	2905	2937	2958	2975
G2	G2-P1C02	2855	2882	2906	2938	2958	2976
G2	G2-P1H01	2856	2882	2907	2939	2959	2976
G2	G2-P1B12	2857	2882	2908	2940	2960	2977
G2	G2-P1B06	2858	2884	2909	2935	2958	2972
G2	G2-P2H10	2859	2882	2910	2941	2961	2978
G2	G2-P1H10	2852	2885	2911	2942	2958	2976
G2	G2-P2C11	2860	2882	2912	2943	2962	2978
G2	G2-P1C09	2861	2886	2913	2944	2963	2979
G2	G2-P1A10	2862	2887	2914	2945	2958	2980
G2	G2-P1B10	2855	2888	2903	2941	2962	2981
G2	G2-P1D07	2855	2889	2915	2946	2958	2982
G2	G2-P1E05	2863	2883	2916	2947	2958	2973
G2	G2-P1D03	2856	2890	2917	2934	2962	2972
G2	G2-P1G12	2864	2891	2917	2946	2964	2972
G2	G2-P2H11	2865	2882	2918	2941	2962	2974
G2	G2-P1C03	2866	2882	2919	2948	2958	2983
G2	G2-P1G07	2867	2892	2920	2946	2962	2984
G2	G2-P1F12	2868	2893	2921	2949	2965	2972
G2	G2-P1G03	2869	2894	2922	2950	2966	2985
G2	G2-P2B08	2870	2882	2923	2943	2967	2986
G2	G2-P2A10	2871	2895	2924	2951	2968	2987
G2	G2-P2D04	2872	2882	2925	2952	2969	2973
G2	G2-P1C06	2873	2882	2926	2943	2958	2988
G2	G2-P2A09	2852	2882	2927	2935	2958	2989
G2	G2-P1B08	2874	2896	2928	2938	2958	2981
G2	G2-P1E03	2875	2897	2929	2953	2961	2990
G2	G2-P2A03	2876	2898	2930	2941	2962	2989
G2	G2-P2F01	2877	2899	2931	2946	2964	2991
G2	G2-P1H11	2878	2900	2932	2946	2958	2992
G2	G2-P1D06	2879	2901	2933	2954	2970	2993

Table 5: VH and VL sequences for scFv selective binders selective for HLA-PEPTIDE Target HLA-A*02:01_LLASSILCA (SEQ ID NO: 2737).

Target group	Clone name	VH (SEQ ID NO)	VL (SEQ ID NO)
G7	G7R3-P1C6	2994	3002
G7	G7R3-P1G10	2995	3003
G7	1-G7R3-P1B4	2996	3004
G7	2-G7R4-P2C2	2997	3005
G7	3-G7R4-P1A3	2998	3006
G7	4-G7R4-B5-P2E9	2999	3007
G7	5-G7R4-B10-P1F8	3000	3008
G7	B7 (G7R3-P3A9)	3001	3009

Table 6: CDR sequences for G7 selective binders selective for HLA-PEPTIDE Target HLA-A*02:01 LLASSILCA (SEQ ID NO: 2737)

Target group	Clone name	CDR-H1 (SEQ ID NO)	CDR-H2 (SEQ ID NO)	CDR-H3 (SEQ ID NO)	CDR-L1 (SEQ ID NO)	CDR-L2 (SEQ ID NO)	CDR-L3 (SEQ ID NO)
G7	G7R3-P1C6	3010	3017	3025	3033	2970	3043
G7	G7R3-P1G10	3011	3018	3026	3034	2958	3044
G7	1-G7R3-P1B4	3012	3019	3027	3035	3039	3045
G7	2-G7R4-P2C2	3013	3020	3028	3036	2962	3046
G7	3-G7R4-P1A3	2879	3021	3029	2934	3040	3047
G7	4-G7R4-B5-P2E9	3014	3022	3030	3037	3041	3048
G7	5-G7R4-B10-P1F8	3015	3023	3031	2946	3042	3049
G7	B7 (G7R3-P3A9)	3016	3024	3032	3038	3041	3050

Table 10: CDR3 and V(D)J sequences of TCR clonotypes confirmed through resorting

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR101	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3351	3656	3962
TCR102	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3352	3657	3963
TCR103	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3054	3353	3658	3964
TCR104	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3352	3659	3963
TCR105	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3055	3354	3660	3965
TCR106	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3056	3355	3661	3966
TCR107	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3057	3356	3662	3967
TCR108	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3058	3357	3663	3968
TCR109	EVDPIGHLY (SEQ	A0101	3059	3358	3664	3969

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR110	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3060	3359	3665	3970
TCR111	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3061	3360	3666	3971
TCR112	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3062	3361	3667	3972
TCR113	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3063	3362	3668	3973
TCR114	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3351	3657	3962
TCR115	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3057	3352	3662	3963
TCR116	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3064	3363	3669	3974
TCR117	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3065	3364	3670	3975
TCR118	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3054	3352	3658	3963
TCR119	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3066	3365	3671	3976
TCR120	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3067	3366	3672	3977
TCR121	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3068	3367	3673	3978
TCR122	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3069	3368	3674	3979
TCR123	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3356	3659	3967
TCR124	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3070	3369	3675	3980
TCR125	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3355	3659	3966
TCR126	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3071	3370	3676	3981
TCR127	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3353	3659	3964
TCR128	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3072	3371	3677	3982
TCR129	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3073	3372	3678	3983
TCR130	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3057	3351	3662	3962
TCR131	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3074	3373	3679	3984
TCR132	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3075	3374	3680	3985
TCR133	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3076	3375	3681	3986
TCR134	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3077	3376	3682	3987
TCR135	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3078	3377	3683	3988
TCR136	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3079	3378	3684	3989
TCR137	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3080	3379	3685	3990
TCR138	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3081	3380	3686	3991
TCR139	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3082	3381	3687	3992
TCR140	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3083	3382	3688	3993
TCR141	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3084	3383	3689	3994
TCR142	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3085	3384	3690	3995

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR143	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3086	3385	3691	3996
TCR144	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3087	3386	3692	3997
TCR145	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3088	3387	3693	3998
TCR146	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3089	3388	3694	3999
TCR147	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3389	3695	4000
TCR148	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3056	3351	3661	3962
TCR149	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3090	3390	3696	4001
TCR150	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3091	3391	3697	4002
TCR151	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3092	3392	3698	4003
TCR152	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3093	3393	3699	4004
TCR153	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3356	3700	3967
TCR154	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3094	3394	3701	4005
TCR155	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3054	3363	3658	3974
TCR156	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3095	3395	3702	4006
TCR157	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3054	3351	3658	3962
TCR158	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3096	3396	3703	4007
TCR159	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3355	3657	3966
TCR160	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3097	3397	3704	4008
TCR161	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3098	3398	3705	4009
TCR162	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3099	3352	3706	3963
TCR163	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3100	3399	3707	4010
TCR164	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3353	3657	3964
TCR165	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3101	3400	3708	4011
TCR166	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3102	3401	3709	4012
TCR167	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3058	3352	3663	3963
TCR168	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3103	3402	3710	4013
TCR169	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3104	3403	3711	4014
TCR170	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3105	3404	3712	4015
TCR171	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3106	3405	3713	4016
TCR172	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3107	3406	3714	4017
TCR173	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3108	3407	3715	4018
TCR174	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3109	3408	3716	4019
TCR175	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3110	3409	3717	4020
TCR176	EVDPIGHLY (SEQ	A0101	3111	3410	3718	4021

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR177	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3112	3411	3719	4022
TCR178	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3113	3412	3720	4023
TCR179	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3058	3351	3663	3962
TCR180	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3354	3659	3965
TCR181	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3072	3353	3677	4024
TCR182	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3413	3721	4025
TCR183	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3114	3414	3722	4026
TCR184	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3058	3355	3663	3966
TCR185	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3415	3659	4027
TCR186	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3114	3353	3722	3964
TCR187	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3115	3416	3723	4028
TCR188	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3116	3417	3724	4029
TCR189	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3117	3418	3725	4030
TCR190	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3118	3419	3726	4031
TCR191	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3119	3420	3727	4032
TCR192	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3120	3352	3728	4033
TCR193	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3121	3421	3729	4034
TCR194	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3054	3367	3658	3978
TCR195	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3122	3422	3730	4035
TCR196	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3123	3423	3731	4036
TCR197	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3124	3424	3732	4037
TCR198	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3112	3351	3719	3962
TCR199	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3060	3352	3665	3963
TCR200	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3059	3351	3664	3962
TCR201	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3071	3355	3676	3966
TCR202	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3125	3425	3733	4038
TCR203	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3126	3426	*3734	4039
TCR204	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3127	3427	3735	4040
TCR205	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3128	3428	3736	4041
TCR206	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3129	3429	3737	4042
TCR207	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3130	3352	3738	3963
TCR208	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3362	3659	3973
TCR209	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3055	3352	3660	3963

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR210	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3131	3430	3739	4043
TCR211	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3132	3431	3740	4044
TCR212	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3133	3432	3741	4045
TCR213	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3053	3381	3657	3992
TCR214	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3134	3433	3742	4046
TCR215	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3061	3351	3666	3962
TCR216	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3104	3352	3711	3963
TCR217	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3055	3351	3660	3962
TCR218	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3058	3353	3663	3964
TCR219	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3135	3434	3743	4047
TCR220	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3052	3435	3744	4048
TCR221	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3136	3436	3745	4049
TCR222	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3137	3437	3746	4050
TCR223	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3138	3438	3747	4051
TCR224	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3139	3439	3748	4052
TCR225	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3140	3440	3749	4053
TCR226	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3141	3441	3750	4054
TCR227	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3142	3442	3751	4055
TCR228	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3143	3443	3752	4056
TCR229	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3144	3444	3753	4057
TCR230	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3145	3445	3754	4058
TCR231	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3136	3444	3755	4057
TCR232	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3146	3446	3756	4059
TCR233	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3147	3447	3757	4060
TCR234	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3148	3448	3758	4061
TCR235	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3149	3449	3759	4062
TCR236	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3150	3450	3760	4063
TCR237	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3151	3436	3761	4049
TCR238	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3139	3436	3748	4049
TCR239	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3152	3451	3762	4064
TCR240	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3153	3452	3763	4065
TCR241	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3154	3453	3764	4066
TCR242	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3155	3454	3765	4067
TCR243	EVDPIGHLY (SEQ	A0101	3137	3440	3746	4053

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR244	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3156	3455	3766	4068
TCR245	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3151	3456	3761	4069
TCR246	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3157	3457	3767	4070
TCR247	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3158	3458	3768	4071
TCR248	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3159	3459	3769	4072
TCR249	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3160	3460	3770	4073
TCR250	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3077	3461	3771	4074
TCR251	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3161	3462	3772	4075
TCR252	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3162	3463	3773	4076
TCR253	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3163	3464	3774	4077
TCR254	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3164	3465	3775	4078
TCR255	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3137	3442	3746	4055
TCR256	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3136	3438	3745	4051
TCR257	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3165	3466	3776	4079
TCR258	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3166	3467	3777	4080
TCR259	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3167	3468	3778	4081
TCR260	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3168	3469	3779	4082
TCR261	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3169	3470	3780	4083
TCR262	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3137	3436	3746	4049
TCR263	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3170	3471	3781	4084
TCR264	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3171	3472	3782	4085
TCR265	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3172	3473	3783	4086
TCR266	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3173	3474	3784	4087
TCR267	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3174	3475	3785	4088
TCR268	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3175	3476	3786	4089
TCR269	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3176	3477	3787	4090
TCR270	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3177	3478	3788	4091
TCR271	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3178	3479	3789	4092
TCR272	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3179	3480	3790	4093
TCR273	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3180	3481	3791	4094
TCR274	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3136	3482	3755	4095
TCR275	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3181	3483	3792	4096
TCR276	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3182	3484	3793	4097

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR277	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3183	3485	3794	4098
TCR278	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3184	3486	3795	4099
TCR279	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3185	3487	3796	4100
TCR280	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3186	3488	3797	4101
TCR281	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3187	3489	3798	4102
TCR282	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3188	3482	3799	4095
TCR283	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3189	3490	3800	4103
TCR284	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3190	3491	3801	4104
TCR285	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3191	3492	3802	4105
TCR286	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3192	3493	3803	4106
TCR287	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3193	3494	3804	4107
TCR288	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3194	3495	3805	4108
TCR289	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3195	3496	3806	4109
TCR290	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3196	3497	3807	4110
TCR291	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3197	3498	3808	4111
TCR292	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3198	3499	3809	4112
TCR293	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3199	3500	3810	4113
TCR294	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3137	3449	3746	4062
TCR295	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3200	3436	3811	4049
TCR296	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3201	3501	3812	4114
TCR297	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3138	3436	3747	4049
TCR298	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3202	3502	3813	4115
TCR299	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3203	3503	3814	4116
TCR300	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3204	3504	3815	4117
TCR301	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3205	3505	3816	4118
TCR302	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3206	3506	3817	4119
TCR303	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3207	3507	3818	4120
TCR304	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3148	3440	3758	4053
TCR305	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3208	3508	3819	4121
TCR306	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3209	3509	3820	4122
TCR307	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3210	3510	3821	4123
TCR308	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3211	3511	3822	4124
TCR309	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3212	3512	3823	4125
TCR310	EVDPIGHLY (SEQ	A0101	3213	3513	3824	4126

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR311	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3214	3514	3825	4127
TCR312	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3215	3515	3826	4128
TCR313	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3216	3516	3827	4129
TCR314	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3517	3828	4130
TCR315	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3218	3518	3829	4131
TCR316	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3219	3519	3830	4132
TCR317	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3220	3520	3831	4133
TCR318	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3221	3521	3832	4134
TCR319	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3518	3828	4131
TCR320	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3222	3522	3833	4135
TCR321	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3223	3523	3834	4136
TCR322	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3224	3524	3835	4137
TCR323	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3225	3525	3836	4138
TCR324	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3226	3526	3837	4139
TCR325	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3227	3527	3838	4140
TCR326	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3228	3528	3839	4141
TCR327	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3229	3529	3840	4142
TCR328	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3230	3530	3841	4143
TCR329	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3525	3828	4138
TCR330	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3231	3531	3842	4144
TCR331	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3232	3532	3843	4145
TCR332	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3233	3520	3844	4133
TCR333	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3530	3828	4143
TCR334	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3234	3533	3845	4146
TCR335	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3235	3534	3846	4147
TCR336	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3532	3828	4145
TCR337	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3236	3535	3847	4148
TCR338	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3237	3536	3848	4149
TCR339	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3238	3537	3849	4150
TCR340	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3239	3538	3850	4151
TCR341	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3240	3539	3851	4152
TCR342	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3241	3540	3852	4153
TCR343	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3242	3541	3853	4154

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR344	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3243	3542	3854	4155
TCR345	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3244	3543	3855	4156
TCR346	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3245	3544	3831	4157
TCR347	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3246	3545	3856	4158
TCR348	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3247	3546	3857	4159
TCR349	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3248	3547	3858	4160
TCR350	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3249	3548	3859	4161
TCR351	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3524	3828	4137
TCR352	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3250	3549	3860	4162
TCR353	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3251	3550	3861	4163
TCR354	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3252	3551	3862	4164
TCR355	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3253	3552	3863	4165
TCR356	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3254	3553	3864	4166
TCR357	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3255	3554	3865	4167
TCR358	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3256	3555	3866	4168
TCR359	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3257	3556	3867	4169
TCR360	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3258	3557	3868	4170
TCR361	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3259	3558	3869	4171
TCR362	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3260	3559	3870	4172
TCR363	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3261	3560	3871	4173
TCR364	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3519	3828	4132
TCR365	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3262	3561	3872	4174
TCR366	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3263	3562	3873	4175
TCR367	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3563	3828	4176
TCR368	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3264	3564	3874	4177
TCR369	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3265	3565	3875	4178
TCR370	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3266	3566	3876	4179
TCR371	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3267	3567	3877	4180
TCR372	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3268	3568	3878	4181
TCR373	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3269	3569	3879	4182
TCR374	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3528	3828	4141
TCR375	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3270	3570	3880	4183
TCR376	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3571	3828	4184
TCR377	EVDPIGHLY (SEQ	A0101	3271	3572	3881	4185

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR378	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3219	3522	3830	4135
TCR379	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3272	3573	3882	4186
TCR380	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3273	3574	3883	4187
TCR381	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3274	3575	3884	4188
TCR382	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3275	3576	3885	4189
TCR383	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3577	3828	4190
TCR384	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3230	3517	3841	4130
TCR385	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3276	3578	3886	4191
TCR386	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3277	3579	3887	4192
TCR387	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3278	3580	3888	4193
TCR388	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3279	3581	3889	4194
TCR389	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3280	3582	3890	4195
TCR390	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3281	3583	3891	4196
TCR391	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3282	3584	3892	4197
TCR392	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3283	3585	3893	4198
TCR393	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3284	3586	3894	4199
TCR394	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3285	3587	3895	4200
TCR395	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3286	3588	3896	4201
TCR396	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3287	3589	3897	4202
TCR397	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3288	3590	3898	4203
TCR398	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3289	3591	3899	4204
TCR399	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3290	3592	3900	4205
TCR400	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3291	3593	3901	4206
TCR401	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3292	3594	3902	4207
TCR402	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3293	3595	3903	4208
TCR403	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3294	3596	3904	4209
TCR404	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3295	3597	3905	4210
TCR405	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3219	3598	3830	4211
TCR406	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3296	3599	3906	4212
TCR407	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3217	3600	3828	4213
TCR408	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3297	3601	3907	4214
TCR409	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3298	3602	3908	4215
TCR410	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3299	3603	3909	4216

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR411	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3300	3604	3910	4217
TCR412	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3301	3605	3911	4218
TCR413	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3302	3606	3912	4219
TCR414	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3303	3607	3913	4220
TCR415	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3304	3608	3914	4221
TCR416	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3305	3609	3915	4222
TCR417	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3306	3610	3916	4223
TCR418	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3307	3611	3917	4224
TCR419	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3289	3595	3899	4208
TCR420	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3308	3612	3918	4225
TCR421	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3309	3613	3919	4226
TCR422	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3310	3614	3920	4227
TCR423	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3311	3615	3921	4228
TCR424	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3312	3616	3922	4229
TCR425	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3313	3617	3923	4230
TCR426	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3314	3618	3924	4231
TCR427	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3289	3619	3899	4232
TCR428	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3315	3620	3925	4233
TCR429	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3316	3621	3926	4234
TCR430	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3317	3622	3927	4235
TCR431	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3318	3623	3928	4236
TCR432	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3319	3624	3929	4237
TCR433	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3320	3625	3930	4238
TCR434	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3321	3626	3931	4239
TCR435	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3322	3627	3932	4240
TCR436	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3323	3628	3933	4241
TCR437	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3324	3629	3934	4242
TCR438	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3325	3602	3935	4215
TCR439	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3326	3630	3936	4243
TCR440	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3327	3631	3937	4244
TCR441	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3328	3632	3938	4245
TCR442	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3289	3598	3899	4211
TCR443	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3329	3633	3939	4246
TCR444	EVDPIGHLY (SEQ	A0101	3330	3634	3940	4247

TCR ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
	ID NO: 3051)					
TCR445	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3331	3635	3941	4248
TCR446	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3332	3636	3942	4249
TCR447	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3333	3637	3943	4250
TCR448	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3334	3638	3944	4251
TCR449	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3335	3639	3945	4252
TCR450	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3336	3640	3946	4253
TCR451	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3337	3641	3947	4254
TCR452	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3338	3642	3948	4255
TCR453	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3290	3596	3900	4209
TCR454	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3339	3643	3949	4256
TCR455	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3290	3601	3900	4214
TCR456	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3340	3644	3950	4257
TCR457	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3289	3611	3899	4224
TCR458	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3341	3645	3951	4258
TCR459	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3342	3646	3952	4259
TCR460	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3343	3647	3953	4260
TCR461	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3142	3648	3751	4261
TCR462	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3344	3649	3954	4262
TCR463	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3345	3650	3955	4263
TCR464	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3290	3614	3956	4264
TCR465	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3346	3651	3957	4265
TCR466	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3347	3652	3958	4266
TCR467	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3348	3653	3959	4267
TCR468	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3349	3654	3960	4268
TCR469	EVDPIGHLY (SEQ ID NO: 3051)	A0101	3350	3655	3961	4269

Table 12: CDR3 and V(D)J sequences of TCR clonotypes confirmed through cloning

TCR Clonotype ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR2	EVDPIGHLY (SEQ ID NO: 3051)	A0101	4273	4287	4302	4317
TCR4	EVDPIGHLY (SEQ ID NO: 3051)	A0101	4274	4288	4303	4318

TCR Clonotype ID #	PEPTIDE	HLA	ALPHA CDR3 (SEQ ID NO)	BETA CDR3 (SEQ ID NO)	FULL LENGTH ALPHA VJ (SEQ ID NO)	FULL LENGTH BETA V(D)J (SEQ ID NO)
TCR53	EVDPIGHLY (SEQ ID NO: 3051)	A0101	4275	4289	4304	4319
TCR54	EVDPIGHLY (SEQ ID NO: 3051)	A0101	4276	4290	4305	4320
TCR19	LLASSILCA (SEQ ID NO: 4270)	A0201	4277	4291	4306	4321
TCR21	LLASSILCA (SEQ ID NO: 4270)	A0201	4278	4292	4307	4322
TCR22	LLASSILCA (SEQ ID NO: 4270)	A0201	4279	4293	4308	4323
TCR18	LLASSILCA (SEQ ID NO: 4270)	A0201	4280	4294	4309	4324
TCR23	LLASSILCA (SEQ ID NO: 4270)	A0201	4281	4295	4310	4325
TCR26	GVYDGEEHSV (SEQ ID NO: 4271)	A0201	4282	4296	4311	4326
TCR28	GVYDGEEHSV (SEQ ID NO: 4271)	A0201	4283	4297	4312	4327
TCR29	GEMSSNSTAL (SEQ ID NO: 4272)	B4402	4284	4298	4313	4328
TCR30	GEMSSNSTAL (SEQ ID NO: 4272)	B4402	4285	4299	4314	4329
TCR32	GEMSSNSTAL (SEQ ID NO: 4272)	B4402	4286	4300	4315	4330
TCR33	GEMSSNSTAL (SEQ ID NO: 4272)	B4402	3138	4301	4316	4331

TABLE A

TABLE A					
Target	**HLA allele/peptide complex**	**SEQ ID NO**	**Protein Name**	**Ensembl id**	**Description**
1	HLA-A*01:01_EVDPIGHLY	1	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
2	HLA-A*29:02_FVQENYLEY	2	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
3	HLA-A*29:02_LVHFLLLKY	3	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
4	HLA-B*44:03_MEVDPIGHLY	4	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
5	HLA-B*35:01_FPVQATIDF	5	DSCR6	ENSG00000183145	Protein ripply3 (Down syndrome critical region protein 6)
6	HLA-A*26:01_EVDPIGHLY	1	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
7	HLA-A*26:01_EVDPIGHVY	6	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
8	HLA-A*29:02_FVQENYLEY	2	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
9	HLA-A*29:02_LVHFLLLKY	3	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
10	HLA-B*44:03_MEVDPIGHVY	7	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
11	HLA-C*02:02_AEMLGSVVGNW	8	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
12	HLA-C*02:02_AEMLGSVVGNW	8	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
13	HLA-A*01:01_EVDPIGHVY	6	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
14	HLA-B*44:02_AEMLERVIKNY	9	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
15	HLA-B*44:03_AEMLERVIKNY	9	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
16	HLA-C*02:02_AEMLERVIKNY	9	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
17	HLA-B*44:03_AETSYVKVL	10	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
18	HLA-A*02:01_ALLEEEEGV	11	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
19	HLA-A*01:01_EVDPASNTY	12	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
20	HLA-A*02:07_KVDELAHFL	13	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
21	HLA-A*30:02_RQVPGSNPARY	14	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
22	HLA-B*35:01_SALPTTISF	15	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
23	HLA-B*46:01_SALPTTISF	15	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)

24	HLA-A*02:07_KVDELAHFLL	16	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
25	HLA-A*02:01_ALFGLLVYL	17	CLD6	ENSG00000184697	Claudin-6 (Skullin)
26	HLA-A*11:01_STSAPAISR	18	CLD6	ENSG00000184697	Claudin-6 (Skullin)
27	HLA-C*02:02_KEVDPASNTY	19	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
28	HLA-B*44:02_AEMLGSVIRNF	20	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
29	HLA-C*02:02_AEMLGSVIRNF	20	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
30	HLA-A*03:01_GLLGDNQIMPK	21	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
31	HLA-B*44:02_AEMLGSVVGNW	8	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
32	HLA-B*27:02_PRALVETSY	22	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
33	HLA-A*01:01_NTDNNLAVY	23	KKLC1	ENSG00000204019	Kita-kyushu lung cancer antigen 1 (KK-LC-1) (Cancer/testis antigen 83)
34	HLA-B*44:03_AEMLGSVVGNW	8	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
35	HLA-B*44:02_AEMLGSVVGNW	8	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
36	HLA-B*44:02_AEMLESVIKNY	24	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
37	HLA-B*44:03_AEMLESVIKNY	24	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
38	HLA-C*02:02_AEMLESVIKNY	24	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
39	HLA-B*44:03_AETSYVKVL	10	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
40	HLA-B*18:01_EELSVMEVY	25	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
41	HLA-A*26:01_EVYDGREHSAY	26	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
42	HLA-A*33:01_EYVIKVSAR	27	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
43	HLA-A*02:01_KVLEYVIKV	28	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
44	HLA-A*02:07_KVLEYVIKV	28	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
45	HLA-A*29:02_LVGFLLLKY	29	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
46	HLA-B*35:01_SAFPTTINF	30	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
47	HLA-C*02:02_SAFPTTINF	30	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
48	HLA-A*29:02_LVHFLLLKY	3	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
49	HLA-A*30:02_STLPTTINY	31	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)

50	HLA-B*18:01_MEVDPIGHVY	7	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
51	HLA-B*51:01_DAAHPGPSV	32	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
52	HLA-B*35:01_FPMGTPDPEY	33	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
53	HLA-A*30:02_RVQHASPAGAY	34	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
54	HLA-A*02:07_SLDPSVTHL	35	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
55	HLA-A*30:02_VQHASPAGAY	36	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
56	HLA-A*30:02_EVDPIGHVY	6	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
57	HLA-A*29:02_IFLDFNHFY	37	PLCX2	ENSG00000240891	PI-PLC X domain-containing protein 2
58	HLA-A*29:02_LVQEKYLEY	38	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
59	HLA-A*30:02_RQVPDSDPARY	39	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
60	HLA-B*44:03_AEMLGSVVGNW	8	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
61	HLA-A*02:01_FLWGPRALIET	40	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
62	HLA-A*02:01_FLWGPRALVET	41	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
63	HLA-B*44:03_AEMLGSVIRNF	20	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
64	HLA-A*29:02_LVQENYLEY	42	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
65	HLA-A*26:01_EVLNAVGVY	43	MAGC2	ENSG00000046774	Melanoma-associated antigen C2 (Cancer/testis antigen 10) (CT10) (Hepatocellular carcinoma-associated antigen 587) (MAGE-C2 antigen) (MAGE-E1 antigen)
66	HLA-A*29:02_GAVSLLLRY	44	Q5T1G4	ENSG00000204179	Protein tyrosine phosphatase, non-receptor type 20A (Tyrosine-protein phosphatase non-receptor type 20) (Fragment)
67	HLA-A*02:07_LLDPVQRNL	45	ZN560	ENSG00000198028	Zinc finger protein 560
68	HLA-C*04:01_TFDSVAVEF	46	ZN560	ENSG00000198028	Zinc finger protein 560
69	HLA-A*01:01_YSDVMLENY	47	ZN560	ENSG00000198028	Zinc finger protein 560
70	HLA-A*02:07_TLDEKVAEL	48	MAGC2	ENSG00000046774	Melanoma-associated antigen C2 (Cancer/testis antigen 10) (CT10) (Hepatocellular carcinoma-associated antigen 587) (MAGE-C2 antigen) (MAGE-E1 antigen)
71	HLA-B*51:01_TAFIGNSI	49	CLD6	ENSG00000184697	Claudin-6 (Skullin)
72	HLA-A*11:01_STLPTTINY	31	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
73	HLA-C*04:01_AFDDIATYF	50	SSX1	ENSG00000126752	Protein SSX1 (Cancer/testis antigen 5.1) (CT5.1) (Synovial sarcoma, X breakpoint 1)
74	HLA-B*35:01_SPASDAYIVF	51	NACA2	ENSG00000253506	Nascent polypeptide-associated complex subunit alpha-2 (Alpha-NAC-like) (Hom s 2.01) (Nascent polypeptide-associated complex subunit alpha-like) (NAC-alpha-like)

75	HLA-A*30:02_VYKSPASDAY	52	NACA2	ENSG00000253506	Nascent polypeptide-associated complex subunit alpha-2 (Alpha-NAC-like) (Hom s 2.01) (Nascent polypeptide-associated complex subunit alpha-like) (NAC-alpha-like)
76	HLA-B*44:03_KEVDPASNTY	19	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
77	HLA-A*30:02_AMNSLSAMY	53	DMBX1	ENSG00000197587	Diencephalon/mesencephalon homeobox protein 1 (Orthodenticle homolog 3) (Paired-like homeobox protein DMBX1)
78	HLA-A*11:01_ASQEDILLK	54	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
79	HLA-A*11:01_ATMTQQLEK	55	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
80	HLA-B*44:03_EEIGVENIREF	56	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
81	HLA-A*11:01_GTVESISVKK	57	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
82	HLA-A*30:02_STSGELIGEY	58	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
83	HLA-A*24:02_VYIAELEKI	59	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
84	HLA-A*11:01_AGQDLSAYLLK	60	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
85	HLA-A*26:01_SVVAHLSTY	61	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
86	HLA-A*11:01_AAAGVSSTK	62	MAGB2	ENSG00000099399	Melanoma-associated antigen B2 (Cancer/testis antigen 3.2) (CT3.2) (DSS-AHC critical interval MAGE superfamily 6) (DAM6) (MAGE XP-2 antigen) (MAGE-B2 antigen)
87	HLA-A*30:02_KVNPNGHTY	63	MAGB2	ENSG00000099399	Melanoma-associated antigen B2 (Cancer/testis antigen 3.2) (CT3.2) (DSS-AHC critical interval MAGE superfamily 6) (DAM6) (MAGE XP-2 antigen) (MAGE-B2 antigen)
88	HLA-B*44:02_AEILESVIRNY	64	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
89	HLA-B*44:03_AEILESVIRNY	64	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
90	HLA-C*02:02_AEILESVIRNY	64	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
91	HLA-A*30:02_RQVPGSDPARY	65	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
92	HLA-C*01:02_SSPSVVASL	66	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
93	HLA-A*01:01_LLDPAQRNLY	67	ZN560	ENSG00000198028	Zinc finger protein 560
94	HLA-A*26:01_EVDPASNTY	12	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
95	HLA-A*26:01_FVQENYLEY	2	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
96	HLA-C*02:02_MEVDPIGHVY	7	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
97	HLA-C*16:01_SALPTTISF	15	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
98	HLA-A*01:01_LTDQPSAY	68	V9GYR9	ENSG00000225362	Cancer/testis antigen 62 (Fragment)
99	HLA-C*04:01_AFDVASFL	69	STRA8	ENSG00000146857	Stimulated by retinoic acid gene 8 protein homolog
100	HLA-A*30:02_SSLPTTMNY	70	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
101	HLA-B*44:03_EEIIPLNRIY	71	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
102	HLA-A*01:01_TSDTDVEVLY	72	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
103	HLA-A*29:02_TFQDIILEARY	73	DMBX1	ENSG00000197587	Diencephalon/mesencephalon homeobox protein 1 (Orthodenticle homolog 3) (Paired-like homeobox protein DMBX1)
104	HLA-A*29:02_YFVQENYLEY	74	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)

105	HLA-A*29:02_WVQENYLEY	75	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
106	HLA-A*33:01_EVRDYVEER	76	GBG1	ENSG00000127928	Guanine nucleotide-binding protein G(T) subunit gamma-T1 (Transducin gamma chain)
107	HLA-C*16:01_SAFPTTINF	30	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
108	HLA-A*02:07_ALFGLLVYL	17	CLD6	ENSG00000184697	Claudin-6 (Skullin)
109	HLA-A*02:01_VLTSGIVFV	77	CLD6	ENSG00000184697	Claudin-6 (Skullin)
110	HLA-B*35:01_FVQENYLEY	2	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
111	HLA-B*51:01_NALSSLKI	78	CX7B2	ENSG00000170516	Cytochrome c oxidase subunit 7B2, mitochondrial (Cytochrome c oxidase polypeptide VIIb2)
112	HLA-B*35:01_NAVLASGTAF	79	CX7B2	ENSG00000170516	Cytochrome c oxidase subunit 7B2, mitochondrial (Cytochrome c oxidase polypeptide VIIb2)
113	HLA-B*27:02_PRALVETSY	22	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
114	HLA-A*11:01_ASAPPQKQK	80	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
115	HLA-A*01:01_EIDNSELLY	81	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
116	HLA-A*02:07_KVDEAVAVL	82	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
117	HLA-A*33:01_NGKQIYVGR	83	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
118	HLA-B*51:01_SPAGPILSI	84	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
119	HLA-B*35:01_LPYASTLGY	85	SOX14	ENSG00000168875	Transcription factor SOX-14 (Protein SOX-28)
120	HLA-A*26:01_DVADKLVTF	86	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
121	HLA-A*11:01_GTVESISVK	87	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
122	HLA-B*18:01_IENQAVPAF	88	X6RD31	ENSG00000234068	P antigen family member 2 (Fragment)
123	HLA-A*03:01_AVLQKFLEH	89	MSLNL	ENSG00000162006	Mesothelin-like protein (Pre-pro-megakaryocyte-potentiating-factor-like)
124	HLA-B*35:01_QPAAPGPAL	90	MSLNL	ENSG00000162006	Mesothelin-like protein (Pre-pro-megakaryocyte-potentiating-factor-like)
125	HLA-B*18:01_DEDQAMRAF	91	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
126	HLA-B*35:01_NPIGDTGVKF	92	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
127	HLA-C*05:01_NADLQSEF	93	V9GYR9	ENSG00000225362	Cancer/testis antigen 62 (Fragment)
128	HLA-B*44:03_SEVSFLEYY	94	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
129	HLA-A*02:01_SLSNRLYYL	95	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
130	HLA-B*44:02_AEMLESVIKNY	24	A0A075B7A9	ENSG00000267978	Melanoma-associated antigen 9 (Fragment)
131	HLA-B*44:03_AEMLESVIKNY	24	A0A075B7A9	ENSG00000267978	Melanoma-associated antigen 9 (Fragment)
132	HLA-C*02:02_AEMLESVIKNY	24	A0A075B7A9	ENSG00000267978	Melanoma-associated antigen 9 (Fragment)
133	HLA-A*02:01_GVYDGEEHSV	96	MAGB2	ENSG00000099399	Melanoma-associated antigen B2 (Cancer/testis antigen 3.2) (CT3.2) (DSS-AHC critical interval MAGE superfamily 6) (DAM6) (MAGE XP-2 antigen) (MAGE-B2 antigen)
134	HLA-B*51:01_DANFIPTV	97	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
135	HLA-A*30:02_SSLPTTMNY	70	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
136	HLA-B*44:03_EELGVMGVY	98	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
137	HLA-B*51:01_YPREGSEV	99	FOXI3	ENSG00000214336	Forkhead box protein I3

138	HLA-B*27:02_GLLGDNQIMPK	21	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
139	HLA-A*11:01_ATDLHGVSR	100	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
140	HLA-B*44:02_TEQLTITGKKW	101	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
141	HLA-B*44:03_TEQLTITGKKW	101	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
142	HLA-B*44:02_AEIEPVSAVW	102	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
143	HLA-B*44:03_AEIEPVSAVW	102	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
144	HLA-C*02:02_AEIEPVSAVW	102	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
145	HLA-B*44:02_SEQQLSQKVF	103	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
146	HLA-B*44:03_SEQQLSQKVF	103	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
147	HLA-C*02:02_SEQQLSQKVF	103	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
148	HLA-A*01:01_LLDPVQRNLY	104	ZN560	ENSG00000198028	Zinc finger protein 560
149	HLA-A*29:02_LYSDINITY	105	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
150	HLA-C*05:01_YADLSPNEL	106	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
151	HLA-B*51:01_YPFKPKLTI	107	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
152	HLA-A*01:01_YSDINITYVNY	108	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
153	HLA-A*01:01_YSDINITY	109	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
154	HLA-A*31:01_QVKIWFQNR	110	NKX12	ENSG00000229544	NK1 transcription factor-related protein 2 (Homeobox protein SAX-1) (NKX-1.1)
155	HLA-B*51:01_TPFYAPRL	111	NKX12	ENSG00000229544	NK1 transcription factor-related protein 2 (Homeobox protein SAX-1) (NKX-1.1)
156	HLA-A*11:01_GTMKIHILQK	112	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
157	HLA-A*29:02_SYFITSLSY	113	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
158	HLA-B*35:01_SALDESNTY	114	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
159	HLA-B*18:01_IESEPLFTY	115	MAGC1	ENSG00000155495	Melanoma-associated antigen C1 (Cancer/testis antigen 7.1) (CT7.1) (MAGE-C1 antigen)
160	HLA-B*18:01_DEALGGTAF	116	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
161	HLA-A*26:01_EVQSDYSSY	117	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
162	HLA-A*29:02_GLFDVFLRF	118	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)

163	HLA-C*01:02_VVIEQSSSL	119	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
164	HLA-A*11:01_SALGVTITK	120	ROP1A	ENSG00000065371	Ropporin-1A (Cancer/testis antigen 91) (CT91) (Rhophilin-associated protein 1A)
165	HLA-A*11:01_GTASLTLPPK	121	CA094	ENSG00000142698	Uncharacterized protein C1orf94
166	HLA-B*44:03_VEVDGPELKF	122	CA094	ENSG00000142698	Uncharacterized protein C1orf94
167	HLA-B*51:01_DAYKFAADV	123	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
168	HLA-A*33:01_DVNNQLNSR	124	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
169	HLA-B*35:01_IPIEPVESM	125	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
170	HLA-A*11:01_SSQTAAQVTK	126	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
171	HLA-C*01:02_QSPQGASAL	127	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
172	HLA-B*46:01_AVLASGTAF	128	CX7B2	ENSG00000170516	Cytochrome c oxidase subunit 7B2, mitochondrial (Cytochrome c oxidase polypeptide VIIb2)
173	HLA-A*26:01_EVVEGKEWGSF	129	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
174	HLA-A*01:01_NSAINPLIY	130	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
175	HLA-A*29:02_RYLQVVLLY	131	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
176	HLA-A*29:02_FQNPHGETLLY	132	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
177	HLA-A*11:01_SVMDLVGSILK	133	LDHC	ENSG00000166796	L-lactate dehydrogenase C chain (LDH-C) (EC 1.1.1.27) (Cancer/testis antigen 32) (CT32) (LDH testis subunit) (LDH-X)
178	HLA-A*33:01_EVRDMSEHVTR	134	PAGE5	ENSG00000158639	P antigen family member 5 (PAGE-5) (Cancer/testis antigen 16.1) (CT16.1) (G antigen family E member 1) (Prostate-associated gene 5 protein)
179	HLA-A*30:02_AALASVGHLY	135	ONEC3	ENSG00000205922	One cut domain family member 3 (One cut homeobox 3) (Transcription factor ONECUT-3) (OC-3)
180	HLA-A*01:01_VTESESGSPEY	136	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
181	HLA-A*02:07_SIDWFMVTV	137	PLAC1	ENSG00000170965	Placenta-specific protein 1
182	HLA-B*18:01_LEEEVVTF	138	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
183	HLA-A*26:01_FVQENYLEY	2	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
184	HLA-A*29:02_LVQEKYLEY	38	MAGB2	ENSG00000099399	Melanoma-associated antigen B2 (Cancer/testis antigen 3.2) (CT3.2) (DSS-AHC critical interval MAGE superfamily 6) (DAM6) (MAGE XP-2 antigen) (MAGE-B2 antigen)
185	HLA-B*35:01_NASGPDPAL	139	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
186	HLA-C*01:02_QSPQGASSL	140	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
187	HLA-B*44:03_SESEMFPKF	141	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)

188	HLA-A*29:02_NFQGIRFHY	142	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
189	HLA-B*51:01_DAAVTHSI	143	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
190	HLA-A*24:02_LYKPDSNEF	144	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
191	HLA-B*35:01_MAAAGIPSM	145	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
192	HLA-B*35:01_MAAGGIPSM	146	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
193	HLA-B*35:01_MAATPIPAM	147	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
194	HLA-B*44:03_NEFAVGTKNY	148	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
195	HLA-C*02:02_NEFAVGTKNY	148	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
196	HLA-A*24:02_QYAAVTHNI	149	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
197	HLA-A*03:01_SLFRAVITK	150	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
198	HLA-A*29:02_FFLPVSVVY	151	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
199	HLA-A*24:02_IYGFFNENF	152	NPFF2	ENSG00000056291	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)
200	HLA-A*33:01_DYIHKNDNVQR	153	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
201	HLA-C*02:02_SALPTTISF	15	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
202	HLA-B*51:01_IPALPLPTI	154	DPPA2	ENSG00000163530	Developmental pluripotency-associated protein 2 (Pluripotent embryonic stem cell-related gene 1 protein)
203	HLA-A*11:01_STSDVKLEK	155	DPPA2	ENSG00000163530	Developmental pluripotency-associated protein 2 (Pluripotent embryonic stem cell-related gene 1 protein)
204	HLA-B*44:03_AEARPVPHW	156	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
205	HLA-B*35:01_MPAVKNVISY	157	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
206	HLA-B*46:01_SAFPTTINF	30	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
207	HLA-B*35:01_SPFSGGPVSF	158	P5F1B	ENSG00000212993	Putative POU domain, class 5, transcription factor 1B (Oct4-pg1) (Octamer-binding protein 3-like) (Octamer-binding transcription factor 3-like)
208	HLA-B*35:01_TAAPATLEL	159	MESP2	ENSG00000188095	Mesoderm posterior protein 2 (Class C basic helix-loop-helix protein 6) (bHLHc6)
209	HLA-B*46:01_TAAAPGSPF	160	NKX12	ENSG00000229544	NK1 transcription factor-related protein 2 (Homeobox protein SAX-1) (NKX-1.1)
210	HLA-B*46:01_IAKVTGVAF	161	J3KR52	ENSG00000185055	EF-hand calcium-binding domain-containing protein 10
211	HLA-A*11:01_ALAETSYVK	162	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
212	HLA-A*30:02_AMIENFNAKY	163	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)
213	HLA-B*18:01_DEDGKIVGY	164	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)
214	HLA-A*26:01_DVPHGHITSL	165	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)

215	HLA-B*35:01_LPENYQMKY	166	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)
216	HLA-A*02:07_ALLEEEEGV	11	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
217	HLA-B*51:01_DAVVIALV	167	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
218	HLA-A*26:01_EVVGVVYVY	168	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
219	HLA-B*35:01_EVVGVVYVY	168	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
220	HLA-B*51:01_FPYLVLTI	169	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
221	HLA-A*29:02_ILLFWKPLRY	170	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
222	HLA-B*18:01_LEVVGVVY	171	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
223	HLA-A*29:02_LLFWKPLRY	172	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
224	HLA-B*51:01_LPQTPLVI	173	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
225	HLA-B*46:01_VAIDQYNTF	174	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
226	HLA-A*01:01_ITDPTDPVDY	175	DCC	ENSG00000187323	Netrin receptor DCC (Colorectal cancer suppressor) (Immunoglobulin superfamily DCC subclass member 1) (Tumor suppressor protein DCC)
227	HLA-A*02:07_LLPASSFSV	176	DCC	ENSG00000187323	Netrin receptor DCC (Colorectal cancer suppressor) (Immunoglobulin superfamily DCC subclass member 1) (Tumor suppressor protein DCC)
228	HLA-A*02:01_SIWEGLVTV	177	DCC	ENSG00000187323	Netrin receptor DCC (Colorectal cancer suppressor) (Immunoglobulin superfamily DCC subclass member 1) (Tumor suppressor protein DCC)
229	HLA-A*30:02_IVNPPPPEY	178	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
230	HLA-A*02:01_FLAPLSFYL	179	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
231	HLA-A*29:02_VNTNVVLRY	180	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
232	HLA-B*18:01_NEFAVGTKNY	148	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
233	HLA-A*11:01_ASVEASKLK	181	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
234	HLA-A*26:01_EVISVQMSM	182	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
235	HLA-B*35:01_TATLLIVRY	183	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
236	HLA-B*44:02_TEDPTGHFLW	184	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)

237	HLA-B*44:03_TEDPTGHFLW	184	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
238	HLA-B*08:01_TIKTKYVL	185	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
239	HLA-B*18:01_YEVISVQM	186	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
240	HLA-A*02:07_ALDPPVDVFV	187	LN28A	ENSG00000131914	Protein lin-28 homolog A (Lin-28A) (Zinc finger CCHC domain-containing protein 1)
241	HLA-B*35:01_HAGEDVAVF	188	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
242	HLA-C*02:02_AETSYVKVL	10	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
243	HLA-A*29:02_AFGDILHRY	189	TRI51	ENSG00000124900	Tripartite motif-containing protein 51 (SPRY domain-containing protein 5)
244	HLA-A*26:01_ENVPLIGKY	190	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
245	HLA-A*11:01_SSIFGLAPGK	191	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
246	HLA-B*51:01_LPTDLFNSV	192	ROP1A	ENSG00000065371	Ropporin-1A (Cancer/testis antigen 91) (CT91) (Rhophilin-associated protein 1A)
247	HLA-A*33:01_DTFSYPIER	193	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
248	HLA-A*26:01_EVPSGVIPNL	194	MAGC2	ENSG00000046774	Melanoma-associated antigen C2 (Cancer/testis antigen 10) (CT10) (Hepatocellular carcinoma-associated antigen 587) (MAGE-C2 antigen) (MAGE-E1 antigen)
249	HLA-A*24:02_LYATVIHDI	195	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
250	HLA-B*35:01_FVQENYLEY	2	MAGA3	ENSG00000221867	Melanoma-associated antigen 3 (Antigen MZ2-D) (Cancer/testis antigen 1.3) (CT1.3) (MAGE-3 antigen)
251	HLA-A*11:01_SSYNRGLISK	196	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
252	HLA-A*02:07_ALDESNTYQL	197	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
253	HLA-B*44:02_AEQRDDILYF	198	CRLF2	ENSG00000205755	Cytokine receptor-like factor 2 (Cytokine receptor-like 2) (IL-XR) (Thymic stromal lymphopoietin protein receptor) (TSLP receptor)
254	HLA-B*44:03_AEQRDDILYF	198	CRLF2	ENSG00000205755	Cytokine receptor-like factor 2 (Cytokine receptor-like 2) (IL-XR) (Thymic stromal lymphopoietin protein receptor) (TSLP receptor)
255	HLA-A*02:01_FLWGPRALAET	199	MAGA4	ENSG00000147381	Melanoma-associated antigen 4 (Cancer/testis antigen 1.4) (CT1.4) (MAGE-4 antigen) (MAGE-41 antigen) (MAGE-X2 antigen)
256	HLA-A*11:01_IVQEPTEEK	200	X6RD31	ENSG00000234068	P antigen family member 2 (Fragment)
257	HLA-B*44:03_EESVLVGYVDY	201	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
258	HLA-B*08:01_EVKARTQEL	202	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
259	HLA-A*11:01_SSDSESEMFPK	203	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
260	HLA-B*35:01_DANFIPTVY	204	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
261	HLA-B*44:03_QESDLRLFL	205	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
262	HLA-A*01:01_YSEKISYVY	206	SSX1	ENSG00000126752	Protein SSX1 (Cancer/testis antigen 5.1) (CT5.1) (Synovial sarcoma, X breakpoint 1)
263	HLA-A*03:01_RVHPVSTMVK	207	LDHC	ENSG00000166796	L-lactate dehydrogenase C chain (LDH-C) (EC 1.1.1.27) (Cancer/testis antigen 32) (CT32) (LDH testis subunit) (LDH-X)
264	HLA-B*44:03_AEDEDGKIVGY	208	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)

265	HLA-B*44:03_EEPLSVTAKY	209	VCX1	ENSG00000182583	Variable charge X-linked protein 1 (Variable charge protein on X with ten repeats) (VCX-10r) (Variably charged protein X-B1) (VCX-B1)
266	HLA-A*29:02_AFLEVVGVVY	210	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
267	HLA-A*29:02_ILTDINWRF	211	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
268	HLA-B*18:01_SEDPILTAF	212	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
269	HLA-B*44:03_SEDPILTAF	212	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
270	HLA-B*44:03_EETPFSRLI	213	INSL6	ENSG00000120210	Insulin-like peptide INSL6 (Insulin-like peptide 6) (Relaxin/insulin-like factor 1) [Cleaved into: Insulin-like peptide INSL6 B chain; Insulin-like peptide INSL6 A chain]
271	HLA-A*24:02_VYIHENAKF	214	INSL6	ENSG00000120210	Insulin-like peptide INSL6 (Insulin-like peptide 6) (Relaxin/insulin-like factor 1) [Cleaved into: Insulin-like peptide INSL6 B chain; Insulin-like peptide INSL6 A chain]
272	HLA-C*01:02_ITPQRQSAL	215	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
273	HLA-B*51:01_EPYPVTKNI	216	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
274	HLA-B*35:01_IAAAFAVDY	217	X6RE50	ENSG00000004809	Solute carrier family 22 member 16 (Fragment)
275	HLA-B*35:01_MPLEVYEM	218	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
276	HLA-B*44:03_AEATQSMNAKY	219	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
277	HLA-C*02:02_AEATQSMNAKY	219	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
278	HLA-A*30:02_ATQSMNAKY	220	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
279	HLA-A*02:07_KLDTVGVFL	221	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
280	HLA-B*44:03_EEIENLYRF	222	MEIG1	ENSG00000197889	Meiosis expressed gene 1 protein homolog
281	HLA-A*29:02_VLLDEGAMLLY	223	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
282	HLA-B*44:03_EEFQVLVKKI	224	S100G	ENSG00000169906	Protein S100-G (Calbindin-D9k) (S100 calcium-binding protein G) (Vitamin D-dependent calcium-binding protein, intestinal) (CABP)
283	HLA-A*02:07_TLDDLFQEL	225	S100G	ENSG00000169906	Protein S100-G (Calbindin-D9k) (S100 calcium-binding protein G) (Vitamin D-dependent calcium-binding protein, intestinal) (CABP)
284	HLA-C*04:01_TYDGMLSDV	226	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
285	HLA-B*18:01_TEFVGATM	227	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
286	HLA-C*01:02_QSPQGASSL	140	MAGA6	ENSG00000197172	Melanoma-associated antigen 6 (Cancer/testis antigen 1.6) (CT1.6) (MAGE-6 antigen) (MAGE3B antigen)
287	HLA-B*51:01_IPFTPPTV	228	A0A1B0GTJ6	ENSG00000268655	HCG1796489
288	HLA-A*11:01_TVADPLPQVAK	229	A0A1B0GTJ6	ENSG00000268655	HCG1796489
289	HLA-A*02:01_TVADPLPQV	230	A0A1B0GTJ6	ENSG00000268655	HCG1796489
290	HLA-A*29:02_GYLVVGFVY	231	X6RE50	ENSG00000004809	Solute carrier family 22 member 16 (Fragment)

291	HLA-A*30:02_GQNLSIHSGQY	232	CRSPL	ENSG00000101074	Peptidase inhibitor R3HDML (Cysteine-rich secretory protein R3HDML)
292	HLA-A*30:02_SVYPPAANMEY	233	CRSPL	ENSG00000101074	Peptidase inhibitor R3HDML (Cysteine-rich secretory protein R3HDML)
293	HLA-A*11:01_SSSSPISNK	234	DMRT1	ENSG00000137090	Doublesex- and mab-3-related transcription factor 1 (DM domain expressed in testis protein 1)
294	HLA-A*29:02_FLSSLFPFRY	235	MAJIN	ENSG00000168070	Membrane-anchored junction protein
295	HLA-B*18:01_QELEVGKEAY	236	MAJIN	ENSG00000168070	Membrane-anchored junction protein
296	HLA-B*44:03_QELEVGKEAY	236	MAJIN	ENSG00000168070	Membrane-anchored junction protein
297	HLA-C*02:02_QELEVGKEAY	236	MAJIN	ENSG00000168070	Membrane-anchored junction protein
298	HLA-B*44:02_SEQPPASLGF	237	MAJIN	ENSG00000168070	Membrane-anchored junction protein
299	HLA-B*44:03_SEQPPASLGF	237	MAJIN	ENSG00000168070	Membrane-anchored junction protein
300	HLA-C*02:02_SEQPPASLGF	237	MAJIN	ENSG00000168070	Membrane-anchored junction protein
301	HLA-B*44:03_GELREISGNQY	238	PDCL2	ENSG00000163440	Phosducin-like protein 2
302	HLA-A*26:01_EVKKEYASM	239	STRA8	ENSG00000146857	Stimulated by retinoic acid gene 8 protein homolog
303	HLA-A*33:01_DYFPVILKR	240	MAGC2	ENSG00000046774	Melanoma-associated antigen C2 (Cancer/testis antigen 10) (CT10) (Hepatocellular carcinoma-associated antigen 587) (MAGE-C2 antigen) (MAGE-E1 antigen)
304	HLA-B*44:03_KEGEPVEFTF	241	LN28B	ENSG00000187772	Protein lin-28 homolog B (Lin-28B)
305	HLA-A*11:01_TVAVTQMNK	242	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
306	HLA-A*02:07_VLDEVDAAL	243	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
307	HLA-A*26:01_DVRIEVGLY	244	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
308	HLA-B*35:01_HPFKPDATY	245	PO4F1	ENSG00000152192	POU domain, class 4, transcription factor 1 (Brain-specific homeobox/POU domain protein 3A) (Brain-3A) (Brn-3A) (Homeobox/POU domain protein RDC-1) (Oct-T1)
309	HLA-A*11:01_AVLSAGPIITR	246	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
310	HLA-A*26:01_DTPDPPTIISY	247	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
311	HLA-B*35:01_FPAERDISVY	248	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
312	HLA-A*26:01_STIPGVSAY	249	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
313	HLA-B*46:01_STIPGVSAY	249	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
314	HLA-A*30:02_AGMTIATSY	250	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
315	HLA-A*33:01_DSLAAVVLQNR	251	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
316	HLA-A*03:01_GTGIAGITK	252	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
317	HLA-A*11:01_GTGIAGITK	252	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
318	HLA-A*11:01_GTGTGIAGITK	253	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
319	HLA-B*18:01_IEAELHISY	254	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
320	HLA-B*44:03_IEAELHISY	254	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env

					polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
321	HLA-B*51:01_LPLTGPLV	255	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
322	HLA-A*01:01_TVDSNQQTY	256	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
323	HLA-A*24:02_TYQTYTHNQF	257	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
324	HLA-B*51:01_DPFFKQQAV	258	ADAM2	ENSG00000104755	Disintegrin and metalloproteinase domain-containing protein 2 (ADAM 2) (Cancer/testis antigen 15) (CT15) (Fertilin subunit beta) (PH-30) (PH30) (PH30-beta)
325	HLA-B*44:03_GEANELLHTF	259	ADAM2	ENSG00000104755	Disintegrin and metalloproteinase domain-containing protein 2 (ADAM 2) (Cancer/testis antigen 15) (CT15) (Fertilin subunit beta) (PH-30) (PH30) (PH30-beta)
326	HLA-C*04:01_NFDSLPVQI	260	ADAM2	ENSG00000104755	Disintegrin and metalloproteinase domain-containing protein 2 (ADAM 2) (Cancer/testis antigen 15) (CT15) (Fertilin subunit beta) (PH-30) (PH30) (PH30-beta)
327	HLA-A*11:01_ATAQPSQVRQK	261	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
328	HLA-A*11:01_SVLSEQFTK	262	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
329	HLA-A*33:01_DIQEPYYGR	263	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
330	HLA-A*01:01_TSDIQEPYY	264	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
331	HLA-A*02:07_FLPDAFVTM	265	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
332	HLA-A*29:02_IFAHLGLDY	266	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
333	HLA-A*02:01_KLFTSVFGV	267	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
334	HLA-C*04:01_YYDLVESTF	268	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
335	HLA-B*08:01_YPVTKNISL	269	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
336	HLA-B*18:01_SEVSFLEY	270	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
337	HLA-A*11:01_ITWDAPAITK	271	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
338	HLA-B*44:03_TEVVEGKEW	272	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
339	HLA-C*02:02_VAIDQYNTF	174	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)

340	HLA-B*35:01_DAWGGNTAY	273	CRBA4	ENSG00000196431	Beta-crystallin A4 (Beta-A4 crystallin)
341	HLA-B*08:01_YPAERLTSF	274	CRBA4	ENSG00000196431	Beta-crystallin A4 (Beta-A4 crystallin)
342	HLA-B*44:03_EEVSNLVNY	275	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
343	HLA-B*18:01_IEAGTSESY	276	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
344	HLA-B*44:03_IEAGTSESY	276	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
345	HLA-A*29:02_IFSNWGHPKY	277	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
346	HLA-A*11:01_VTMEHISEK	278	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
347	HLA-A*02:01_YLSEALQEA	279	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
348	HLA-A*26:01_EVVGELVAKF	280	TFDP3	ENSG00000183434	Transcription factor Dp family member 3 (Cancer/testis antigen 30) (CT30) (Hepatocellular carcinoma-associated antigen 661)
349	HLA-A*02:01_GMMDDYTYV	281	NKAI3	ENSG00000185942	Sodium/potassium-transporting ATPase subunit beta-1-interacting protein 3 (Na(+)/K(+)-transporting ATPase subunit beta-1-interacting protein 3) (Protein FAM77D)
350	HLA-B*44:03_AEMAVGLVVF	282	COX8C	ENSG00000187581	Cytochrome c oxidase subunit 8C, mitochondrial (Cytochrome c oxidase polypeptide 8 isoform 3) (Cytochrome c oxidase polypeptide VIII isoform 3) (COX VIII-3) (Cytochrome c oxidase subunit 8-3) (COX8-3) (Cytochrome c oxidase subunit VIIIC)
351	HLA-C*02:02_AEMAVGLVVF	282	COX8C	ENSG00000187581	Cytochrome c oxidase subunit 8C, mitochondrial (Cytochrome c oxidase polypeptide 8 isoform 3) (Cytochrome c oxidase polypeptide VIII isoform 3) (COX VIII-3) (Cytochrome c oxidase subunit 8-3) (COX8-3) (Cytochrome c oxidase subunit VIIIC)
352	HLA-B*44:03_SENDIPSVAF	283	DC4L2	ENSG00000176566	DDB1- and CUL4-associated factor 4-like protein 2 (WD repeat-containing protein 21C)
353	HLA-A*33:01_NNFPHSIAR	284	KKLC1	ENSG00000204019	Kita-kyushu lung cancer antigen 1 (KK-LC-1) (Cancer/testis antigen 83)
354	HLA-A*31:01_RGNEVISVMNR	285	PPBN	ENSG00000163286	Alkaline phosphatase, placental-like (EC 3.1.3.1) (ALP-1) (Alkaline phosphatase Nagao isozyme) (Germ cell alkaline phosphatase) (GCAP) (Placental alkaline phosphatase-like) (PLAP-like)
355	HLA-A*11:01_KTYETNLEIKK	286	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
356	HLA-A*11:01_AALDNTNIGK	287	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
357	HLA-A*29:02_ALASVGHLY	288	ONEC3	ENSG00000205922	One cut domain family member 3 (One cut homeobox 3) (Transcription factor ONECUT-3) (OC-3)
358	HLA-A*26:01_EVSNKIVGY	289	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
359	HLA-A*29:02_SFLDASFVY	290	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
360	HLA-A*11:01_TVSQAKVQVNK	291	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
361	HLA-A*26:01_ELKQDISSF	292	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
362	HLA-B*18:01_VENEFKAEY	293	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
363	HLA-A*29:02_SFSNVWHLY	294	VRTN	ENSG00000133980	Vertnin
364	HLA-A*03:01_ATAQPSQVRQK	261	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
365	HLA-B*51:01_DAAINSHI	295	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
366	HLA-A*29:02_VALENFFRY	296	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
367	HLA-B*44:03_AEMLTNVISRY	297	MAGC1	ENSG00000155495	Melanoma-associated antigen C1 (Cancer/testis antigen 7.1) (CT7.1) (MAGE-C1 antigen)

368	HLA-B*44:03_DEDGKIVGY	164	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)
369	HLA-A*11:01_KTLGKIAEK	298	SG1D1	ENSG00000168515	Secretoglobin family 1D member 1 (Lipophilin-A)
370	HLA-A*24:02_YYDLVESTF	268	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
371	HLA-A*30:02_AQAFTSGKY	299	TRI51	ENSG00000124900	Tripartite motif-containing protein 51 (SPRY domain-containing protein 5)
372	HLA-B*18:01_DEEDMQAVETY	300	PDCL2	ENSG00000163440	Phosducin-like protein 2
373	HLA-A*30:02_STKSVSTSY	301	5HT1F	ENSG00000179097	5-hydroxytryptamine receptor 1F (5-HT-1F) (5-HT1F) (Serotonin receptor 1F)
374	HLA-A*02:01_LVIDTVTEV	302	SPERT	ENSG00000174015	Spermatid-associated protein (Protein chibby homolog 2)
375	HLA-C*05:01_VIDTVTEV	303	SPERT	ENSG00000174015	Spermatid-associated protein (Protein chibby homolog 2)
376	HLA-B*51:01_YPLNRFSSV	304	SPERT	ENSG00000174015	Spermatid-associated protein (Protein chibby homolog 2)
377	HLA-B*35:01_YPAERLTSF	274	CRBA4	ENSG00000196431	Beta-crystallin A4 (Beta-A4 crystallin)
378	HLA-B*18:01_TEIVLENNY	305	R4GMQ3	ENSG00000107831	Fibroblast growth factor 8
379	HLA-A*01:01_YTALQNAKY	306	R4GMQ3	ENSG00000107831	Fibroblast growth factor 8
380	HLA-A*33:01_DSFQKVILR	307	ZN728	ENSG00000269067	Zinc finger protein 728
381	HLA-B*44:03_SEPQIVPITF	308	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
382	HLA-B*44:02_EEIIPLNRIY	71	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
383	HLA-A*24:02_IYTGVTVSF	309	LMIP	ENSG00000105370	Lens fiber membrane intrinsic protein (MP18) (MP19) (MP20)
384	HLA-A*29:02_SFAHQGLWRY	310	LMIP	ENSG00000105370	Lens fiber membrane intrinsic protein (MP18) (MP19) (MP20)
385	HLA-B*44:03_EEIPQEIQRL	311	LRIQ4	ENSG00000188306	Leucine-rich repeat and IQ domain-containing protein 4 (Leucine-rich repeat-containing protein 64)
386	HLA-A*01:01_YIENNHLEY	312	LRIQ4	ENSG00000188306	Leucine-rich repeat and IQ domain-containing protein 4 (Leucine-rich repeat-containing protein 64)
387	HLA-A*01:01_HSEELDPQKY	313	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
388	HLA-B*44:02_AEMLESVIKNY	24	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
389	HLA-B*44:03_AEMLESVIKNY	24	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
390	HLA-C*02:02_AEMLESVIKNY	24	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
391	HLA-B*44:03_AETSYVKVL	10	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
392	HLA-A*02:01_ALDEKVAEL	314	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
393	HLA-A*02:07_ALDEKVAEL	314	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
394	HLA-A*02:01_GLYDGREHSV	315	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
395	HLA-B*44:03_SESSTILVVRY	316	SPNXB	ENSG00000227234	Sperm protein associated with the nucleus on the X chromosome B1 (Cancer/testis antigen 11.2) (CT11.2) (Nuclear-associated protein SPAN-Xb) (SPANX-B) (SPANX family member B1) (SPANX family member F1)
396	HLA-A*01:01_QTEFPTTYY	317	GFY	ENSG00000261949	Golgi-associated olfactory signaling regulator (Protein Goofy)
397	HLA-B*18:01_TEFPTTYY	318	GFY	ENSG00000261949	Golgi-associated olfactory signaling regulator (Protein Goofy)
398	HLA-A*01:01_TSDPQISTSLY	319	GFY	ENSG00000261949	Golgi-associated olfactory signaling regulator (Protein Goofy)
399	HLA-A*02:07_VLDEEVSNL	320	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
400	HLA-B*46:01_FLITQATAY	321	NBPF4	ENSG00000196427	Neuroblastoma breakpoint family member 4
401	HLA-A*30:02_ALQGALGLY	322	PPAT	ENSG00000142513	Testicular acid phosphatase (EC 3.1.3.2)
402	HLA-B*51:01_YPMDPHKEV	323	PPAT	ENSG00000142513	Testicular acid phosphatase (EC 3.1.3.2)

403	HLA-B*51:01_LAFLVGQSI	324	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
404	HLA-B*35:01_MPSEVSEVL	325	E9PRF5	ENSG00000233436	BTB/POZ domain-containing protein 18 (Fragment)
405	HLA-A*02:07_KLFTSVFGV	267	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
406	HLA-B*35:01_TAAAFTISY	326	S22AD	ENSG00000172940	Solute carrier family 22 member 13 (Organic cation transporter-like 3) (ORCTL-3)
407	HLA-A*29:02_FFLHPISFY	327	MBOA4	ENSG00000177669	Ghrelin O-acyltransferase (EC 2.3.1.-) (Membrane-bound O-acyltransferase domain-containing protein 4) (O-acyltransferase domain-containing protein 4)
408	HLA-A*11:01_ASQISSETLIK	328	DPPA3	ENSG00000187569	Developmental pluripotency-associated protein 3 (Stella-related protein)
409	HLA-A*11:01_ASALFQSNK	329	RNS10	ENSG00000182545	Inactive ribonuclease-like protein 10
410	HLA-B*18:01_SEESVLVGY	330	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
411	HLA-A*26:01_ETSYVKVLEY	331	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
412	HLA-B*18:01_DEGISSLF	332	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
413	HLA-A*03:01_KVNSPIRMK	333	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
414	HLA-B*35:01_LPYDIINAF	334	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
415	HLA-C*05:01_NVDEGISSL	335	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
416	HLA-A*11:01_SVLQQLTPMNK	336	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
417	HLA-B*35:01_TPIQTSLAY	337	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
418	HLA-B*35:01_EALTPHSSY	338	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
419	HLA-A*01:01_FTEIVLENNY	339	R4GMQ3	ENSG00000107831	Fibroblast growth factor 8
420	HLA-B*44:03_AEVPIEPHW	340	GCNT7	ENSG00000124091	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 (EC 2.4.1.-)
421	HLA-B*35:01_LPFTIISM	341	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
422	HLA-B*35:01_DPSQFNPTY	342	DPPA3	ENSG00000187569	Developmental pluripotency-associated protein 3 (Stella-related protein)
423	HLA-B*44:03_AEILKNEAY	343	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
424	HLA-C*02:02_AEILKNEAY	343	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
425	HLA-B*44:02_AENQGLVLKF	344	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
426	HLA-B*44:03_AENQGLVLKF	344	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
427	HLA-A*02:01_ALFETLIQL	345	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
428	HLA-A*26:01_ESIEYVQTF	346	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
429	HLA-A*26:01_EVIPITNSEL	347	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
430	HLA-B*51:01_LPALKIVMI	348	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
431	HLA-B*18:01_NEMSVISNM	349	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
432	HLA-A*01:01_NTEGLHHLY	350	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
433	HLA-A*24:02_NYIIKGNLF	351	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3

434	HLA-A*02:01_QIADIVTSV	352	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
435	HLA-C*01:02_VIPITNSEL	353	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
436	HLA-B*18:01_SENDIPSVAF	283	DC4L2	ENSG00000176566	DDB1- and CUL4-associated factor 4-like protein 2 (WD repeat-containing protein 21C)
437	HLA-C*01:02_AAPAGPGEL	354	FOXI3	ENSG00000214336	Forkhead box protein I3
438	HLA-C*02:02_AESSSKRSF	355	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
439	HLA-B*18:01_TEFVGATMF	356	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
440	HLA-A*29:02_VYVGDALLY	357	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
441	HLA-B*51:01_HPLNGQPLI	358	LUZP4	ENSG00000102021	Leucine zipper protein 4 (Cancer/testis antigen 28) (CT-28) (CT28) (Tumor antigen HOM-TES-85)
442	HLA-A*02:07_LLDGFMITL	359	PASD1	ENSG00000166049	Circadian clock protein PASD1 (Cancer/testis antigen 63) (CT63) (OX-TES-1) (PAS domain-containing protein 1)
443	HLA-A*24:02_VYQKIILKF	360	PASD1	ENSG00000166049	Circadian clock protein PASD1 (Cancer/testis antigen 63) (CT63) (OX-TES-1) (PAS domain-containing protein 1)
444	HLA-B*35:01_EPLSVTASY	361	VCX3	ENSG00000169059	Variable charge X-linked protein 3 (Variable charge protein on X with eight repeats) (VCX-8r) (Variably charged protein X-A) (VCX-A)
445	HLA-B*51:01_DAFVPFSI	362	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
446	HLA-A*26:01_ETVSTTLRY	363	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
447	HLA-A*01:01_GTETVSTTLRY	364	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
448	HLA-A*02:01_FLWGPRALVET	41	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
449	HLA-A*11:01_AVNPELAPVMK	365	SPT22	ENSG00000141255	Spermatogenesis-associated protein 22 (Testis development protein NYD-SP20)
450	HLA-C*16:01_SAVTPGPYY	366	SPT22	ENSG00000141255	Spermatogenesis-associated protein 22 (Testis development protein NYD-SP20)
451	HLA-A*31:01_RVQVWFQNR	367	ALX3	ENSG00000156150	Homeobox protein aristaless-like 3 (Proline-rich transcription factor ALX3)
452	HLA-A*02:07_KMAELVHFL	368	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
453	HLA-A*29:02_IFINKEDSLLY	369	C295L	ENSG00000178404	CEP295 N-terminal-like protein (KIAA1731 N-terminal like protein)
454	HLA-A*02:01_GLWEIENNPTV	370	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
455	HLA-A*03:01_SAYGMPMYK	371	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
456	HLA-A*11:01_SAYGMPMYK	371	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
457	HLA-B*35:01_AAAAAAATY	372	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
458	HLA-A*03:01_RVAVPVLVK	373	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
459	HLA-A*30:02_SQFPHGAMGSY	374	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
460	HLA-B*51:01_DAVAAMSV	375	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
461	HLA-A*29:02_NWAPPEYYLY	376	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
462	HLA-B*18:01_TEETIKAEF	377	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
463	HLA-A*29:02_WAPPEYYLY	378	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
464	HLA-C*02:02_KEVDPTGHSF	379	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)

465	HLA-B*18:01_DEEQNLVAF	380	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
466	HLA-B*44:03_EEAANSGYSW	381	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
467	HLA-C*02:02_EEAANSGYSW	381	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
468	HLA-B*44:03_EEQNLVAFQY	382	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
469	HLA-A*11:01_STEDEEQLLQK	383	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
470	HLA-C*16:01_ASIDREIAM	384	PRD13	ENSG00000112238	PR domain zinc finger protein 13 (EC 2.1.1.-) (PR domain-containing protein 13)
471	HLA-A*03:01_RLGPVPGTFK	385	PRD13	ENSG00000112238	PR domain zinc finger protein 13 (EC 2.1.1.-) (PR domain-containing protein 13)
472	HLA-A*11:01_SSSQTAAQVTK	386	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
473	HLA-B*44:02_AEMAVGLVVF	282	COX8C	ENSG00000187581	Cytochrome c oxidase subunit 8C, mitochondrial (Cytochrome c oxidase polypeptide 8 isoform 3) (Cytochrome c oxidase polypeptide VIII isoform 3) (COX VIII-3) (Cytochrome c oxidase subunit 8-3) (COX8-3) (Cytochrome c oxidase subunit VIIIC)
474	HLA-A*02:07_FLDLQVNSL	387	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
475	HLA-A*29:02_VLREIEDEWLY	388	DPPA3	ENSG00000187569	Developmental pluripotency-associated protein 3 (Stella-related protein)
476	HLA-B*18:01_DESITFHSI	389	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
477	HLA-B*18:01_EEVARFLTY	390	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
478	HLA-B*44:03_EEVARFLTY	390	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
479	HLA-A*26:01_EVASAVSAF	391	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
480	HLA-A*02:07_LLPGSIHFV	392	PTX4	ENSG00000251692	Pentraxin-4
481	HLA-B*44:03_EEQLLQKVM	393	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
482	HLA-A*02:07_KVLEFLAKV	394	MAGB2	ENSG00000099399	Melanoma-associated antigen B2 (Cancer/testis antigen 3.2) (CT3.2) (DSS-AHC critical interval MAGE superfamily 6) (DAM6) (MAGE XP-2 antigen) (MAGE-B2 antigen)
483	HLA-A*02:07_SLDDIIIYKEL	395	LUZP4	ENSG00000102021	Leucine zipper protein 4 (Cancer/testis antigen 28) (CT-28) (CT28) (Tumor antigen HOM-TES-85)
484	HLA-B*44:03_KEGEAVEFTF	396	LN28A	ENSG00000131914	Protein lin-28 homolog A (Lin-28A) (Zinc finger CCHC domain-containing protein 1)
485	HLA-B*18:01_DEGAMLLY	397	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
486	HLA-A*11:01_KTYETNLEIK	398	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
487	HLA-A*01:01_LLDEGAMLLY	399	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)

488	HLA-B*35:01_TPLVIAISY	400	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
489	HLA-B*44:03_VEVGEVKSW	401	RFPLB	ENSG00000251258	Ret finger protein-like 4B (RING finger protein 211)
490	HLA-C*02:02_VEVGEVKSW	401	RFPLB	ENSG00000251258	Ret finger protein-like 4B (RING finger protein 211)
491	HLA-B*44:03_WEVEVGEVKSW	402	RFPLB	ENSG00000251258	Ret finger protein-like 4B (RING finger protein 211)
492	HLA-A*26:01_TTAPGTVHSY	403	Q5JUY5	ENSG00000117400	Thrombopoietin receptor
493	HLA-C*16:01_ASSQVPRVM	404	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
494	HLA-A*01:01_WSDSSVTTY	405	CD051	ENSG00000237136	Uncharacterized protein C4orf51
495	HLA-C*02:02_KAFDDIATY	406	SSX1	ENSG00000126752	Protein SSX1 (Cancer/testis antigen 5.1) (CT5.1) (Synovial sarcoma, X breakpoint 1)
496	HLA-A*29:02_HVSNLVFAY	407	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
497	HLA-A*29:02_ILGSVWLAY	408	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
498	HLA-B*44:03_KEFGGPFFW	409	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
499	HLA-B*35:01_LPFTIPTSM	410	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
500	HLA-A*11:01_VVNQGKGMFK	411	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
501	HLA-A*24:02_VYGAFPVQL	412	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
502	HLA-A*01:01_YTSDGNTKY	413	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
503	HLA-A*24:02_VYGSYLYKL	414	DPPA5	ENSG00000203909	Developmental pluripotency-associated 5 protein (hDPPA5) (Embryonal stem cell-specific gene 1 protein) (ESG-1)
504	HLA-A*30:02_QISEVEPKY	415	NAA11	ENSG00000156269	N-alpha-acetyltransferase 11 (EC 2.3.1.255) (N-terminal acetyltransferase complex ARD1 subunit homolog B) (hARD2) (NatA catalytic subunit Naa11)
505	HLA-A*29:02_HAPNLPYRY	416	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
506	HLA-B*35:01_LPFDGSPKITY	417	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
507	HLA-B*51:01_LPFDGSPKI	418	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
508	HLA-A*11:01_SVIGGPSTYK	419	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
509	HLA-A*03:01_TIYNTTQPRQK	420	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
510	HLA-B*35:01_EAFLSPEY	421	PPAT	ENSG00000142513	Testicular acid phosphatase (EC 3.1.3.2)
511	HLA-C*16:01_AAMNIARAL	422	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
512	HLA-A*11:01_ASYEIGYILK	423	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
513	HLA-A*26:01_EVVGGAVRVQY	424	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
514	HLA-B*46:01_LVKEGLASY	425	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
515	HLA-A*02:01_ALYDGLTLV	426	VRTN	ENSG00000133980	Vertnin

516	HLA-A*02:01_SLLKLIVEL	427	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
517	HLA-B*35:01_IASNYNVSY	428	PTX4	ENSG00000251692	Pentraxin-4
518	HLA-A*30:02_RQAPGSDPVRY	429	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
519	HLA-B*44:02_AEMLTNVISRY	297	MAGC1	ENSG00000155495	Melanoma-associated antigen C1 (Cancer/testis antigen 7.1) (CT7.1) (MAGE-C1 antigen)
520	HLA-B*46:01_STKSVSTSY	301	5HT1F	ENSG00000179097	5-hydroxytryptamine receptor 1F (5-HT-1F) (5-HT1F) (Serotonin receptor 1F)
521	HLA-B*35:01_MAATGVSSM	430	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
522	HLA-A*33:01_DTSPLLLGR	431	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
523	HLA-A*29:02_HVSPSPLIY	432	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
524	HLA-B*35:01_HVSPSPLIY	432	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
525	HLA-A*29:02_WVNGLTLRY	433	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
526	HLA-A*11:01_GTISFVQYK	434	J3KR52	ENSG00000185055	EF-hand calcium-binding domain-containing protein 10
527	HLA-C*04:01_AFVTMTGGF	435	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
528	HLA-A*29:02_NLWEKKGLLLY	436	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
529	HLA-A*26:01_EVISQLTRV	437	SYCY1	ENSG00000242950	Syncytin-1 (Endogenous retrovirus group W member 1) (Env-W) (Envelope polyprotein gPr73) (Enverin) (HERV-7q Envelope protein) (HERV-W envelope protein) (HERV-W_7q21.2 provirus ancestral Env polyprotein) (Syncytin) [Cleaved into: Surface protein (SU) (gp50); Transmembrane protein (TM) (gp24)]
530	HLA-A*01:01_YTEQDLYSY	438	SYCY1	ENSG00000242950	Syncytin-1 (Endogenous retrovirus group W member 1) (Env-W) (Envelope polyprotein gPr73) (Enverin) (HERV-7q Envelope protein) (HERV-W envelope protein) (HERV-W_7q21.2 provirus ancestral Env polyprotein) (Syncytin) [Cleaved into: Surface protein (SU) (gp50); Transmembrane protein (TM) (gp24)]
531	HLA-A*24:02_NYFLDPVTI	439	TRI51	ENSG00000124900	Tripartite motif-containing protein 51 (SPRY domain-containing protein 5)
532	HLA-A*02:07_AVDEESPFL	440	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
533	HLA-B*51:01_TPYHLSTVV	441	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
534	HLA-A*01:01_NLDHYTNAY	442	GLYL3	ENSG00000203972	Glycine N-acyltransferase-like protein 3 (EC 2.3.1.-)
535	HLA-B*51:01_DAFDVASFL	443	STRA8	ENSG00000146857	Stimulated by retinoic acid gene 8 protein homolog
536	HLA-A*29:02_RTFPITGLRY	444	DYTN	ENSG00000232125	Dystrotelin
537	HLA-A*01:01_FTEEDLHFVLY	445	PRD14	ENSG00000147596	PR domain zinc finger protein 14 (EC 2.1.1.-) (PR domain-containing protein 14)
538	HLA-A*29:02_IFVSPKGVLAY	446	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
539	HLA-B*44:03_QEGQLPLLF	447	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
540	HLA-A*02:01_LLAQQPIYV	448	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
541	HLA-B*51:01_LPFTIISM	341	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)

542	HLA-A*11:01_AVIEHMQEK	449	AXDN1	ENSG00000162779	Axonemal dynein light chain domain-containing protein 1
543	HLA-B*44:03_EEIIKNIQKLY	450	AXDN1	ENSG00000162779	Axonemal dynein light chain domain-containing protein 1
544	HLA-A*02:01_YLIDHPVSL	451	AXDN1	ENSG00000162779	Axonemal dynein light chain domain-containing protein 1
545	HLA-A*02:07_YLIDHPVSL	451	AXDN1	ENSG00000162779	Axonemal dynein light chain domain-containing protein 1
546	HLA-A*24:02_IYISNSIYF	452	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
547	HLA-A*11:01_VVTGNVPLK	453	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
548	HLA-A*11:01_ASMSLPPPK	454	U3KQD4	ENSG00000105549	Testicular haploid-expressed gene protein (Theg homolog (Mouse), isoform CRA_a)
549	HLA-C*16:01_VASPRIISL	455	U3KQD4	ENSG00000105549	Testicular haploid-expressed gene protein (Theg homolog (Mouse), isoform CRA_a)
550	HLA-A*29:02_MILDNHALY	456	TDT	ENSG00000107447	DNA nucleotidylexotransferase (EC 2.7.7.31) (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase)
551	HLA-A*02:07_TLDEKVDEL	457	MAGC1	ENSG00000155495	Melanoma-associated antigen C1 (Cancer/testis antigen 7.1) (CT7.1) (MAGE-C1 antigen)
552	HLA-B*35:01_LAFGGHIAF	458	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
553	HLA-A*30:02_ALASVGHLY	288	ONEC3	ENSG00000205922	One cut domain family member 3 (One cut homeobox 3) (Transcription factor ONECUT-3) (OC-3)
554	HLA-B*35:01_APLGAAAAY	459	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
555	HLA-A*29:02_GLFTHTIFY	460	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
556	HLA-B*51:01_VPKAKIITI	461	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
557	HLA-A*01:01_HTEDKPYKY	462	ZN729	ENSG00000196350	Zinc finger protein 729
558	HLA-A*01:01_HSDSERQYY	463	FGF16	ENSG00000196468	Fibroblast growth factor 16 (FGF-16)
559	HLA-A*02:07_SLDWDLHGF	464	FGF16	ENSG00000196468	Fibroblast growth factor 16 (FGF-16)
560	HLA-A*31:01_QVKIWFQNR	110	HXB1	ENSG00000120094	Homeobox protein Hox-B1 (Homeobox protein Hox-2I)
561	HLA-A*11:01_TSLDVPLIGK	465	ACHB4	ENSG00000117971	Neuronal acetylcholine receptor subunit beta-4
562	HLA-B*44:03_EEDLHFVLY	466	PRD14	ENSG00000147596	PR domain zinc finger protein 14 (EC 2.1.1.-) (PR domain-containing protein 14)
563	HLA-B*46:01_SVVAHLSTY	61	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
564	HLA-B*44:03_SEAQDKSKLW	467	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)
565	HLA-A*29:02_AVYNGQWKY	468	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
566	HLA-A*11:01_SVTSVFDEK	469	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
567	HLA-A*02:01_ALMEVTVYL	470	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
568	HLA-B*44:03_EELANVLPISY	471	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)

569	HLA-B*44:03_SEAGLTANQY	472	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
570	HLA-C*02:02_SEAGLTANQY	472	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
571	HLA-A*29:02_VFYILQLAY	473	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
572	HLA-A*11:01_STVDPMKLYEK	474	GCM1	ENSG00000137270	Chorion-specific transcription factor GCMa (hGCMa) (GCM motif protein 1) (Glial cells missing homolog 1)
573	HLA-B*35:01_SAVTPGPYY	366	SPT22	ENSG00000141255	Spermatogenesis-associated protein 22 (Testis development protein NYD-SP20)
574	HLA-A*02:07_YLDLRNTGL	475	LRC52	ENSG00000162763	Leucine-rich repeat-containing protein 52 (BK channel auxiliary gamma subunit LRRC52)
575	HLA-A*11:01_ATIDVTTVER	476	PCDC1	ENSG00000248383	Protocadherin alpha-C1 (PCDH-alpha-C1)
576	HLA-B*51:01_DPLELHKI	477	PCDC1	ENSG00000248383	Protocadherin alpha-C1 (PCDH-alpha-C1)
577	HLA-A*02:07_TVADPLPQV	230	A0A1B0GTJ6	ENSG00000268655	HCG1796489
578	HLA-B*35:01_SPEAGLAEY	478	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
579	HLA-B*51:01_IPMDGTAVI	479	CALI	ENSG00000185972	Calicin
580	HLA-A*01:01_GSEVSFLEY	480	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
581	HLA-B*44:02_KEFGGPFFW	409	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
582	HLA-A*11:01_AAGALPLLK	481	GSX2	ENSG00000180613	GS homeobox 2 (Genetic-screened homeobox 2) (Homeobox protein GSH-2)
583	HLA-A*11:01_ATYLNLSEK	482	GSX2	ENSG00000180613	GS homeobox 2 (Genetic-screened homeobox 2) (Homeobox protein GSH-2)
584	HLA-B*51:01_MPPPLVMSV	483	GSX2	ENSG00000180613	GS homeobox 2 (Genetic-screened homeobox 2) (Homeobox protein GSH-2)
585	HLA-A*31:01_QVKIWFQNR	110	GSX2	ENSG00000180613	GS homeobox 2 (Genetic-screened homeobox 2) (Homeobox protein GSH-2)
586	HLA-B*51:01_VPPWNPQLI	484	ADIG	ENSG00000182035	Adipogenin
587	HLA-C*04:01_MFDNGSFL	485	FOXE3	ENSG00000186790	Forkhead box protein E3 (Forkhead-related protein FKHL12) (Forkhead-related transcription factor 8) (FREAC-8)
588	HLA-A*11:01_KSGDLVFAK	486	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
589	HLA-A*31:01_ATKSGLVVR	487	GCNT7	ENSG00000124091	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 (EC 2.4.1.-)
590	HLA-B*51:01_LAPPIGNSI	488	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
591	HLA-B*44:03_EEGEDRDGHAW	489	NALP7	ENSG00000167634	NACHT, LRR and PYD domains-containing protein 7 (Nucleotide-binding oligomerization domain protein 12) (PYRIN-containing APAF1-like protein 3)
592	HLA-A*24:02_EYLKDPVTI	490	TRI60	ENSG00000176979	Tripartite motif-containing protein 60 (RING finger protein 129) (RING finger protein 33)
593	HLA-B*44:03_SEFEQIRLF	491	TRI60	ENSG00000176979	Tripartite motif-containing protein 60 (RING finger protein 129) (RING finger protein 33)
594	HLA-B*18:01_SEVSFLEYY	94	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
595	HLA-A*11:01_AGISSTITR	492	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
596	HLA-B*18:01_EETRVLAF	493	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
597	HLA-A*11:01_SSEQSPLQK	494	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
598	HLA-A*02:01_ALYSGDLHAA	495	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
599	HLA-B*18:01_EEFSLQKSY	496	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
600	HLA-B*44:03_EEFSLQKSY	496	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
601	HLA-C*02:02_EEFSLQKSY	496	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
602	HLA-A*02:07_FLDSLLATL	497	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
603	HLA-B*35:01_HAEDISNIM	498	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1

604	HLA-A*11:01_STVGFGDVVAK	499	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
605	HLA-B*35:01_TAFSTGTVF	500	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
606	HLA-A*02:07_TVDSVTAFL	501	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
607	HLA-A*11:01_GVAALTPVQK	502	ANHX	ENSG00000227059	Anomalous homeobox protein
608	HLA-A*02:01_HLLDNADVAL	503	ANHX	ENSG00000227059	Anomalous homeobox protein
609	HLA-A*02:07_LLDNADVAL	504	ANHX	ENSG00000227059	Anomalous homeobox protein
610	HLA-C*02:02_IEAELHISY	254	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
611	HLA-B*18:01_TETPGTAY	505	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
612	HLA-C*01:02_TGPSGNAL	506	S22AD	ENSG00000172940	Solute carrier family 22 member 13 (Organic cation transporter-like 3) (ORCTL-3)
613	HLA-A*11:01_ASFLTTVFK	507	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
614	HLA-A*24:02_IYIGNIEHL	508	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
615	HLA-B*51:01_DAFPISLI	509	CXA10	ENSG00000135355	Gap junction alpha-10 protein (Connexin-62) (Cx62)
616	HLA-A*30:02_KTLAEISDRY	510	X1WI33	ENSG00000170788	DPY30 domain-containing protein 1 (Fragment)
617	HLA-A*11:01_VTMEQLRQK	511	X1WI33	ENSG00000170788	DPY30 domain-containing protein 1 (Fragment)
618	HLA-B*08:01_HAYHKVTL	512	CF010	ENSG00000204296	Uncharacterized protein C6orf10
619	HLA-A*01:01_QSEMYISRY	513	CF010	ENSG00000204296	Uncharacterized protein C6orf10
620	HLA-A*01:01_SSEQSARLLDY	514	CF010	ENSG00000204296	Uncharacterized protein C6orf10
621	HLA-A*11:01_ATAQPSQVR	515	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
622	HLA-A*26:01_DIISEQKVSEF	516	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
623	HLA-A*02:01_ALLGILISV	517	IZUM2	ENSG00000161652	Izumo sperm-egg fusion protein 2
624	HLA-A*24:02_LYTKAHETF	518	MSLNL	ENSG00000162006	Mesothelin-like protein (Pre-pro-megakaryocyte-potentiating-factor-like)
625	HLA-A*24:02_SYLLGWTTF	519	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
626	HLA-C*02:02_AEIEPVSAV	520	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
627	HLA-A*11:01_VIIDHGSGFLK	521	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
628	HLA-B*51:01_MPYTEAVI	522	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
629	HLA-B*35:01_LPVPLDSAF	523	ASCL4	ENSG00000187855	Achaete-scute homolog 4 (ASH-4) (hASH4) (Achaete-scute-like protein 4) (Class A basic helix-loop-helix protein 44) (bHLHa44)
630	HLA-B*44:03_QELLERQAW	524	ASCL4	ENSG00000187855	Achaete-scute homolog 4 (ASH-4) (hASH4) (Achaete-scute-like protein 4) (Class A basic helix-loop-helix protein 44) (bHLHa44)
631	HLA-B*51:01_DAYLSYTKV	525	IRPL2	ENSG00000189108	X-linked interleukin-1 receptor accessory protein-like 2 (IL-1 receptor accessory protein-like 2) (IL-1-RAPL-2) (IL-1RAPL-2) (IL1RAPL-2) (IL1RAPL-2-related protein) (Interleukin-1 receptor 9) (IL-1R-9) (IL-1R9) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1)
632	HLA-A*11:01_STNLKMVSK	526	IRPL2	ENSG00000189108	X-linked interleukin-1 receptor accessory protein-like 2 (IL-1 receptor accessory protein-like 2) (IL-1-RAPL-2) (IL-1RAPL-2) (IL1RAPL-2) (IL1RAPL-2-related protein) (Interleukin-1 receptor 9) (IL-1R-9) (IL-1R9) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1)
633	HLA-A*02:07_ALDPPVDVF	527	LN28A	ENSG00000131914	Protein lin-28 homolog A (Lin-28A) (Zinc finger CCHC domain-containing protein 1)

634	HLA-B*35:01_YPLSPTISL	528	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
635	HLA-A*03:01_HILTHANTNK	529	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
636	HLA-A*26:01_SVTTYTGSY	530	CD051	ENSG00000237136	Uncharacterized protein C4orf51
637	HLA-A*29:02_AFLIIVFSY	531	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
638	HLA-A*29:02_FFVGIFDIKY	532	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
639	HLA-A*29:02_FVGIFDIKY	533	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
640	HLA-A*02:07_ILDDNPITRI	534	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
641	HLA-A*24:02_LYTLTTNFF	535	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
642	HLA-B*35:01_MPLTDGISSF	536	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
643	HLA-B*44:03_TEDIGSKGY	537	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
644	HLA-A*29:02_GYWGVRLKY	538	KCNV2	ENSG00000168263	Potassium voltage-gated channel subfamily V member 2 (Voltage-gated potassium channel subunit Kv8.2)
645	HLA-B*18:01_LEEKMIAAY	539	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
646	HLA-A*02:07_SLDEALQRV	540	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
647	HLA-A*29:02_AVWPLELAY	541	UBP41	ENSG00000161133	Putative ubiquitin carboxyl-terminal hydrolase 41 (EC 3.4.19.12) (Deubiquitinating enzyme 41) (Ubiquitin thioesterase 41) (Ubiquitin-specific-processing protease 41)
648	HLA-B*46:01_LAFGGHIAF	458	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
649	HLA-A*01:01_DTELGSSEY	542	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
650	HLA-A*02:07_GLPDIMKPIKL	543	GP139	ENSG00000180269	Probable G-protein coupled receptor 139 (G(q)-coupled orphan receptor GPRg1) (G-protein-coupled receptor PGR3)
651	HLA-B*51:01_LPANILTVI	544	GP139	ENSG00000180269	Probable G-protein coupled receptor 139 (G(q)-coupled orphan receptor GPRg1) (G-protein-coupled receptor PGR3)
652	HLA-A*02:01_SLAETPASA	545	GALP	ENSG00000197487	Galanin-like peptide
653	HLA-A*30:02_SIQQLVPEY	546	C144L	ENSG00000205212	Putative coiled-coil domain-containing protein 144 N-terminal-like
654	HLA-B*18:01_DELEKQIVY	547	E9PBZ7	ENSG00000242715	Coiled-coil domain-containing protein 169
655	HLA-B*51:01_FPLPLAREV	548	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)

656	HLA-A*11:01_SSMALPSPHK	549	FOXR1	ENSG00000176302	Forkhead box protein R1 (Forkhead box protein N5)
657	HLA-A*26:01_DVAEAIAFF	550	A0A1B0GVH6	ENSG00000226792	Long intergenic non-protein coding RNA 371
658	HLA-A*26:01_DTAVLITRY	551	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
659	HLA-C*04:01_NFDGATTL	552	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
660	HLA-A*03:01_STNLPLTQK	553	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
661	HLA-A*11:01_STNLPLTQK	553	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
662	HLA-A*24:02_NYFIDPVTI	554	TRI48	ENSG00000150244	Tripartite motif-containing protein 48 (RING finger protein 101)
663	HLA-B*51:01_DPITFSFI	555	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
664	HLA-A*26:01_EVISVQVQDV	556	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
665	HLA-A*02:01_SLFESLEYL	557	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
666	HLA-B*46:01_FLITQATAY	321	NBPF6	ENSG00000186086	Neuroblastoma breakpoint family member 6
667	HLA-A*03:01_RTFPITGLRY	444	DYTN	ENSG00000232125	Dystrotelin
668	HLA-C*02:02_AELQASLSKY	558	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
669	HLA-A*29:02_IFSDQETFY	559	PRD14	ENSG00000147596	PR domain zinc finger protein 14 (EC 2.1.1.-) (PR domain-containing protein 14)
670	HLA-A*03:01_AVYNSPQFKK	560	FBX39	ENSG00000177294	F-box only protein 39
671	HLA-A*11:01_AVYNSPQFKK	560	FBX39	ENSG00000177294	F-box only protein 39
672	HLA-A*11:01_AVYNSPQFK	561	FBX39	ENSG00000177294	F-box only protein 39
673	HLA-B*51:01_SAYGNATSV	562	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
674	HLA-A*26:01_FTVDSNQQTY	563	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
675	HLA-A*30:02_AVAPHHSGVY	564	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
676	HLA-A*11:01_SVSIIGFHK	565	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
677	HLA-A*31:01_QSFPPKVNR	566	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
678	HLA-A*02:01_FIHEDLNTV	567	RNS10	ENSG00000182545	Inactive ribonuclease-like protein 10
679	HLA-A*29:02_NFFEEVFIY	568	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
680	HLA-B*44:02_EEMQIQKSQW	569	NTM2G	ENSG00000188152	NUT family member 2G
681	HLA-B*44:03_EEMQIQKSQW	569	NTM2G	ENSG00000188152	NUT family member 2G
682	HLA-A*01:01_TSDPGLLSY	570	NTM2G	ENSG00000188152	NUT family member 2G
683	HLA-B*18:01_EESVLVGY	571	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
684	HLA-B*51:01_DAHNTHVGI	572	WNT9B	ENSG00000158955	Protein Wnt-9b (Protein Wnt-14b) (Protein Wnt-15)
685	HLA-A*29:02_GFKETAFLY	573	WNT9B	ENSG00000158955	Protein Wnt-9b (Protein Wnt-14b) (Protein Wnt-15)
686	HLA-A*24:02_VYMEDSPSF	574	WNT9B	ENSG00000158955	Protein Wnt-9b (Protein Wnt-14b) (Protein Wnt-15)

687	HLA-A*11:01_AVAAKMEVK	575	SG1D1	ENSG00000168515	Secretoglobin family 1D member 1 (Lipophilin-A)
688	HLA-A*29:02_AFLKMIYSY	576	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
689	HLA-B*18:01_NEAKFITF	577	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
690	HLA-B*51:01_LPKLPKPYI	578	PSG1	ENSG00000231924	Pregnancy-specific beta-1-glycoprotein 1 (PS-beta-G-1) (PSBG-1) (Pregnancy-specific glycoprotein 1) (CD66 antigen-like family member F) (Fetal liver non-specific cross-reactive antigen 1/2) (FL-NCA-1/2) (PSG95) (Pregnancy-specific beta-1 glycoprotein C/D) (PS-beta-C/D) (CD antigen CD66f)
691	HLA-B*51:01_LPTTAQVTI	579	PSG1	ENSG00000231924	Pregnancy-specific beta-1-glycoprotein 1 (PS-beta-G-1) (PSBG-1) (Pregnancy-specific glycoprotein 1) (CD66 antigen-like family member F) (Fetal liver non-specific cross-reactive antigen 1/2) (FL-NCA-1/2) (PSG95) (Pregnancy-specific beta-1 glycoprotein C/D) (PS-beta-C/D) (CD antigen CD66f)
692	HLA-B*51:01_LPYYSTSII	580	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
693	HLA-B*51:01_LPYYSTSI	581	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
694	HLA-A*11:01_VTLAKPVNK	582	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
695	HLA-A*11:01_STEPGISNIK	583	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
696	HLA-A*03:01_VVTGNVPLK	453	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
697	HLA-A*30:02_DLNDVTHVY	584	DDX53	ENSG00000184735	Probable ATP-dependent RNA helicase DDX53 (EC 3.6.4.13) (Cancer-associated gene protein) (Cancer/testis antigen 26) (CT26) (DEAD box protein 53) (DEAD box protein CAGE)
698	HLA-A*31:01_RVQVWFQNR	367	ESX1	ENSG00000123576	Homeobox protein ESX1 (Extraembryonic, spermatogenesis, homeobox 1) [Cleaved into: Homeobox protein ESX1-N; Homeobox protein ESX1-C]
699	HLA-A*03:01_KLFIPQITTK	585	PSG8	ENSG00000124467	Pregnancy-specific beta-1-glycoprotein 8 (PS-beta-G-8) (PSBG-8) (Pregnancy-specific glycoprotein 8)
700	HLA-B*51:01_LPKLPKPYI	578	PSG8	ENSG00000124467	Pregnancy-specific beta-1-glycoprotein 8 (PS-beta-G-8) (PSBG-8) (Pregnancy-specific glycoprotein 8)
701	HLA-B*51:01_YPKLPKPYI	586	PSG8	ENSG00000124467	Pregnancy-specific beta-1-glycoprotein 8 (PS-beta-G-8) (PSBG-8) (Pregnancy-specific glycoprotein 8)
702	HLA-B*35:01_LPLVTVVY	587	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
703	HLA-A*24:02_NYGVLHVTF	588	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
704	HLA-B*18:01_DETEIRSFF	589	DAZL	ENSG00000092345	Deleted in azoospermia-like (DAZ homolog) (DAZ-like autosomal) (Deleted in azoospermia-like 1) (SPGY-like-autosomal)
705	HLA-B*18:01_DETEIRSF	590	DAZL	ENSG00000092345	Deleted in azoospermia-like (DAZ homolog) (DAZ-like autosomal) (Deleted in azoospermia-like 1) (SPGY-like-autosomal)
706	HLA-B*35:01_SPVQVITGY	591	DAZL	ENSG00000092345	Deleted in azoospermia-like (DAZ homolog) (DAZ-like autosomal) (Deleted in azoospermia-like 1) (SPGY-like-autosomal)
707	HLA-B*51:01_DAYIPGGPLTV	592	OVOL3	ENSG00000105261	Putative transcription factor ovo-like protein 3
708	HLA-A*30:02_KVHGQPASYAY	593	OVOL3	ENSG00000105261	Putative transcription factor ovo-like protein 3
709	HLA-A*30:02_KVHGQPASY	594	OVOL3	ENSG00000105261	Putative transcription factor ovo-like protein 3

710	HLA-B*35:01_SPAPSLESY	595	MSGN1	ENSG00000151379	Mesogenin-1 (Paraxial mesoderm-specific mesogenin1) (pMesogenin1) (pMsgn1)
711	HLA-A*02:01_TLADALHTL	596	MSGN1	ENSG00000151379	Mesogenin-1 (Paraxial mesoderm-specific mesogenin1) (pMesogenin1) (pMsgn1)
712	HLA-B*51:01_LPAVQAPVI	597	TEKT5	ENSG00000153060	Tektin-5
713	HLA-B*08:01_YSAARAVSL	598	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
714	HLA-A*24:02_VYFGHDSELF	599	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
715	HLA-B*51:01_IGYVTPDI	600	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
716	HLA-B*51:01_LPLQFLVV	601	WFD13	ENSG00000168634	WAP four-disulfide core domain protein 13
717	HLA-B*51:01_LPPTSSISI	602	AR13A	ENSG00000174225	ADP-ribosylation factor-like protein 13A
718	HLA-A*24:02_PYPDVTFTL	603	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
719	HLA-B*44:03_GEYPDYQQW	604	CRGB	ENSG00000182187	Gamma-crystallin B (Gamma-B-crystallin) (Gamma-crystallin 1-2)
720	HLA-C*02:02_GEYPDYQQW	604	CRGB	ENSG00000182187	Gamma-crystallin B (Gamma-B-crystallin) (Gamma-crystallin 1-2)
721	HLA-B*35:01_MPVPGQHSM	605	AMELX	ENSG00000125363	Amelogenin, X isoform
722	HLA-C*16:01_AAVQRAAEL	606	TF2LX	ENSG00000153779	Homeobox protein TGIF2LX (TGF-beta-induced transcription factor 2-like protein) (TGFB-induced factor 2-like protein, X-linked) (TGIF-like on the X)
723	HLA-A*29:02_AIFQGYFAY	607	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
724	HLA-A*11:01_AQFSSSAIQK	608	SOX14	ENSG00000168875	Transcription factor SOX-14 (Protein SOX-28)
725	HLA-A*29:02_AFAPTFLVY	609	S22AO	ENSG00000197658	Solute carrier family 22 member 24
726	HLA-B*51:01_DAVRIKTSI	610	S22AO	ENSG00000197658	Solute carrier family 22 member 24
727	HLA-B*51:01_FPILAVPVI	611	S22AO	ENSG00000197658	Solute carrier family 22 member 24
728	HLA-C*16:01_SASVHHNEL	612	S22AO	ENSG00000197658	Solute carrier family 22 member 24
729	HLA-A*11:01_SVSGLVLSH	613	S22AO	ENSG00000197658	Solute carrier family 22 member 24
730	HLA-B*35:01_HPAVTPDAY	614	AP2D	ENSG00000008197	Transcription factor AP-2-delta (AP2-delta) (Activating enhancer-binding protein 2-delta) (Transcription factor AP-2-beta-like 1)
731	HLA-B*35:01_SVANSTVAY	615	AP2D	ENSG00000008197	Transcription factor AP-2-delta (AP2-delta) (Activating enhancer-binding protein 2-delta) (Transcription factor AP-2-beta-like 1)
732	HLA-A*01:01_YSSSSPLTY	616	AP2D	ENSG00000008197	Transcription factor AP-2-delta (AP2-delta) (Activating enhancer-binding protein 2-delta) (Transcription factor AP-2-beta-like 1)
733	HLA-B*51:01_DAPPAILTF	617	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
734	HLA-B*18:01_EEIAFSTY	618	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
735	HLA-A*26:01_EINPHMSSY	619	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
736	HLA-A*11:01_SSYVPIFEK	620	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
737	HLA-A*11:01_STIDEYVHR	621	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
738	HLA-A*11:01_STMGGFGVGK	622	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
739	HLA-A*02:07_TIDEYVHRI	623	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
740	HLA-A*30:02_TLNNNIAKAGY	624	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)

741	HLA-A*11:01_AISITPVHK	625	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
742	HLA-B*44:03_AESPLEVPQSF	626	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
743	HLA-A*02:07_ALDQKVAFL	627	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
744	HLA-A*26:01_EVLNLTGVY	628	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
745	HLA-A*29:02_LFIKLGLTY	629	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
746	HLA-A*29:02_SLAEQILAKY	630	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
747	HLA-A*11:01_SSSSEQSPLQK	631	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
748	HLA-B*51:01_LPNTSIHGI	632	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
749	HLA-B*51:01_YPNSPVQVI	633	DAZL	ENSG00000092345	Deleted in azoospermia-like (DAZ homolog) (DAZ-like autosomal) (Deleted in azoospermia-like 1) (SPGY-like-autosomal)
750	HLA-B*35:01_HAAGFGPEL	634	MBOA4	ENSG00000177669	Ghrelin O-acyltransferase (EC 2.3.1.-) (Membrane-bound O-acyltransferase domain-containing protein 4) (O-acyltransferase domain-containing protein 4)
751	HLA-A*29:02_GVLILLVRY	635	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
752	HLA-A*02:01_GLYGINEDIFL	636	LDH6A	ENSG00000166800	L-lactate dehydrogenase A-like 6A (EC 1.1.1.27)
753	HLA-B*46:01_LMIPNITQY	637	LDH6A	ENSG00000166800	L-lactate dehydrogenase A-like 6A (EC 1.1.1.27)
754	HLA-A*11:01_SVADLTESILK	638	LDH6A	ENSG00000166800	L-lactate dehydrogenase A-like 6A (EC 1.1.1.27)
755	HLA-A*02:01_TLWEIQKELKL	639	LDH6A	ENSG00000166800	L-lactate dehydrogenase A-like 6A (EC 1.1.1.27)
756	HLA-B*35:01_MPHEVTHSM	640	V9GZ31	ENSG00000177414	Ubiquitin-conjugating enzyme E2 U (Fragment)
757	HLA-A*03:01_ATFQTTLPTLK	641	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
758	HLA-A*11:01_ATFQTTLPTLK	641	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
759	HLA-B*18:01_LETDIHLSY	642	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
760	HLA-A*02:07_VLDQNRSTL	643	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
761	HLA-B*44:03_QEGSSGMELSW	644	TEX19	ENSG00000182459	Testis-expressed protein 19
762	HLA-C*16:01_IEAELHISY	254	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
763	HLA-B*51:01_VPLSTVNRV	645	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
764	HLA-B*35:01_AAAAAGLAY	646	BHE23	ENSG00000125533	Class E basic helix-loop-helix protein 23 (bHLHe23) (Class B basic helix-loop-helix protein 4) (bHLHb4)
765	HLA-B*51:01_IPYAHSPSV	647	BHE23	ENSG00000125533	Class E basic helix-loop-helix protein 23 (bHLHe23) (Class B basic helix-loop-helix protein 4) (bHLHb4)
766	HLA-B*18:01_EEFNVLEM	648	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
767	HLA-B*51:01_LPPGGIPGI	649	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
768	HLA-C*02:02_KEADPTGHSY	650	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
769	HLA-A*01:01_HTEDKPYKY	462	ZNF99	ENSG00000213973	Zinc finger protein 99
770	HLA-A*02:01_ILYDLKIAL	651	ZNF99	ENSG00000213973	Zinc finger protein 99
771	HLA-A*03:01_KVFNNSSTLMK	652	ZNF99	ENSG00000213973	Zinc finger protein 99

772	HLA-C*02:02_AEQQPQPQF	653	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
773	HLA-B*51:01_IPLGTMSTI	654	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
774	HLA-B*18:01_QEFLNVQEY	655	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
775	HLA-B*44:03_QEFLNVQEY	655	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
776	HLA-B*18:01_TEAELMQQF	656	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
777	HLA-B*44:03_TEAELMQQF	656	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
778	HLA-C*05:01_VTDDPQKF	657	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
779	HLA-A*29:02_SLPDKVFIKY	658	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
780	HLA-A*26:01_EVAERGTAY	659	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
781	HLA-A*29:02_FFSGPKTYKY	660	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
782	HLA-B*44:03_GEADIMISF	661	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
783	HLA-C*02:02_GEADIMISF	661	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
784	HLA-B*35:01_LPASGLAVF	662	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
785	HLA-A*11:01_SSFDAVTMLGK	663	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
786	HLA-A*01:01_STDPSALMY	664	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
787	HLA-A*29:02_YFFSGPKTYKY	665	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
788	HLA-A*24:02_IYSGNSYYF	666	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
789	HLA-A*33:01_DMQAVETYR	667	PDCL2	ENSG00000163440	Phosducin-like protein 2
790	HLA-A*31:01_ASWARIAAR	668	DPPA2	ENSG00000163530	Developmental pluripotency-associated protein 2 (Pluripotent embryonic stem cell-related gene 1 protein)
791	HLA-B*44:03_KEDNPSGHTY	669	MAGB1	ENSG00000214107	Melanoma-associated antigen B1 (Cancer/testis antigen 3.1) (CT3.1) (DSS-AHC critical interval MAGE superfamily 10) (DAM10) (MAGE-B1 antigen) (MAGE-XP antigen)
792	HLA-A*03:01_TVAVTQMNK	242	ACTL8	ENSG00000117148	Actin-like protein 8 (Cancer/testis antigen 57) (CT57)
793	HLA-A*31:01_AVRGSDTLWYR	670	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
794	HLA-B*08:01_YQKEKNVSI	671	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
795	HLA-C*04:01_FFDSIIAEL	672	A0A1B0GVH6	ENSG00000226792	Long intergenic non-protein coding RNA 371
796	HLA-B*27:02_VDQIALPNLK	673	DYTN	ENSG00000232125	Dystrotelin
797	HLA-A*33:01_DTFRSISTR	674	WNT8B	ENSG00000075290	Protein Wnt-8b
798	HLA-B*27:02_GRGAIADTF	675	WNT8B	ENSG00000075290	Protein Wnt-8b
799	HLA-B*44:03_AESEGTKAVL	676	H2BWT	ENSG00000123569	Histone H2B type W-T (H2B histone family member W testis-specific)
800	HLA-C*02:02_AESEGTKAVL	676	H2BWT	ENSG00000123569	Histone H2B type W-T (H2B histone family member W testis-specific)

801	HLA-A*03:01_SLYAIQQQRK	677	H2BWT	ENSG00000123569	Histone H2B type W-T (H2B histone family member W testis-specific)
802	HLA-B*18:01_DEAGMLSYF	678	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
803	HLA-B*18:01_DEAGMLSY	679	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
804	HLA-B*44:03_EEEKLFLSY	680	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
805	HLA-B*08:01_ELLTKTSL	681	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
806	HLA-A*01:01_HSDEAGMLSY	682	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
807	HLA-A*31:01_IVTNVLENR	683	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
808	HLA-A*33:01_IVTNVLENR	683	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
809	HLA-A*30:02_QGIKDLHAY	684	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
810	HLA-B*44:03_SEEEKLFLSY	685	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
811	HLA-B*18:01_SEIEAAGF	686	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
812	HLA-A*11:01_ASVLIFANK	687	K7EM39	ENSG00000141748	Putative ADP-ribosylation factor-like protein 5C (Fragment)
813	HLA-B*44:03_EEQSLQKLY	688	SPT21	ENSG00000187144	Spermatogenesis-associated protein 21
814	HLA-A*01:01_QSSERTLSY	689	SPT21	ENSG00000187144	Spermatogenesis-associated protein 21
815	HLA-A*11:01_ITQDLVQEK	690	MAGB1	ENSG00000214107	Melanoma-associated antigen B1 (Cancer/testis antigen 3.1) (CT3.1) (DSS-AHC critical interval MAGE superfamily 10) (DAM10) (MAGE-B1 antigen) (MAGE-XP antigen)
816	HLA-A*29:02_FVADSFPFY	691	FOXI3	ENSG00000214336	Forkhead box protein I3
817	HLA-B*18:01_DEGEHLVF	692	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
818	HLA-A*26:01_EVATAVNTR	693	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
819	HLA-A*02:07_ILPLRFVEL	694	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
820	HLA-A*02:01_TVTEKIYYL	695	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
821	HLA-A*26:01_EVTNHNIRLF	696	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
822	HLA-A*24:02_EYQEIFQQL	697	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
823	HLA-A*29:02_LTFPVRPFFY	698	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
824	HLA-B*35:01_MPQPVNPEL	699	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
825	HLA-A*24:02_NYLVDPVTI	700	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
826	HLA-A*11:01_SVSFLNVTK	701	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
827	HLA-B*44:03_GEYPDYQQW	604	CRGC	ENSG00000163254	Gamma-crystallin C (Gamma-C-crystallin) (Gamma-crystallin 2-1) (Gamma-crystallin 3)
828	HLA-C*02:02_GEYPDYQQW	604	CRGC	ENSG00000163254	Gamma-crystallin C (Gamma-C-crystallin) (Gamma-crystallin 2-1) (Gamma-crystallin 3)
829	HLA-B*44:03_EEITQGNTL	702	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
830	HLA-A*31:01_ITQGNTLLRAR	703	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
831	HLA-B*35:01_LPEPFKIAY	704	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
832	HLA-A*02:07_QVDDLIETV	705	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
833	HLA-A*11:01_VTSLPSGLQK	706	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
834	HLA-A*29:02_YLPEPFKIAY	707	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
835	HLA-A*29:02_EVVGVVYVY	168	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
836	HLA-B*35:01_TVQGVVTSF	708	CT55	ENSG00000169551	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)
837	HLA-A*11:01_ASLQDILSH	709	S22AD	ENSG00000172940	Solute carrier family 22 member 13 (Organic cation transporter-like 3) (ORCTL-3)
838	HLA-A*01:01_YTESRSFNY	710	EP3B	ENSG00000181552	Epididymal secretory protein E3-beta (Human epididymis-specific protein 3-beta) (HE3-beta)
839	HLA-A*02:07_LLDDIMAEV	711	TSPY1	ENSG00000258992	Testis-specific Y-encoded protein 1 (Cancer/testis antigen 78) (CT78)
840	HLA-A*02:01_SLDEALQRV	540	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
841	HLA-B*51:01_DAVEALYKV	712	CBPA5	ENSG00000158525	Carboxypeptidase A5 (EC 3.4.17.-)

842	HLA-A*01:01_YLESHGLAY	713	CBPA5	ENSG00000158525	Carboxypeptidase A5 (EC 3.4.17.-)
843	HLA-A*02:07_LLDDIMAEV	711	C9JPU3	ENSG00000168757	Testis-specific Y-encoded protein 2
844	HLA-A*30:02_AVQTSYTSY	714	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
845	HLA-B*44:03_NEVVVSFKW	715	LY6L	ENSG00000261667	Lymphocyte antigen 6L (Lymphocyte antigen 6 complex locus protein L)
846	HLA-A*26:01_DAPPAILTF	617	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
847	HLA-A*30:02_NVNGQTISLY	716	LMTD1	ENSG00000152936	Lamin tail domain-containing protein 1 (Intermediate filament tail domain-containing protein 1)
848	HLA-A*02:01_SLDASPFSV	717	LMTD1	ENSG00000152936	Lamin tail domain-containing protein 1 (Intermediate filament tail domain-containing protein 1)
849	HLA-A*11:01_STATITKEK	718	LMTD1	ENSG00000152936	Lamin tail domain-containing protein 1 (Intermediate filament tail domain-containing protein 1)
850	HLA-A*11:01_STTGQLTSK	719	LMTD1	ENSG00000152936	Lamin tail domain-containing protein 1 (Intermediate filament tail domain-containing protein 1)
851	HLA-B*51:01_IPLTIISI	720	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
852	HLA-B*51:01_LPALEPVI	721	PRS48	ENSG00000189099	Serine protease 48 (EC 3.4.21.-) (Epidermis-specific serine protease-like protein)
853	HLA-B*44:03_SEGTKVPAW	722	CLC6A	ENSG00000205846	C-type lectin domain family 6 member A (C-type lectin superfamily member 10) (Dendritic cell-associated C-type lectin 2) (DC-associated C-type lectin 2) (Dectin-2)
854	HLA-A*30:02_YQGSIVHEY	723	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
855	HLA-B*08:01_HMAHKVNSL	724	MROH9	ENSG00000117501	Maestro heat-like repeat-containing protein family member 9
856	HLA-A*02:07_IVDAIYRQL	725	MROH9	ENSG00000117501	Maestro heat-like repeat-containing protein family member 9
857	HLA-A*30:02_KVNSLLDAY	726	MROH9	ENSG00000117501	Maestro heat-like repeat-containing protein family member 9
858	HLA-B*08:01_NPKTKSSL	727	MROH9	ENSG00000117501	Maestro heat-like repeat-containing protein family member 9
859	HLA-B*18:01_SESLAAVF	728	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
860	HLA-B*51:01_IPYLQTVSV	729	OX2R	ENSG00000137252	Orexin receptor type 2 (Ox-2-R) (Ox2-R) (Ox2R) (Hypocretin receptor type 2)
861	HLA-A*02:01_SLADVLVTI	730	OX2R	ENSG00000137252	Orexin receptor type 2 (Ox-2-R) (Ox2-R) (Ox2R) (Hypocretin receptor type 2)
862	HLA-A*26:01_EVITTVYGY	731	ZAN	ENSG00000146839	Zonadhesin
863	HLA-A*02:01_FLQEVITTV	732	ZAN	ENSG00000146839	Zonadhesin
864	HLA-A*30:02_GQSPGAALHIY	733	ZAN	ENSG00000146839	Zonadhesin
865	HLA-B*18:01_LEIEIPTTY	734	ZAN	ENSG00000146839	Zonadhesin
866	HLA-A*30:02_SGHGVSSRY	735	ZAN	ENSG00000146839	Zonadhesin
867	HLA-B*18:01_VEVTVPSSY	736	ZAN	ENSG00000146839	Zonadhesin
868	HLA-A*02:01_GLMAVNQEV	737	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
869	HLA-B*44:03_EEPLSVTASY	738	VCX3	ENSG00000169059	Variable charge X-linked protein 3 (Variable charge protein on X with eight repeats) (VCX-8r) (Variably charged protein X-A) (VCX-A)
870	HLA-B*18:01_EESPFLVAV	739	HDGL1	ENSG00000112273	Hepatoma-derived growth factor-like protein 1 (PWWP domain-containing protein 1)
871	HLA-B*18:01_DEMGVVGY	740	OTOR	ENSG00000125879	Otoraplin (Fibrocyte-derived protein) (Melanoma inhibitory activity-like protein)
872	HLA-B*44:03_HEAFGGINW	741	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
873	HLA-A*29:02_FFLSMVNNY	742	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
874	HLA-A*29:02_IFSQHTFKY	743	IFNK	ENSG00000147896	Interferon kappa (IFN-kappa)

875	HLA-C*02:02_QEINTKSAF	744	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
876	HLA-B*44:03_SESSTILVVRY	316	SPNXC	ENSG00000198573	Sperm protein associated with the nucleus on the X chromosome C (Cancer/testis antigen 11.3) (CT11.3) (Cancer/testis-associated protein CTp11) (Nuclear-associated protein SPAN-Xc) (SPANX-C) (SPANX family member C)
877	HLA-A*24:02_SYLGISAVSEF	745	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
878	HLA-A*11:01_ATQRDLIATQK	746	LUZP4	ENSG00000102021	Leucine zipper protein 4 (Cancer/testis antigen 28) (CT-28) (CT28) (Tumor antigen HOM-TES-85)
879	HLA-B*46:01_AVKKGSTAY	747	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
880	HLA-A*33:01_DARVVINR	748	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
881	HLA-B*51:01_TAYHVSLIV	749	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
882	HLA-B*18:01_VEDPVTVEY	750	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
883	HLA-B*46:01_VVIEQSSSL	119	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
884	HLA-B*44:02_AEARPVPHW	156	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
885	HLA-C*05:01_NADLQSEFL	751	V9GYR9	ENSG00000225362	Cancer/testis antigen 62 (Fragment)
886	HLA-B*35:01_HAFDGTILF	752	PIWL1	ENSG00000125207	Piwi-like protein 1 (EC 3.1.26.-)
887	HLA-A*30:02_KTGPSRSSY	753	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
888	HLA-A*03:01_AVYNSPQFK	561	FBX39	ENSG00000177294	F-box only protein 39
889	HLA-A*11:01_ASAVQLPEK	754	CB091	ENSG00000205086	Uncharacterized protein C2orf91
890	HLA-A*11:01_ATPSADFLLK	755	E9PHT4	ENSG00000206199	Protein ANKUB1
891	HLA-A*11:01_AVASAFKEK	756	E9PHT4	ENSG00000206199	Protein ANKUB1
892	HLA-A*29:02_GYSHPSFFY	757	E9PHT4	ENSG00000206199	Protein ANKUB1
893	HLA-A*26:01_ETTDIKGLF	758	CD051	ENSG00000237136	Uncharacterized protein C4orf51
894	HLA-A*30:02_AQLGGLSDGY	759	HXB1	ENSG00000120094	Homeobox protein Hox-B1 (Homeobox protein Hox-2I)
895	HLA-B*44:03_TELEKEFHF	760	HXB1	ENSG00000120094	Homeobox protein Hox-B1 (Homeobox protein Hox-2I)
896	HLA-B*44:03_EEDVWVIIHLY	761	PDCL2	ENSG00000163440	Phosducin-like protein 2
897	HLA-A*03:01_ALQLVPGSPK	762	WFD13	ENSG00000168634	WAP four-disulfide core domain protein 13
898	HLA-B*35:01_MAGASIPAM	763	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
899	HLA-B*18:01_FEAGTSVTY	764	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
900	HLA-A*30:02_KAFDDIATY	406	SSX1	ENSG00000126752	Protein SSX1 (Cancer/testis antigen 5.1) (CT5.1) (Synovial sarcoma, X breakpoint 1)
901	HLA-A*02:01_SQDSFIPGV	765	CER1	ENSG00000147869	Cerberus (Cerberus-related protein) (DAN domain family member 4)
902	HLA-B*51:01_MPYAHGPSV	766	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
903	HLA-B*44:03_SEQDLQQLRL	767	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
904	HLA-C*01:02_SSPLSAASL	768	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
905	HLA-A*11:01_STQGDMMQK	769	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
906	HLA-A*11:01_TTADVALLK	770	PRS48	ENSG00000189099	Serine protease 48 (EC 3.4.21.-) (Epidermis-specific serine protease-like protein)
907	HLA-B*35:01_NAFKFSSTF	771	ZN729	ENSG00000196350	Zinc finger protein 729

908	HLA-B*44:03_AETDNLDHY	772	GLYL3	ENSG00000203972	Glycine N-acyltransferase-like protein 3 (EC 2.3.1.-)
909	HLA-A*30:02_TTHIANHSY	773	Q5JUY5	ENSG00000117400	Thrombopoietin receptor
910	HLA-A*11:01_ATVEEDFQPFR	774	PRD14	ENSG00000147596	PR domain zinc finger protein 14 (EC 2.1.1.-) (PR domain-containing protein 14)
911	HLA-B*44:03_AEFPNSFVTL	775	ADA18	ENSG00000168619	Disintegrin and metalloproteinase domain-containing protein 18 (ADAM 18) (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tMDC III)
912	HLA-A*29:02_FLPQNFLVY	776	ADA18	ENSG00000168619	Disintegrin and metalloproteinase domain-containing protein 18 (ADAM 18) (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tMDC III)
913	HLA-B*18:01_DEQQIINSF	777	PP2D1	ENSG00000183977	Protein phosphatase 2C-like domain-containing protein 1
914	HLA-A*24:02_IYNPENVETF	778	PP2D1	ENSG00000183977	Protein phosphatase 2C-like domain-containing protein 1
915	HLA-A*01:01_LSDSNYSKY	779	PP2D1	ENSG00000183977	Protein phosphatase 2C-like domain-containing protein 1
916	HLA-A*11:01_STSEPNLTK	780	PP2D1	ENSG00000183977	Protein phosphatase 2C-like domain-containing protein 1
917	HLA-A*30:02_ITQDLVQEKY	781	MAGB1	ENSG00000214107	Melanoma-associated antigen B1 (Cancer/testis antigen 3.1) (CT3.1) (DSS-AHC critical interval MAGE superfamily 10) (DAM10) (MAGE-B1 antigen) (MAGE-XP antigen)
918	HLA-A*11:01_AVMTKPKVK	782	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
919	HLA-A*31:01_IVKVPILNR	783	TEX37	ENSG00000172073	Testis-expressed sequence 37 protein (Testis-specific conserved protein of 21 kDa)
920	HLA-B*35:01_LAVAVPVVY	784	NPBW1	ENSG00000183729	Neuropeptides B/W receptor type 1 (G-protein coupled receptor 7)
921	HLA-A*11:01_SVIDVQLGK	785	IRPL2	ENSG00000189108	X-linked interleukin-1 receptor accessory protein-like 2 (IL-1 receptor accessory protein-like 2) (IL-1-RAPL-2) (IL-1RAPL-2) (IL1RAPL-2) (IL1RAPL-2-related protein) (Interleukin-1 receptor 9) (IL-1R-9) (IL-1R9) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1)
922	HLA-B*51:01_SAFGYLHSI	786	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
923	HLA-A*11:01_ASGPPAKAK	787	VCX3B	ENSG00000205642	Variable charge X-linked protein 3B (Variably charged protein X-C) (VCX-C)
924	HLA-B*44:03_EEPLSVTAKY	209	VCX3B	ENSG00000205642	Variable charge X-linked protein 3B (Variably charged protein X-C) (VCX-C)
925	HLA-A*24:02_AYIPKLLQLF	788	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
926	HLA-A*11:01_GTIPGPIAQR	789	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
927	HLA-A*03:01_KTNPSVFFVK	790	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
928	HLA-A*11:01_STLGGVNMK	791	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
929	HLA-B*51:01_VPADSFRTI	792	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
930	HLA-B*44:03_EEMNILAKL	793	TRI60	ENSG00000176979	Tripartite motif-containing protein 60 (RING finger protein 129) (RING finger protein 33)
931	HLA-B*44:02_QELLERQAW	524	ASCL4	ENSG00000187855	Achaete-scute homolog 4 (ASH-4) (hASH4) (Achaete-scute-like protein 4) (Class A basic helix-loop-helix protein 44) (bHLHa44)
932	HLA-A*11:01_SVQEIYNFTR	794	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
933	HLA-A*03:01_VLNQPGILK	795	A0A1B0GUY1	ENSG00000248109	Uncharacterized protein
934	HLA-A*11:01_SIAPNIFLK	796	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
935	HLA-C*05:01_IADVDVQEV	797	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
936	HLA-A*11:01_ASGPPAPAR	798	NGN1	ENSG00000181965	Neurogenin-1 (NGN-1) (Class A basic helix-loop-helix protein 6) (bHLHa6) (Neurogenic basic-helix-loop-helix protein) (Neurogenic differentiation factor 3) (NeuroD3)
937	HLA-B*51:01_LPLYVKEI	799	SGCZ	ENSG00000185053	Zeta-sarcoglycan (Zeta-SG) (ZSG1)

938	HLA-A*29:02_TFPITGLRY	800	DYTN	ENSG00000232125	Dystrotelin
939	HLA-B*44:03_SEAGVYVLRF	801	S14L3	ENSG00000100012	SEC14-like protein 3 (Tocopherol-associated protein 2)
940	HLA-B*35:01_YPVTLNVLY	802	PSG8	ENSG00000124467	Pregnancy-specific beta-1-glycoprotein 8 (PS-beta-G-8) (PSBG-8) (Pregnancy-specific glycoprotein 8)
941	HLA-B*18:01_SEKISYVY	803	SSX1	ENSG00000126752	Protein SSX1 (Cancer/testis antigen 5.1) (CT5.1) (Synovial sarcoma, X breakpoint 1)
942	HLA-A*26:01_EVITSAPGAM	804	DPPA2	ENSG00000163530	Developmental pluripotency-associated protein 2 (Pluripotent embryonic stem cell-related gene 1 protein)
943	HLA-C*02:02_SENDIPSVAF	283	DC4L2	ENSG00000176566	DDB1- and CUL4-associated factor 4-like protein 2 (WD repeat-containing protein 21C)
944	HLA-C*02:02_EEMQIQKSQW	569	NTM2G	ENSG00000188152	NUT family member 2G
945	HLA-A*26:01_QVINGEMQFY	805	NTM1B	ENSG00000203740	Alpha N-terminal protein methyltransferase 1B (EC 2.1.1.299) (Methyltransferase-like protein 11B) (X-Pro-Lys N-terminal protein methyltransferase 1B) (NTM1B)
946	HLA-A*02:07_YLLEKIPLV	806	NTM1B	ENSG00000203740	Alpha N-terminal protein methyltransferase 1B (EC 2.1.1.299) (Methyltransferase-like protein 11B) (X-Pro-Lys N-terminal protein methyltransferase 1B) (NTM1B)
947	HLA-A*11:01_ASVQGELAQLK	807	PTX4	ENSG00000251692	Pentraxin-4
948	HLA-A*26:01_EVDPAGHSY	808	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
949	HLA-A*01:01_NSDNVGYASY	809	V9GYJ5	ENSG00000188611	Neutral ceramidase (Fragment)
950	HLA-A*26:01_QVADINLMGY	810	V9GYJ5	ENSG00000188611	Neutral ceramidase (Fragment)
951	HLA-B*46:01_AAAAAGLAY	646	BHE23	ENSG00000125533	Class E basic helix-loop-helix protein 23 (bHLHe23) (Class B basic helix-loop-helix protein 4) (bHLHb4)
952	HLA-A*11:01_KTADIISEQK	811	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
953	HLA-A*11:01_QTLNNNIAK	812	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
954	HLA-C*02:02_GEMPSERQY	813	AXDN1	ENSG00000162779	Axonemal dynein light chain domain-containing protein 1
955	HLA-A*03:01_ITWDAPAITK	271	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
956	HLA-B*51:01_LPQGSMSSI	814	CF010	ENSG00000204296	Uncharacterized protein C6orf10
957	HLA-B*44:03_SEQSARLLDY	815	CF010	ENSG00000204296	Uncharacterized protein C6orf10
958	HLA-A*11:01_ASFTSFNPK	816	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
959	HLA-C*01:02_QYPVGTASL	817	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
960	HLA-C*02:02_QEFLNVQEY	655	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
961	HLA-C*16:01_IEAIRAEY	818	TRI51	ENSG00000124900	Tripartite motif-containing protein 51 (SPRY domain-containing protein 5)
962	HLA-C*01:02_SSPEGTREL	819	CA094	ENSG00000142698	Uncharacterized protein C1orf94
963	HLA-A*11:01_AVSSAALTH	820	WNT9B	ENSG00000158955	Protein Wnt-9b (Protein Wnt-14b) (Protein Wnt-15)
964	HLA-A*11:01_GTLAMILTK	821	OVCH1	ENSG00000187950	Ovochymase-1 (EC 3.4.21.-)
965	HLA-A*03:01_SVYDNVRSVGK	822	OVCH1	ENSG00000187950	Ovochymase-1 (EC 3.4.21.-)
966	HLA-A*11:01_SVYDNVRSVGK	822	OVCH1	ENSG00000187950	Ovochymase-1 (EC 3.4.21.-)
967	HLA-A*29:02_YMSPDIALLY	823	OVCH1	ENSG00000187950	Ovochymase-1 (EC 3.4.21.-)
968	HLA-B*35:01_DAWSGSNAY	824	CRBA1	ENSG00000108255	Beta-crystallin A3 [Cleaved into: Beta-crystallin A3, isoform A1, Delta4 form; Beta-crystallin A3, isoform A1, Delta7 form; Beta-crystallin A3, isoform A1, Delta8 form]
969	HLA-B*44:03_YEVLTPLKW	825	AMELX	ENSG00000125363	Amelogenin, X isoform
970	HLA-B*35:01_NASNDTYLY	826	CSTL1	ENSG00000125823	Cystatin-like 1 (RCET11)
971	HLA-B*44:03_AEAITAPLF	827	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
972	HLA-C*02:02_AEAITAPLF	827	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
973	HLA-A*31:01_AVQIWFENR	828	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)

974	HLA-A*02:07_IVPSFTFPNV	829	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
975	HLA-A*01:01_QSEKEPGQQY	830	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
976	HLA-B*44:03_SEKEPGQQY	831	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
977	HLA-C*02:02_SEKEPGQQY	831	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
978	HLA-B*35:01_LPVLENVSY	832	NYAP2	ENSG00000144460	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2
979	HLA-B*35:01_MVNAAVNTY	833	NYAP2	ENSG00000144460	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2
980	HLA-A*02:01_FLIEQIDVL	834	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
981	HLA-A*24:02_SYLPGLLYKF	835	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
982	HLA-A*24:02_LYASWMYQL	836	TEX19	ENSG00000182459	Testis-expressed protein 19
983	HLA-A*11:01_AAGIIVIAK	837	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
984	HLA-A*11:01_HVSDPGLPGK	838	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
985	HLA-A*29:02_IFGEMVHLY	839	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
986	HLA-A*11:01_IVDSSPGIGK	840	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
987	HLA-A*01:01_TSDSNLNKY	841	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
988	HLA-A*11:01_VSDPGLPGK	842	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
989	HLA-B*44:03_AEAELTGGSEW	843	C9J420	ENSG00000186038	5-hydroxytryptamine receptor 3E (Fragment)
990	HLA-B*51:01_LPTSGTPLI	844	C9J420	ENSG00000186038	5-hydroxytryptamine receptor 3E (Fragment)
991	HLA-B*35:01_VPTQVNISF	845	C9J420	ENSG00000186038	5-hydroxytryptamine receptor 3E (Fragment)
992	HLA-A*03:01_SVSGLVLSH	613	S22AO	ENSG00000197658	Solute carrier family 22 member 24
993	HLA-C*02:02_TESSVKDPVAW	846	MAGB1	ENSG00000214107	Melanoma-associated antigen B1 (Cancer/testis antigen 3.1) (CT3.1) (DSS-AHC critical interval MAGE superfamily 10) (DAM10) (MAGE-B1 antigen) (MAGE-XP antigen)
994	HLA-A*03:01_RSYSPAPGKQK	847	NOBOX	ENSG00000106410	Homeobox protein NOBOX
995	HLA-B*35:01_EAAPESLDVVY	848	R113B	ENSG00000139797	RING finger protein 113B (Zinc finger protein 183-like 1)
996	HLA-A*29:02_LALSIGTPYRY	849	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)

997	HLA-B*51:01_MPLQVPPQI	850	KCNH5	ENSG00000140015	Potassium voltage-gated channel subfamily H member 5 (Ether-a-go-go potassium channel 2) (hEAG2) (Voltage-gated potassium channel subunit Kv10.2)
998	HLA-A*31:01_QVKIWFQNR	110	GBX1	ENSG00000164900	Homeobox protein GBX-1 (Gastrulation and brain-specific homeobox protein 1)
999	HLA-B*51:01_MAYEKRVLI	851	SG1D1	ENSG00000168515	Secretoglobin family 1D member 1 (Lipophilin-A)
1000	HLA-A*24:02_VYTVWTALW	852	NKAI3	ENSG00000185942	Sodium/potassium-transporting ATPase subunit beta-1-interacting protein 3 (Na(+)/K(+)-transporting ATPase subunit beta-1-interacting protein 3) (Protein FAM77D)
1001	HLA-B*44:03_KEADPTGHSY	650	MAGA1	ENSG00000198681	Melanoma-associated antigen 1 (Antigen MZ2-E) (Cancer/testis antigen 1.1) (CT1.1) (MAGE-1 antigen)
1002	HLA-A*11:01_GSFGGVLQK	853	SKOR2	ENSG00000215474	SKI family transcriptional corepressor 2 (Functional Smad-suppressing element on chromosome 18) (Fussel-18) (LBX1 corepressor 1-like protein) (Ladybird homeobox corepressor 1-like protein)
1003	HLA-B*51:01_IPYAASLI	854	SKOR2	ENSG00000215474	SKI family transcriptional corepressor 2 (Functional Smad-suppressing element on chromosome 18) (Fussel-18) (LBX1 corepressor 1-like protein) (Ladybird homeobox corepressor 1-like protein)
1004	HLA-A*02:07_FLYEVFAQL	855	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
1005	HLA-C*16:01_NASTRNVVF	856	PTX4	ENSG00000251692	Pentraxin-4
1006	HLA-A*11:01_QTQLIPVQK	857	ZP4	ENSG00000116996	Zona pellucida sperm-binding protein 4 (Zona pellucida glycoprotein 4) (Zp-4) (Zona pellucida protein B) [Cleaved into: Processed zona pellucida sperm-binding protein 4]
1007	HLA-B*44:03_AEDLAKAQRW	858	Q5T1N2	ENSG00000162641	Protein AKNAD1
1008	HLA-A*11:01_KSYQGQSPQK	859	Q5T1N2	ENSG00000162641	Protein AKNAD1
1009	HLA-B*51:01_LPYDGDLSQI	860	Q5T1N2	ENSG00000162641	Protein AKNAD1
1010	HLA-A*11:01_SSSSYIFQK	861	Q5T1N2	ENSG00000162641	Protein AKNAD1
1011	HLA-B*44:03_MEDESNKLW	862	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
1012	HLA-A*29:02_IVGENSLEY	863	ZFP42	ENSG00000179059	Zinc finger protein 42 homolog (Zfp-42) (Reduced expression protein 1) (REX-1) (hREX-1) (Zinc finger protein 754)
1013	HLA-B*51:01_LPKLPIPYI	864	PSG9	ENSG00000183668	Pregnancy-specific beta-1-glycoprotein 9 (PS-beta-G-9) (PSBG-9) (Pregnancy-specific glycoprotein 9) (PS34) (Pregnancy-specific beta-1 glycoprotein B) (PS-beta-B) (Pregnancy-specific beta-1-glycoprotein 11) (PS-beta-G-11) (PSBG-11) (Pregnancy-specific glycoprotein 11) (Pregnancy-specific glycoprotein 7) (PSG7)
1014	HLA-B*44:03_QEWTDYRLTW	865	ACHB4	ENSG00000117971	Neuronal acetylcholine receptor subunit beta-4
1015	HLA-B*46:01_AAAAAAATY	372	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1016	HLA-B*51:01_DANLANTII	866	SPI2A	ENSG00000147059	Spindlin-2A (Protein DXF34) (Spindlin-like protein 2A) (SPIN-2) (SPIN-2A)
1017	HLA-B*51:01_DANLANTI	867	SPI2A	ENSG00000147059	Spindlin-2A (Protein DXF34) (Spindlin-like protein 2A) (SPIN-2) (SPIN-2A)
1018	HLA-B*44:03_KEGDEPITQW	868	SPI2A	ENSG00000147059	Spindlin-2A (Protein DXF34) (Spindlin-like protein 2A) (SPIN-2) (SPIN-2A)
1019	HLA-B*51:01_DPMLTAAAI	869	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1020	HLA-B*18:01_EEFEHVGY	870	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1021	HLA-B*51:01_FPIPVPVI	871	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1022	HLA-B*18:01_NETEVIVF	872	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)

1023	HLA-B*44:03_SESQKTVTF	873	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1024	HLA-C*02:02_SESQKTVTF	873	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1025	HLA-B*35:01_EPLSVTAKY	874	VCX1	ENSG00000182583	Variable charge X-linked protein 1 (Variable charge protein on X with ten repeats) (VCX-10r) (Variably charged protein X-B1) (VCX-B1)
1026	HLA-C*02:02_TEVVEGKEW	272	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
1027	HLA-A*24:02_VYLPKIPSW	875	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
1028	HLA-B*51:01_MPLLPSTV	876	CRSPL	ENSG00000101074	Peptidase inhibitor R3HDML (Cysteine-rich secretory protein R3HDML)
1029	HLA-A*29:02_NFPQFPETLSY	877	MROH9	ENSG00000117501	Maestro heat-like repeat-containing protein family member 9
1030	HLA-B*18:01_NESSLVEQM	878	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
1031	HLA-A*11:01_KTITHIVAK	879	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
1032	HLA-A*02:07_LVDEILEEL	880	SHP1L	ENSG00000157060	Testicular spindle-associated protein SHCBP1L (SHC SH2 domain-binding protein 1-like protein)
1033	HLA-A*11:01_GTQDPGLLVPK	881	SP7	ENSG00000170374	Transcription factor Sp7 (Zinc finger protein osterix)
1034	HLA-B*44:03_EEIVLGQRL	882	XKR3	ENSG00000172967	XK-related protein 3 (X Kell blood group-related 3) (XTES)
1035	HLA-A*26:01_EVISRVVTL	883	XKR3	ENSG00000172967	XK-related protein 3 (X Kell blood group-related 3) (XTES)
1036	HLA-A*11:01_NTYASTLYK	884	FGF16	ENSG00000196468	Fibroblast growth factor 16 (FGF-16)
1037	HLA-A*26:01_EVISVVLKY	885	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1038	HLA-A*29:02_EVISVVLKY	885	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1039	HLA-B*18:01_IETEFKNDY	886	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1040	HLA-B*44:02_SEKEPGQQY	831	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
1041	HLA-A*29:02_IVISAYFLY	887	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
1042	HLA-A*02:07_VMDEVQKFL	888	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
1043	HLA-A*29:02_AFPHHPMGMLY	889	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1044	HLA-A*11:01_ASMSVTPVYK	890	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1045	HLA-A*30:02_ASMSVTPVY	891	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1046	HLA-B*18:01_DEVQILVF	892	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1047	HLA-A*33:01_DVINSIEIVSR	893	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1048	HLA-A*26:01_ETFSLVEGSGY	894	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1049	HLA-A*33:01_EYSENYILR	895	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1050	HLA-A*24:02_FYNSIGEKF	896	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1051	HLA-B*35:01_HPASMSVTPVY	897	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like

1052	HLA-B*18:01_IEIPIAMY	898	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1053	HLA-A*02:01_ILDDKTAMV	899	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1054	HLA-A*02:07_ILDDKTAMV	899	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1055	HLA-A*01:01_ISDNLRITY	900	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1056	HLA-A*11:01_IVTGVGVAR	901	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1057	HLA-A*24:02_IYNHPDVKETF	902	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1058	HLA-A*24:02_KYLESSATF	903	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1059	HLA-B*51:01_LPFHADVEI	904	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1060	HLA-A*02:01_LQTDIVTGV	905	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1061	HLA-B*35:01_NASLTSIIY	906	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1062	HLA-A*02:01_QLASAIVTL	907	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1063	HLA-A*11:01_QTNLVFVHK	908	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1064	HLA-A*11:01_QTTLVAIAK	909	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1065	HLA-B*44:03_SEAVVVRAM	910	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1066	HLA-B*18:01_SEQGVVTITY	911	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1067	HLA-B*44:02_SEQGVVTITY	911	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1068	HLA-B*44:03_SEQGVVTITY	911	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1069	HLA-C*02:02_SEQGVVTITY	911	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1070	HLA-A*02:01_SLGHTLVTV	912	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1071	HLA-A*26:01_STASIFLAY	913	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1072	HLA-A*29:02_STASIFLAY	913	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1073	HLA-B*35:01_TPMEQQDEY	914	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1074	HLA-A*29:02_VFEKLQLFY	915	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1075	HLA-A*24:02_VYVITVDVF	916	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1076	HLA-A*02:07_YVDDSPLEL	917	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1077	HLA-C*05:01_YVDDSPLEL	917	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1078	HLA-A*01:01_ETDALDIDY	918	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
1079	HLA-A*11:01_GTQSTHESLK	919	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
1080	HLA-A*02:01_QLLDGFMITL	920	PASD1	ENSG00000166049	Circadian clock protein PASD1 (Cancer/testis antigen 63) (CT63) (OX-TES-1) (PAS domain-containing protein 1)
1081	HLA-A*01:01_KTELETALY	921	GG6L2	ENSG00000174450	Golgin subfamily A member 6-like protein 2
1082	HLA-B*51:01_LPPSLQSSL	922	GG6L2	ENSG00000174450	Golgin subfamily A member 6-like protein 2
1083	HLA-C*02:02_AESPLEVPQSF	626	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
1084	HLA-B*46:01_AGMTIATSY	250	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
1085	HLA-A*24:02_VYGDPHYVTF	923	ZAN	ENSG00000146839	Zonadhesin
1086	HLA-A*29:02_LFWKPLRY	924	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
1087	HLA-B*08:01_QVLVKKISQ	925	S100G	ENSG00000169906	Protein S100-G (Calbindin-D9k) (S100 calcium-binding protein G) (Vitamin D-dependent calcium-binding protein, intestinal) (CABP)
1088	HLA-B*27:02_GRTVAVAEY	926	KR204	ENSG00000206105	Putative keratin-associated protein 20-4
1089	HLA-B*51:01_DAPSKGPSI	927	CL071	ENSG00000214700	Uncharacterized protein C12orf71
1090	HLA-A*02:07_YVDNVSARV	928	GFRA4	ENSG00000125861	GDNF family receptor alpha-4 (GDNF receptor alpha-4) (GDNFR-alpha-4) (GFR-alpha-4) (Persephin receptor)
1091	HLA-A*01:01_VLDDGSIDY	929	LYZL2	ENSG00000151033	Lysozyme-like protein 2 (Lysozyme-2) (EC 3.2.1.17)
1092	HLA-A*30:02_AVFEAGTSVTY	930	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
1093	HLA-A*02:01_FLIPYVIAL	931	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)

1094	HLA-A*29:02_FVSPKGVLAY	932	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
1095	HLA-A*30:02_GQALLLAEY	933	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
1096	HLA-B*35:01_DPYATITY	934	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
1097	HLA-A*29:02_FFSDFGLLWY	935	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
1098	HLA-B*51:01_FPLATQLNV	936	PRR27	ENSG00000187533	Proline-rich protein 27
1099	HLA-A*01:01_YTDTGLPSY	937	PRR27	ENSG00000187533	Proline-rich protein 27
1100	HLA-A*24:02_IYPTVDREHF	938	RFA4	ENSG00000204086	Replication protein A 30 kDa subunit (RP-A p30) (Replication factor A protein 4) (RF-A protein 4)
1101	HLA-A*29:02_LLNPVIATY	939	CB061	ENSG00000239605	Uncharacterized protein C2orf61
1102	HLA-A*30:02_LLNPVIATY	939	CB061	ENSG00000239605	Uncharacterized protein C2orf61
1103	HLA-B*46:01_LLNPVIATY	939	CB061	ENSG00000239605	Uncharacterized protein C2orf61
1104	HLA-A*01:01_LTDTPIPGTY	940	CB061	ENSG00000239605	Uncharacterized protein C2orf61
1105	HLA-A*26:01_EVIGPDGIITV	941	ROP1A	ENSG00000065371	Ropporin-1A (Cancer/testis antigen 91) (CT91) (Rhophilin-associated protein 1A)
1106	HLA-B*18:01_NESPQTNEF	942	TPTE2	ENSG00000132958	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 (EC 3.1.3.67) (Lipid phosphatase TPIP) (TPTE and PTEN homologous inositol lipid phosphatase)
1107	HLA-A*29:02_YFAQVKHLY	943	TPTE2	ENSG00000132958	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 (EC 3.1.3.67) (Lipid phosphatase TPIP) (TPTE and PTEN homologous inositol lipid phosphatase)
1108	HLA-A*33:01_EANSMNTLR	944	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
1109	HLA-A*01:01_GSDDHQYIY	945	DMP1	ENSG00000152592	Dentin matrix acidic phosphoprotein 1 (DMP-1) (Dentin matrix protein 1)
1110	HLA-C*02:02_AEVNVKGLF	946	LMTD1	ENSG00000152936	Lamin tail domain-containing protein 1 (Intermediate filament tail domain-containing protein 1)
1111	HLA-A*26:01_ETSDIQEPYY	947	I22R2	ENSG00000164485	Interleukin-22 receptor subunit alpha-2 (IL-22 receptor subunit alpha-2) (IL-22R-alpha-2) (IL-22RA2) (Cytokine receptor class-II member 10) (Cytokine receptor family 2 member 10) (CRF2-10) (Cytokine receptor family type 2, soluble 1) (CRF2-S1) (Interleukin-22-binding protein) (IL-22BP) (IL22BP) (ZcytoR16)
1112	HLA-A*02:07_LVIDTVTEV	302	SPERT	ENSG00000174015	Spermatid-associated protein (Protein chibby homolog 2)
1113	HLA-A*11:01_ASQKAIIFK	948	MAGB6	ENSG00000176746	Melanoma-associated antigen B6 (Cancer/testis antigen 3.4) (CT3.4) (MAGE-B6 antigen)
1114	HLA-A*01:01_ITEDLVQDKY	949	MAGB6	ENSG00000176746	Melanoma-associated antigen B6 (Cancer/testis antigen 3.4) (CT3.4) (MAGE-B6 antigen)
1115	HLA-C*02:02_KEMDSSGESY	950	MAGB6	ENSG00000176746	Melanoma-associated antigen B6 (Cancer/testis antigen 3.4) (CT3.4) (MAGE-B6 antigen)
1116	HLA-A*26:01_ELYEGTLGKY	951	SG1C1	ENSG00000188076	Secretoglobin family 1C member 1 (Secretoglobin RYD5)
1117	HLA-B*08:01_QPMHKAEL	952	SG1C1	ENSG00000188076	Secretoglobin family 1C member 1 (Secretoglobin RYD5)
1118	HLA-B*44:02_EEIENLYRF	222	MEIG1	ENSG00000197889	Meiosis expressed gene 1 protein homolog
1119	HLA-B*51:01_IPILQKPLI	953	NANGN	ENSG00000205857	NANOG neighbor homeobox (Homeobox protein C14)
1120	HLA-B*44:02_SEDEQNGKQKW	954	NANGN	ENSG00000205857	NANOG neighbor homeobox (Homeobox protein C14)
1121	HLA-B*44:03_SEDEQNGKQKW	954	NANGN	ENSG00000205857	NANOG neighbor homeobox (Homeobox protein C14)
1122	HLA-C*02:02_SEDEQNGKQKW	954	NANGN	ENSG00000205857	NANOG neighbor homeobox (Homeobox protein C14)
1123	HLA-A*02:01_WLTPVIPAL	955	NANGN	ENSG00000205857	NANOG neighbor homeobox (Homeobox protein C14)
1124	HLA-B*27:02_TLQSILAIVK	956	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1125	HLA-C*05:01_IADIVTSVF	957	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
1126	HLA-B*44:03_NEAYIPKLL	958	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
1127	HLA-C*04:01_TYDEQFQGM	959	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3

1128	HLA-B*18:01_DEDSIFAHY	960	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
1129	HLA-A*11:01_ITQGNTLLR	961	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
1130	HLA-B*44:03_WEVDVEKATRW	962	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
1131	HLA-A*02:07_ALPNKLEEL	963	UTS2B	ENSG00000188958	Urotensin-2B (Urotensin II-related peptide) (Urotensin IIB) (U-IIB) (UIIB) (Urotensin-2 domain-containing protein)
1132	HLA-B*44:03_NEIFPDKKY	964	UTS2B	ENSG00000188958	Urotensin-2B (Urotensin II-related peptide) (Urotensin IIB) (U-IIB) (UIIB) (Urotensin-2 domain-containing protein)
1133	HLA-B*51:01_NPYFQNKVI	965	TSPY1	ENSG00000258992	Testis-specific Y-encoded protein 1 (Cancer/testis antigen 78) (CT78)
1134	HLA-A*30:02_TTAPGTVHSY	403	Q5JUY5	ENSG00000117400	Thrombopoietin receptor
1135	HLA-B*51:01_LPALLASLI	966	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
1136	HLA-B*44:02_SEFEQIRLF	491	TRI60	ENSG00000176979	Tripartite motif-containing protein 60 (RING finger protein 129) (RING finger protein 33)
1137	HLA-A*02:01_LLSQDILQV	967	ADIG	ENSG00000182035	Adipogenin
1138	HLA-A*30:02_GQHGSGSSYSY	968	HORN	ENSG00000197915	Hornerin
1139	HLA-B*44:02_AEDFKIQNW	969	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1140	HLA-A*26:01_EIYEILSPSY	970	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1141	HLA-A*26:01_EVASLQNKF	971	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1142	HLA-A*11:01_GTTVDILQK	972	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1143	HLA-B*35:01_IAAAAAAAY	973	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1144	HLA-A*02:07_LLPPLIPSL	974	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1145	HLA-B*35:01_YPYGDPHVIDY	975	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1146	HLA-B*51:01_YPYGDPHVI	976	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1147	HLA-A*29:02_YFAQVKHLY	943	TPTE	ENSG00000274391	Putative tyrosine-protein phosphatase TPTE (EC 3.1.3.48) (Cancer/testis antigen 44) (CT44) (Transmembrane phosphatase with tensin homology) (Tumor antigen BJ-HCC-5)
1148	HLA-A*11:01_RSYSPAPGK	977	NOBOX	ENSG00000106410	Homeobox protein NOBOX
1149	HLA-A*30:02_AQKNTFVSY	978	CCD62	ENSG00000130783	Coiled-coil domain-containing protein 62 (Protein TSP-NY) (Protein aaa)
1150	HLA-A*02:01_TLSNTLVEL	979	CCD62	ENSG00000130783	Coiled-coil domain-containing protein 62 (Protein TSP-NY) (Protein aaa)
1151	HLA-A*03:01_RVWNMTATRPK	980	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
1152	HLA-B*35:01_LPNTVTDAL	981	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
1153	HLA-A*29:02_YLLGWTTFLLY	982	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
1154	HLA-A*03:01_RIFEKYAAK	983	S100G	ENSG00000169906	Protein S100-G (Calbindin-D9k) (S100 calcium-binding protein G) (Vitamin D-dependent calcium-binding protein, intestinal) (CABP)
1155	HLA-B*35:01_FPTEVTYTL	984	HSF5	ENSG00000176160	Heat shock factor protein 5 (HSF 5) (Heat shock transcription factor 5) (HSTF 5)
1156	HLA-B*35:01_NPSPSSVVF	985	HSF5	ENSG00000176160	Heat shock factor protein 5 (HSF 5) (Heat shock transcription factor 5) (HSTF 5)
1157	HLA-A*02:07_KVLEFVAKV	986	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
1158	HLA-A*11:01_SSSEQSPLQK	987	FOXR2	ENSG00000189299	Forkhead box protein R2 (Forkhead box protein N6)
1159	HLA-B*44:02_EEFSLQKSY	496	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
1160	HLA-A*03:01_SVIGGPSTYK	419	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
1161	HLA-A*26:01_SVIGGPSTY	988	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
1162	HLA-A*26:01_EIKGTVTEF	989	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
1163	HLA-A*02:07_LLDHVLIEM	990	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
1164	HLA-B*44:03_AEQQPQPQF	653	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)

1165	HLA-A*30:02_STLPFQSAKY	991	OPRD	ENSG00000116329	Delta-type opioid receptor (D-OR-1) (DOR-1)
1166	HLA-A*26:01_EVNPTTHSY	992	MAGB4	ENSG00000120289	Melanoma-associated antigen B4 (MAGE-B4 antigen)
1167	HLA-A*30:02_EVNPTTHSY	992	MAGB4	ENSG00000120289	Melanoma-associated antigen B4 (MAGE-B4 antigen)
1168	HLA-A*30:02_AAAAAAAAATY	993	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1169	HLA-A*02:01_FLITGIVQV	994	GP119	ENSG00000147262	Glucose-dependent insulinotropic receptor (G-protein coupled receptor 119)
1170	HLA-A*02:07_ALDVEFYTL	995	SL9C2	ENSG00000162753	Sodium/hydrogen exchanger 11 (Na(+)/H(+) exchanger 11) (NHE-11) (Solute carrier family 9 member 11) (Solute carrier family 9 member C2)
1171	HLA-C*04:01_IYDVSTYM	996	SL9C2	ENSG00000162753	Sodium/hydrogen exchanger 11 (Na(+)/H(+) exchanger 11) (NHE-11) (Solute carrier family 9 member 11) (Solute carrier family 9 member C2)
1172	HLA-B*51:01_LAYHVQNEI	997	TERB2	ENSG00000167014	Telomere repeats-binding bouquet formation protein 2
1173	HLA-A*26:01_FTSSQVQRY	998	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1174	HLA-A*26:01_EVFPQSHHF	999	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
1175	HLA-B*35:01_SAWETITIY	1000	MC5R	ENSG00000176136	Melanocortin receptor 5 (MC5-R) (MC-2)
1176	HLA-A*26:01_EIYGGHHSAF	1001	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
1177	HLA-B*35:01_YPAPLESLDY	1002	PRA10	ENSG00000187545	PRAME family member 10
1178	HLA-C*02:02_AEVGGVFASL	1003	FGF16	ENSG00000196468	Fibroblast growth factor 16 (FGF-16)
1179	HLA-B*44:03_AEAITAPLF	827	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1180	HLA-C*02:02_AEAITAPLF	827	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1181	HLA-A*31:01_AVQIWFENR	828	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1182	HLA-A*02:07_IVPSFTFPNV	829	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1183	HLA-A*01:01_QSEKEPGQQY	830	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1184	HLA-B*44:03_SEKEPGQQY	831	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1185	HLA-C*02:02_SEKEPGQQY	831	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1186	HLA-A*03:01_GVLNQPGILK	1004	A0A1B0GUY1	ENSG00000248109	Uncharacterized protein
1187	HLA-B*35:01_LPAALSSEQM	1005	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
1188	HLA-B*44:03_EEAQLAIRI	1006	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
1189	HLA-B*18:01_DEADFSEHTTY	1007	Q5T1N2	ENSG00000162641	Protein AKNAD1
1190	HLA-A*03:01_KSYQGQSPQK	859	Q5T1N2	ENSG00000162641	Protein AKNAD1
1191	HLA-B*18:01_SEKIVYVY	1008	SSX3	ENSG00000165584	Protein SSX3 (Cancer/testis antigen 5.3) (CT5.3)
1192	HLA-A*26:01_ETPTSRQLSEY	1009	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
1193	HLA-B*51:01_NPYFQNKVI	965	C9JPU3	ENSG00000168757	Testis-specific Y-encoded protein 2
1194	HLA-B*44:03_QEINTKSAF	744	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
1195	HLA-A*11:01_ASEDNLTSLLK	1010	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
1196	HLA-A*02:01_FLYHDSTDIGL	1011	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
1197	HLA-B*51:01_MPMSEVSQV	1012	U3KQD4	ENSG00000105549	Testicular haploid-expressed gene protein (Theg homolog (Mouse), isoform CRA_a)
1198	HLA-A*02:01_TLTITVPAV	1013	U3KQD4	ENSG00000105549	Testicular haploid-expressed gene protein (Theg homolog (Mouse), isoform CRA_a)
1199	HLA-A*30:02_ISNPLLIGRY	1014	TTLL2	ENSG00000120440	Probable tubulin polyglutamylase TTLL2 (EC 6.-.-.-) (Testis-specific protein NYD-TSPG) (Tubulin--tyrosine ligase-like protein 2)

1200	HLA-A*24:02_KYISNPLLI	1015	TTLL2	ENSG00000120440	Probable tubulin polyglutamylase TTLL2 (EC 6.-.-.-) (Testis-specific protein NYD-TSPG) (Tubulin--tyrosine ligase-like protein 2)
1201	HLA-A*24:02_VYQEGLVRF	1016	TTLL2	ENSG00000120440	Probable tubulin polyglutamylase TTLL2 (EC 6.-.-.-) (Testis-specific protein NYD-TSPG) (Tubulin--tyrosine ligase-like protein 2)
1202	HLA-C*16:01_AAAAAGLAY	646	BHE23	ENSG00000125533	Class E basic helix-loop-helix protein 23 (bHLHe23) (Class B basic helix-loop-helix protein 4) (bHLHb4)
1203	HLA-C*16:01_AAAAAAATY	372	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1204	HLA-A*29:02_GVLGANLLY	1017	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1205	HLA-C*02:02_IEAGTSESY	276	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
1206	HLA-A*11:01_TTYTGSYRK	1018	CD051	ENSG00000237136	Uncharacterized protein C4orf51
1207	HLA-A*02:07_LLDGQWHHI	1019	PTX4	ENSG00000251692	Pentraxin-4
1208	HLA-B*35:01_LPNENFQSLY	1020	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
1209	HLA-B*44:02_EEDVWVIIHLY	761	PDCL2	ENSG00000163440	Phosducin-like protein 2
1210	HLA-B*35:01_TATSTGQLY	1021	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
1211	HLA-B*44:02_SEKEPGQQY	831	RHF2B	ENSG00000203989	Rhox homeobox family member 2B
1212	HLA-B*51:01_MPAAAALI	1022	DYTN	ENSG00000232125	Dystrotelin
1213	HLA-A*24:02_KYLYVTSSF	1023	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
1214	HLA-A*03:01_GTMKIHILQK	112	V9GZ46	ENSG00000124092	Transcriptional repressor CTCFL
1215	HLA-A*03:01_SSYVPIFEK	620	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
1216	HLA-B*35:01_MPFAISTSL	1024	S7A13	ENSG00000164893	Solute carrier family 7 member 13 (Sodium-independent aspartate/glutamate transporter 1) (X-amino acid transporter 2)
1217	HLA-B*44:03_EEASVYSQW	1025	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1218	HLA-C*02:02_EEASVYSQW	1025	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1219	HLA-A*02:01_RLWPEGTPIYL	1026	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1220	HLA-A*02:07_VLDGVKVQL	1027	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1221	HLA-A*11:01_VTQEVIRHK	1028	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1222	HLA-A*02:01_FLSDNTIEV	1029	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
1223	HLA-A*24:02_NYNEAKFITF	1030	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
1224	HLA-B*18:01_VEWEVHGM	1031	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
1225	HLA-B*44:02_KEGEPVEFTF	241	LN28B	ENSG00000187772	Protein lin-28 homolog B (Lin-28B)
1226	HLA-B*44:02_AESPLEVPQSF	626	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
1227	HLA-A*31:01_TTLGIDYVNPR	1032	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1228	HLA-A*03:01_HVSPSPLIY	432	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
1229	HLA-A*24:02_NYTDFSGSSF	1033	TSN16	ENSG00000130167	Tetraspanin-16 (Tspan-16) (Tetraspanin TM4-B) (Transmembrane 4 superfamily member 16)
1230	HLA-B*18:01_YEAFLSPEY	1034	PPAT	ENSG00000142513	Testicular acid phosphatase (EC 3.1.3.2)
1231	HLA-A*02:01_ALAAVDIAV	1035	PO4F1	ENSG00000152192	POU domain, class 4, transcription factor 1 (Brain-specific homeobox/POU domain protein 3A) (Brain-3A) (Brn-3A) (Homeobox/POU domain protein RDC-1) (Oct-T1)
1232	HLA-B*18:01_DENLIYVI	1036	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1233	HLA-A*31:01_QVKIWFQNR	110	NKX26	ENSG00000180053	Homeobox protein Nkx-2.6 (Homeobox protein NK-2 homolog F)

1234	HLA-B*44:02_GEYPDYQQW	604	CRGB	ENSG00000182187	Gamma-crystallin B (Gamma-B-crystallin) (Gamma-crystallin 1-2)
1235	HLA-A*11:01_AVHNEDKLMAK	1037	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1236	HLA-A*31:01_AVKKPFDLR	1038	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1237	HLA-B*18:01_DEYGNTTLHY	1039	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1238	HLA-A*11:01_ISQDEILTNK	1040	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1239	HLA-B*18:01_LEEEVTTY	1041	RTP2	ENSG00000198471	Receptor-transporting protein 2 (3CxxC-type zinc finger protein 2)
1240	HLA-A*02:07_LVDNLITSL	1042	RTP2	ENSG00000198471	Receptor-transporting protein 2 (3CxxC-type zinc finger protein 2)
1241	HLA-C*16:01_AAVSDPRVY	1043	A0A0U1RRI6	ENSG00000224109	Centromere protein V-like 3
1242	HLA-A*11:01_ATLENLLSH	1044	PRAM4	ENSG00000243073	PRAME family member 4
1243	HLA-A*30:02_TVNKLNHAY	1045	A0A1B0GW35	ENSG00000250821	HCG2040572
1244	HLA-A*01:01_QSEQSSVRY	1046	SACA1	ENSG00000118434	Sperm acrosome membrane-associated protein 1 (Sperm acrosomal membrane-associated protein 32)
1245	HLA-A*29:02_ILSPIEETY	1047	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1246	HLA-A*02:01_GLLSDLVYL	1048	LRC52	ENSG00000162763	Leucine-rich repeat-containing protein 52 (BK channel auxiliary gamma subunit LRRC52)
1247	HLA-A*11:01_GTNGFQLLR	1049	A0A0B4J218	ENSG00000164871,EI G00000178287	Sperm-associated antigen 11A (Sperm-associated antigen 11B) (Fragment)
1248	HLA-A*11:01_GTNGFQLLR	1049	SG11B	ENSG00000164871	Sperm-associated antigen 11B (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)
1249	HLA-A*02:07_LLPPRTPPYQV	1050	SG11B	ENSG00000164871	Sperm-associated antigen 11B (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)
1250	HLA-B*51:01_VPPGIRNTI	1051	SG11B	ENSG00000164871	Sperm-associated antigen 11B (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)
1251	HLA-B*35:01_VPSYPGNTY	1052	PRR27	ENSG00000187533	Proline-rich protein 27
1252	HLA-A*30:02_RLLPPVSGGY	1053	CP26C	ENSG00000187553	Cytochrome P450 26C1 (EC 1.14.-.-)
1253	HLA-B*51:01_YPISPKVI	1054	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1254	HLA-A*11:01_GVLNQPGILK	1004	A0A1B0GUY1	ENSG00000248109	Uncharacterized protein
1255	HLA-C*02:02_AAAAAAATY	372	NKX24	ENSG00000125816	Homeobox protein Nkx-2.4 (Homeobox protein NK-2 homolog D)
1256	HLA-B*51:01_DAWLFGALV	1055	GALR3	ENSG00000128310	Galanin receptor type 3 (GAL3-R) (GALR-3)
1257	HLA-A*26:01_DVATFAAGY	1056	GALR3	ENSG00000128310	Galanin receptor type 3 (GAL3-R) (GALR-3)
1258	HLA-A*02:01_QLWGHTIQV	1057	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
1259	HLA-A*02:01_SLSPVSATL	1058	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
1260	HLA-B*08:01_DLVQRNVSI	1059	LDH6A	ENSG00000166800	L-lactate dehydrogenase A-like 6A (EC 1.1.1.27)
1261	HLA-A*11:01_GSIDDGNFQK	1060	ADA18	ENSG00000168619	Disintegrin and metalloproteinase domain-containing protein 18 (ADAM 18) (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tMDC III)
1262	HLA-A*11:01_KAMAHLIQK	1061	GPC6A	ENSG00000173612	G-protein coupled receptor family C group 6 member A (hGPRC6A) (G-protein coupled receptor GPCR33) (hGPCR33)
1263	HLA-A*03:01_RLSAESKDLLK	1062	OLIG3	ENSG00000177468	Oligodendrocyte transcription factor 3 (Oligo3) (Class B basic helix-loop-helix protein 7) (bHLHb7) (Class E basic helix-loop-helix protein 20) (bHLHe20)
1264	HLA-B*35:01_QPLLHVTAY	1063	CH086	ENSG00000196166	Uncharacterized protein C8orf86
1265	HLA-A*02:07_ALDNIVTQF	1064	CD022	ENSG00000197826	Uncharacterized protein C4orf22
1266	HLA-A*02:01_FLDSQITTV	1065	CD022	ENSG00000197826	Uncharacterized protein C4orf22
1267	HLA-A*02:07_FLDSQITTV	1065	CD022	ENSG00000197826	Uncharacterized protein C4orf22
1268	HLA-A*30:02_SSSGLSSSY	1066	HORN	ENSG00000197915	Hornerin
1269	HLA-B*51:01_LPPLIPSL	1067	CP096	ENSG00000205832	Uncharacterized protein C16orf96
1270	HLA-B*51:01_DALKQSLVV	1068	PCDG8	ENSG00000253767	Protocadherin gamma-A8 (PCDH-gamma-A8)
1271	HLA-B*44:03_EEVQAFLQTY	1069	PCDG8	ENSG00000253767	Protocadherin gamma-A8 (PCDH-gamma-A8)
1272	HLA-A*30:02_GTMGLSARY	1070	PCDG8	ENSG00000253767	Protocadherin gamma-A8 (PCDH-gamma-A8)
1273	HLA-A*02:01_YLVTKVVAV	1071	PCDG8	ENSG00000253767	Protocadherin gamma-A8 (PCDH-gamma-A8)
1274	HLA-B*44:03_DETEIRSFF	589	DAZL	ENSG00000092345	Deleted in azoospermia-like (DAZ homolog) (DAZ-like autosomal) (Deleted in azoospermia-like 1) (SPGY-like-autosomal)

1275	HLA-B*51:01_IPPSFVKMV	1072	PP13	ENSG00000105198	Galactoside-binding soluble lectin 13 (Galectin-13) (Gal-13) (Placental tissue protein 13) (PP13) (Placental protein 13)
1276	HLA-A*03:01_RLGPLTTSH	1073	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
1277	HLA-A*01:01_VTDTLVEVLLY	1074	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
1278	HLA-A*24:02_EYAGNFQGI	1075	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
1279	HLA-B*51:01_DSYVFVNTL	1076	MAGC1	ENSG00000155495	Melanoma-associated antigen C1 (Cancer/testis antigen 7.1) (CT7.1) (MAGE-C1 antigen)
1280	HLA-A*24:02_LYLPEPFKI	1077	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
1281	HLA-A*02:07_YLPEPFKIA	1078	CC049	ENSG00000163632	Putative uncharacterized protein C3orf49
1282	HLA-B*46:01_MVILGVTSF	1079	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
1283	HLA-B*08:01_MPAVKNVI	1080	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
1284	HLA-A*29:02_LLSLVGFVY	1081	NKAI3	ENSG00000185942	Sodium/potassium-transporting ATPase subunit beta-1-interacting protein 3 (Na(+)/K(+)-transporting ATPase subunit beta-1-interacting protein 3) (Protein FAM77D)
1285	HLA-C*02:02_AELTGGSEW	1082	C9J420	ENSG00000186038	5-hydroxytryptamine receptor 3E (Fragment)
1286	HLA-A*29:02_IFIIITDLSLY	1083	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1287	HLA-C*02:02_SAINPVLYY	1084	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1288	HLA-A*30:02_RVAELINASY	1085	DC8L1	ENSG00000226372	DDB1- and CUL4-associated factor 8-like protein 1 (WD repeat-containing protein 42B)
1289	HLA-B*35:01_TAASSDIEM	1086	DC8L1	ENSG00000226372	DDB1- and CUL4-associated factor 8-like protein 1 (WD repeat-containing protein 42B)
1290	HLA-B*18:01_NEYFSTKY	1087	A14EL	ENSG00000268223	ARL14 effector protein-like
1291	HLA-A*33:01_DTNIIANR	1088	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
1292	HLA-A*11:01_QVASQEDILLK	1089	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
1293	HLA-B*18:01_IEAIRAEY	818	TRI51	ENSG00000124900	Tripartite motif-containing protein 51 (SPRY domain-containing protein 5)
1294	HLA-A*01:01_VSDSTYYSSFY	1090	DMRT1	ENSG00000137090	Doublesex- and mab-3-related transcription factor 1 (DM domain expressed in testis protein 1)
1295	HLA-A*02:01_FLGPATAHL	1091	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1296	HLA-A*24:02_IYSVRVVNF	1092	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1297	HLA-A*31:01_RVLPWADRTAR	1093	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
1298	HLA-B*35:01_NPLGDIASL	1094	CG072	ENSG00000164500	Uncharacterized protein C7orf72
1299	HLA-B*51:01_FPYVVLVI	1095	SC6A5	ENSG00000165970	Sodium- and chloride-dependent glycine transporter 2 (GlyT-2) (GlyT2) (Solute carrier family 6 member 5)
1300	HLA-A*02:07_GLPIFFLEV	1096	SC6A5	ENSG00000165970	Sodium- and chloride-dependent glycine transporter 2 (GlyT-2) (GlyT2) (Solute carrier family 6 member 5)
1301	HLA-B*51:01_TAYPNVTMV	1097	SC6A5	ENSG00000165970	Sodium- and chloride-dependent glycine transporter 2 (GlyT-2) (GlyT2) (Solute carrier family 6 member 5)
1302	HLA-B*51:01_WAFVTPTI	1098	SC6A5	ENSG00000165970	Sodium- and chloride-dependent glycine transporter 2 (GlyT-2) (GlyT2) (Solute carrier family 6 member 5)
1303	HLA-A*11:01_QTLEELNTVLK	1099	PERL	ENSG00000167419	Lactoperoxidase (LPO) (EC 1.11.1.7) (Salivary peroxidase) (SPO)
1304	HLA-A*01:01_FTSSQVQRY	998	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1305	HLA-C*02:02_AEAELTGGSEW	843	C9J420	ENSG00000186038	5-hydroxytryptamine receptor 3E (Fragment)
1306	HLA-A*29:02_RNLPPPLYY	1100	PRR27	ENSG00000187533	Proline-rich protein 27
1307	HLA-A*02:01_KVLEFVAKV	986	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
1308	HLA-B*35:01_FPTGAILTL	1101	PTX4	ENSG00000251692	Pentraxin-4

1309	HLA-B*44:03_NEQESLLSRY	1102	TULP2	ENSG00000104804	Tubby-related protein 2 (Cancer/testis antigen 65) (CT65) (Tubby-like protein 2)
1310	HLA-B*51:01_DALLAQKV	1103	PRA12	ENSG00000116726	PRAME family member 12
1311	HLA-B*44:03_SESDLKHLSW	1104	PRA12	ENSG00000116726	PRAME family member 12
1312	HLA-A*11:01_ASQVPSHSPK	1105	ZSC10	ENSG00000130182	Zinc finger and SCAN domain-containing protein 10 (Zinc finger protein 206)
1313	HLA-B*27:02_LRNQLDQQF	1106	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
1314	HLA-A*02:01_ALADFMLSL	1107	GPR32	ENSG00000142511	Probable G-protein coupled receptor 32
1315	HLA-A*29:02_YITFVFLSY	1108	GPR32	ENSG00000142511	Probable G-protein coupled receptor 32
1316	HLA-A*11:01_STSTVPLAH	1109	PO4F1	ENSG00000152192	POU domain, class 4, transcription factor 1 (Brain-specific homeobox/POU domain protein 3A) (Brain-3A) (Brn-3A) (Homeobox/POU domain protein RDC-1) (Oct-T1)
1317	HLA-B*44:02_GEYPDYQQW	604	CRGC	ENSG00000163254	Gamma-crystallin C (Gamma-C-crystallin) (Gamma-crystallin 2-1) (Gamma-crystallin 3)
1318	HLA-A*31:01_AVAVWVHVR	1110	CG033	ENSG00000170279	Uncharacterized protein C7orf33
1319	HLA-A*29:02_SYLDLLTLSY	1111	CG033	ENSG00000170279	Uncharacterized protein C7orf33
1320	HLA-A*01:01_YLDLLTLSY	1112	CG033	ENSG00000170279	Uncharacterized protein C7orf33
1321	HLA-A*24:02_NYAPPVVKF	1113	V9GZ31	ENSG00000177414	Ubiquitin-conjugating enzyme E2 U (Fragment)
1322	HLA-A*02:07_GLPWRFEEL	1114	TEX19	ENSG00000182459	Testis-expressed protein 19
1323	HLA-A*26:01_EVIAGLERF	1115	H9KVA5	ENSG00000187959	Putative cleavage and polyadenylation-specificity factor subunit 4-like protein
1324	HLA-B*35:01_FAFEKDVEM	1116	H9KVA5	ENSG00000187959	Putative cleavage and polyadenylation-specificity factor subunit 4-like protein
1325	HLA-A*26:01_EVASAVSAFGY	1117	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
1326	HLA-A*29:02_IFSAINPVLY	1118	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1327	HLA-A*29:02_SAINPVLYY	1084	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1328	HLA-A*26:01_EVYDEDPFAY	1119	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
1329	HLA-B*18:01_TENIVAVM	1120	RN148	ENSG00000235631	RING finger protein 148
1330	HLA-B*18:01_NENSLVSF	1121	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
1331	HLA-A*02:07_VQDDTLHNV	1122	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1332	HLA-B*46:01_YSHVQGISY	1123	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
1333	HLA-A*26:01_ESAGVMSVY	1124	CCG5	ENSG00000075429	Voltage-dependent calcium channel gamma-5 subunit (Neuronal voltage-gated calcium channel gamma-5 subunit) (Transmembrane AMPAR regulatory protein gamma-5) (TARP gamma-5)
1334	HLA-B*35:01_EPYLEGISY	1125	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
1335	HLA-C*16:01_SASGPGLAF	1126	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
1336	HLA-A*02:07_ILDVIGVKV	1127	ADA29	ENSG00000168594	Disintegrin and metalloproteinase domain-containing protein 29 (ADAM 29) (Cancer/testis antigen 73) (CT73)
1337	HLA-A*11:01_STLTVDIANK	1128	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
1338	HLA-C*16:01_VVTGHQQSF	1129	DC4L2	ENSG00000176566	DDB1- and CUL4-associated factor 4-like protein 2 (WD repeat-containing protein 21C)
1339	HLA-B*44:03_QEVVGELVAKF	1130	TFDP3	ENSG00000183434	Transcription factor Dp family member 3 (Cancer/testis antigen 30) (CT30) (Hepatocellular carcinoma-associated antigen 661)
1340	HLA-B*35:01_LPGPQQQAF	1131	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)
1341	HLA-A*02:01_YLLEKIPLV	806	NTM1B	ENSG00000203740	Alpha N-terminal protein methyltransferase 1B (EC 2.1.1.299) (Methyltransferase-like protein 11B) (X-Pro-Lys N-terminal protein methyltransferase 1B) (NTM1B)
1342	HLA-B*44:02_AENESVIIRL	1132	TDR15	ENSG00000218819	Tudor domain-containing protein 15

1343	HLA-B*44:03_AENESVIIRL	1132	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1344	HLA-C*02:02_AENESVIIRL	1132	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1345	HLA-A*11:01_AILLQVIAK	1133	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1346	HLA-A*02:01_ALLGQVVYA	1134	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1347	HLA-A*26:01_AVITEINGY	1135	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1348	HLA-B*51:01_DARIFQLSI	1136	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1349	HLA-B*51:01_DPYEIGQTA	1137	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1350	HLA-A*26:01_DVISLMLQAGY	1138	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1351	HLA-B*44:03_EEVYISHIY	1139	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1352	HLA-A*01:01_EVDIVFVDY	1140	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1353	HLA-B*18:01_FEVEFIDY	1141	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1354	HLA-A*11:01_GSMNSNQQLFK	1142	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1355	HLA-B*35:01_IPTDSSSEF	1143	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1356	HLA-B*44:03_KEVDIVFVDY	1144	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1357	HLA-A*11:01_KTVDYFTSK	1145	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1358	HLA-A*24:02_KYVDDKVLVF	1146	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1359	HLA-B*51:01_LPKSLAVNI	1147	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1360	HLA-A*01:01_PTDSSSEFQVY	1148	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1361	HLA-B*35:01_QALLGQVVY	1149	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1362	HLA-A*11:01_QTQESTVNSK	1150	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1363	HLA-A*24:02_QYITLSETF	1151	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1364	HLA-A*02:01_RLAEIVYNI	1152	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1365	HLA-A*31:01_SAKEFLMNR	1153	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1366	HLA-B*44:03_SEFKNPFTL	1154	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1367	HLA-C*02:02_SEFKNPFTL	1154	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1368	HLA-C*02:02_SETSVSDVNSF	1155	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1369	HLA-A*03:01_SLNKKGILK	1156	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1370	HLA-A*11:01_SVNLQNFPK	1157	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1371	HLA-A*30:02_VINKPSPVTY	1158	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1372	HLA-A*02:07_VLDKLQPSL	1159	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1373	HLA-A*29:02_YGFSFYIRY	1160	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1374	HLA-B*08:01_YINEKIKVL	1161	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1375	HLA-A*02:07_YVDDKVLVFL	1162	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1376	HLA-A*02:07_YVDDKVLVF	1163	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1377	HLA-A*31:01_ATLQPRGITR	1164	V9GYR9	ENSG00000225362	Cancer/testis antigen 62 (Fragment)
1378	HLA-A*02:01_YLHEQVKTI	1165	FHL17	ENSG00000132446	Ferritin heavy polypeptide-like 17 (Cancer/testis antigen 38) (CT38)
1379	HLA-B*18:01_QEHLVIAEM	1166	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
1380	HLA-A*31:01_NGKQIYVGR	83	PABP3	ENSG00000151846	Polyadenylate-binding protein 3 (PABP-3) (Poly(A)-binding protein 3) (Testis-specific poly(A)-binding protein)
1381	HLA-B*35:01_AAASLFEVY	1167	OTOP1	ENSG00000163982	Otopetrin-1
1382	HLA-A*30:02_ATIAVVVVY	1168	OTOP1	ENSG00000163982	Otopetrin-1
1383	HLA-B*35:01_HAAASLFEVY	1169	OTOP1	ENSG00000163982	Otopetrin-1
1384	HLA-B*51:01_LPYSILAI	1170	OTOP1	ENSG00000163982	Otopetrin-1
1385	HLA-A*30:02_ASLDSITHRY	1171	CD045	ENSG00000164123	Uncharacterized protein C4orf45
1386	HLA-A*30:02_ASNRSLPAKY	1172	CD045	ENSG00000164123	Uncharacterized protein C4orf45
1387	HLA-B*35:01_TPDPPTIISY	1173	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
1388	HLA-A*03:01_ALYPALPKSGK	1174	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
1389	HLA-B*44:03_LETDIHLSY	642	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
1390	HLA-B*18:01_SEAGLTANQY	472	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
1391	HLA-A*33:01_DVFSPSHKTTR	1175	CL040	ENSG00000180116	Uncharacterized protein C12orf40
1392	HLA-A*33:01_DYYPSSSER	1176	CL040	ENSG00000180116	Uncharacterized protein C12orf40
1393	HLA-A*02:01_ILMEEGGIYSL	1177	CL040	ENSG00000180116	Uncharacterized protein C12orf40
1394	HLA-A*01:01_STDEIRQSDY	1178	CL040	ENSG00000180116	Uncharacterized protein C12orf40
1395	HLA-B*08:01_TLFERLNSL	1179	CL040	ENSG00000180116	Uncharacterized protein C12orf40
1396	HLA-A*24:02_NYSPVTGKF	1180	OTOL1	ENSG00000182447	Otolin-1
1397	HLA-A*02:07_TLDPADFFL	1181	OTOL1	ENSG00000182447	Otolin-1

1398	HLA-B*44:03_AEIAINVHL	1182	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1399	HLA-C*02:02_AEIAINVHL	1182	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1400	HLA-C*02:02_AEYTGAQQKL	1183	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1401	HLA-A*03:01_AINVHLSTLK	1184	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1402	HLA-B*18:01_DENEVATSM	1185	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1403	HLA-A*01:01_FSDLQKGYY	1186	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1404	HLA-B*44:03_MEVDVQEKL	1187	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1405	HLA-A*01:01_VADDGVTQY	1188	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1406	HLA-A*01:01_VLDPAGDWYY	1189	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1407	HLA-B*35:01_YPNITDPEY	1190	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1408	HLA-A*29:02_AFLTSTLLF	1191	PLET1	ENSG00000188771	Placenta-expressed transcript 1 protein
1409	HLA-B*18:01_DEYYTITL	1192	PLET1	ENSG00000188771	Placenta-expressed transcript 1 protein
1410	HLA-B*18:01_TEVEIQAF	1193	PLET1	ENSG00000188771	Placenta-expressed transcript 1 protein
1411	HLA-B*18:01_YENVAKVGF	1194	ZN560	ENSG00000198028	Zinc finger protein 560
1412	HLA-C*02:02_AENQGLVLKF	344	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
1413	HLA-A*02:07_LLDDIMAEV	711	F2Z2I4	ENSG00000228927,EN G00000236424	Testis-specific Y-encoded protein 10 (Testis-specific Y-encoded protein 3)
1414	HLA-A*02:07_LLDDIMAEV	711	TSPY3	ENSG00000228927	Testis-specific Y-encoded protein 3
1415	HLA-A*01:01_ATEVSTWFY	1195	AT5L2	ENSG00000249222	ATP synthase subunit g 2, mitochondrial (ATPase subunit g 2)
1416	HLA-A*02:01_NLVEKTPAL	1196	AT5L2	ENSG00000249222	ATP synthase subunit g 2, mitochondrial (ATPase subunit g 2)
1417	HLA-B*35:01_TPALVNAAVTY	1197	AT5L2	ENSG00000249222	ATP synthase subunit g 2, mitochondrial (ATPase subunit g 2)
1418	HLA-A*02:07_ALDGISQVL	1198	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1419	HLA-B*35:01_DAYPEIEKF	1199	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1420	HLA-B*51:01_DAYPEIEKF	1199	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1421	HLA-B*44:03_EEGELEKLF	1200	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1422	HLA-A*03:01_KTYDAPSALPK	1201	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1423	HLA-A*11:01_KTYDAPSALPK	1201	PTTG2	ENSG00000250254	Securin-2 (Pituitary tumor-transforming gene 2 protein)
1424	HLA-A*29:02_SVYVGDALLY	1202	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
1425	HLA-A*02:07_EMFPKFTEV	1203	BRDT	ENSG00000137948	Bromodomain testis-specific protein (Cancer/testis antigen 9) (CT9) (RING3-like protein)

1426	HLA-A*11:01_AVVDGIQYK	1204	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1427	HLA-A*33:01_DTHAVVTAR	1205	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1428	HLA-A*26:01_EVVAIGTGEY	1206	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1429	HLA-A*11:01_ISNPVLPPK	1207	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1430	HLA-A*11:01_SISNPVLPPK	1208	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1431	HLA-A*31:01_SLAAFIIER	1209	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1432	HLA-B*35:01_HAGPNVYKF	1210	MAJIN	ENSG00000168070	Membrane-anchored junction protein
1433	HLA-B*44:02_AESDVTRFLF	1211	HYPM	ENSG00000187516	Huntingtin-interacting protein M (Huntingtin yeast partner M)
1434	HLA-B*44:03_AESDVTRFLF	1211	HYPM	ENSG00000187516	Huntingtin-interacting protein M (Huntingtin yeast partner M)
1435	HLA-B*44:02_AESDVTRFL	1212	HYPM	ENSG00000187516	Huntingtin-interacting protein M (Huntingtin yeast partner M)
1436	HLA-B*44:03_AESDVTRFL	1212	HYPM	ENSG00000187516	Huntingtin-interacting protein M (Huntingtin yeast partner M)
1437	HLA-A*31:01_QVKTWFQNR	1213	BSH	ENSG00000188909	Brain-specific homeobox protein homolog
1438	HLA-B*51:01_YPLMPTPTL	1214	BSH	ENSG00000188909	Brain-specific homeobox protein homolog
1439	HLA-B*18:01_EEETLKTLY	1215	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1440	HLA-B*44:03_EEETLKTLY	1215	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1441	HLA-C*05:01_IADEAVKL	1216	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1442	HLA-A*30:02_KQKFGEITDTY	1217	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1443	HLA-A*29:02_KVLGEKETLLY	1218	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1444	HLA-B*44:02_SEEETLKTLY	1219	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1445	HLA-B*44:03_SEEETLKTLY	1219	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1446	HLA-C*02:02_SEEETLKTLY	1219	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1447	HLA-B*35:01_TAITTSEQY	1220	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1448	HLA-A*11:01_TSVDHGISK	1221	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1449	HLA-A*11:01_TTSEQYYSK	1222	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1450	HLA-A*01:01_VSEEETLKTLY	1223	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1451	HLA-B*51:01_DAPKEINI	1224	RGS21	ENSG00000253148	Regulator of G-protein signaling 21 (RGS21)
1452	HLA-A*02:01_GLDAFRIFL	1225	RGS21	ENSG00000253148	Regulator of G-protein signaling 21 (RGS21)
1453	HLA-A*02:07_GLDAFRIFL	1225	RGS21	ENSG00000253148	Regulator of G-protein signaling 21 (RGS21)
1454	HLA-B*51:01_LPIEGQEI	1226	BLID	ENSG00000259571	BH3-like motif-containing cell death inducer (Breast cancer cell protein 2)
1455	HLA-A*24:02_LYIGATGQF	1227	TCF24	ENSG00000261787	Transcription factor 24 (TCF-24)
1456	HLA-C*05:01_FTDEGDQLF	1228	SE1L2	ENSG00000101251	Protein sel-1 homolog 2 (Suppressor of lin-12-like protein 2) (Sel-1L2)
1457	HLA-A*29:02_GLHGLGLLY	1229	SE1L2	ENSG00000101251	Protein sel-1 homolog 2 (Suppressor of lin-12-like protein 2) (Sel-1L2)
1458	HLA-A*24:02_LYIKSLPTF	1230	SE1L2	ENSG00000101251	Protein sel-1 homolog 2 (Suppressor of lin-12-like protein 2) (Sel-1L2)
1459	HLA-B*35:01_NALGFLSSY	1231	SE1L2	ENSG00000101251	Protein sel-1 homolog 2 (Suppressor of lin-12-like protein 2) (Sel-1L2)
1460	HLA-B*44:03_TEIVLENNY	305	R4GMQ3	ENSG00000107831	Fibroblast growth factor 8
1461	HLA-B*18:01_TEDIGPQF	1232	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
1462	HLA-A*02:07_FLQEVITTV	732	ZAN	ENSG00000146839	Zonadhesin
1463	HLA-A*01:01_HGDAHLQEY	1233	FATE1	ENSG00000147378	Fetal and adult testis-expressed transcript protein (Cancer/testis antigen 43) (CT43) (Tumor antigen BJ-HCC-2)
1464	HLA-A*11:01_STKPDMIQK	1234	IFNK	ENSG00000147896	Interferon kappa (IFN-kappa)
1465	HLA-B*35:01_QPLQPSSPVAY	1235	PASD1	ENSG00000166049	Circadian clock protein PASD1 (Cancer/testis antigen 63) (CT63) (OX-TES-1) (PAS domain-containing protein 1)
1466	HLA-A*02:01_SLGPVVQV	1236	PASD1	ENSG00000166049	Circadian clock protein PASD1 (Cancer/testis antigen 63) (CT63) (OX-TES-1) (PAS domain-containing protein 1)
1467	HLA-A*30:02_AVSISTVGY	1237	KCNV2	ENSG00000168263	Potassium voltage-gated channel subfamily V member 2 (Voltage-gated potassium channel subunit Kv8.2)
1468	HLA-B*44:03_EEEQLQQARW	1238	CC185	ENSG00000178395	Coiled-coil domain-containing protein 185
1469	HLA-B*44:02_EEQLQQARW	1239	CC185	ENSG00000178395	Coiled-coil domain-containing protein 185
1470	HLA-B*44:03_EEQLQQARW	1239	CC185	ENSG00000178395	Coiled-coil domain-containing protein 185
1471	HLA-B*35:01_FPVQATIDFY	1240	DSCR6	ENSG00000183145	Protein ripply3 (Down syndrome critical region protein 6)

1472	HLA-C*02:02_KEGEPVEFTF	241	LN28B	ENSG00000187772	Protein lin-28 homolog B (Lin-28B)
1473	HLA-B*18:01_LEQLVLMY	1241	CS067	ENSG00000188032	UPF0575 protein C19orf67
1474	HLA-A*30:02_RVAELINASY	1085	DC8L2	ENSG00000189186	DDB1- and CUL4-associated factor 8-like protein 2 (WD repeat-containing protein 42C)
1475	HLA-A*26:01_HVAGEQMAEY	1242	BTNL2	ENSG00000204290	Butyrophilin-like protein 2 (BTL-II)
1476	HLA-B*18:01_TEMQMEEY	1243	BTNL2	ENSG00000204290	Butyrophilin-like protein 2 (BTL-II)
1477	HLA-A*01:01_VTEMQMEEY	1244	BTNL2	ENSG00000204290	Butyrophilin-like protein 2 (BTL-II)
1478	HLA-B*18:01_MEFKAVIY	1245	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1479	HLA-A*24:02_YYLNDLDRI	1246	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1480	HLA-A*24:02_RYILENHDF	1247	RFPLB	ENSG00000251258	Ret finger protein-like 4B (RING finger protein 211)
1481	HLA-A*30:02_TLQEGITGVY	1248	S35G6	ENSG00000259224	Solute carrier family 35 member G6 (Acyl-malonyl-condensing enzyme 1-like protein 3) (Transmembrane protein 21B)
1482	HLA-A*02:01_TLQEGITGV	1249	S35G6	ENSG00000259224	Solute carrier family 35 member G6 (Acyl-malonyl-condensing enzyme 1-like protein 3) (Transmembrane protein 21B)
1483	HLA-A*33:01_EYGNIPVVR	1250	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1484	HLA-A*03:01_GIADPNQSAK	1251	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
1485	HLA-A*11:01_ATLELNETQVK	1252	HXB1	ENSG00000120094	Homeobox protein Hox-B1 (Homeobox protein Hox-2I)
1486	HLA-B*46:01_SINKSGASY	1253	TTLL2	ENSG00000120440	Probable tubulin polyglutamylase TTLL2 (EC 6.-.-.-) (Testis-specific protein NYD-TSPG) (Tubulin--tyrosine ligase-like protein 2)
1487	HLA-B*18:01_EEEKLFLSY	680	APOL5	ENSG00000128313	Apolipoprotein L5 (Apolipoprotein L-V) (ApoL-V)
1488	HLA-B*35:01_FPIVGDVAL	1254	TSN16	ENSG00000130167	Tetraspanin-16 (Tspan-16) (Tetraspanin TM4-B) (Transmembrane 4 superfamily member 16)
1489	HLA-A*02:07_MLDDIPEDNTL	1255	SPT22	ENSG00000141255	Spermatogenesis-associated protein 22 (Testis development protein NYD-SP20)
1490	HLA-C*16:01_AAFVSSRVL	1256	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1491	HLA-A*11:01_ATGSANMTK	1257	SPI2A	ENSG00000147059	Spindlin-2A (Protein DXF34) (Spindlin-like protein 2A) (SPIN-2) (SPIN-2A)
1492	HLA-A*30:02_GVQTFTSGKY	1258	TRI49	ENSG00000168930	Tripartite motif-containing protein 49 (RING finger protein 18) (Testis-specific RING-finger protein)
1493	HLA-B*35:01_MPQPLNPEL	1259	TRI49	ENSG00000168930	Tripartite motif-containing protein 49 (RING finger protein 18) (Testis-specific RING-finger protein)
1494	HLA-A*24:02_NYFIDPVTI	554	TRI49	ENSG00000168930	Tripartite motif-containing protein 49 (RING finger protein 18) (Testis-specific RING-finger protein)
1495	HLA-A*11:01_SSQPSPSDPK	1260	VCX3	ENSG00000169059	Variable charge X-linked protein 3 (Variable charge protein on X with eight repeats) (VCX-8r) (Variably charged protein X-A) (VCX-A)
1496	HLA-B*44:03_AEYTGAQQKL	1183	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1497	HLA-A*29:02_ILLDPVQRNLY	1261	ZN560	ENSG00000198028	Zinc finger protein 560
1498	HLA-A*11:01_AGESGKSTIVK	1262	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1499	HLA-A*26:01_EIIIYGPAY	1263	PSG1	ENSG00000231924	Pregnancy-specific beta-1-glycoprotein 1 (PS-beta-G-1) (PSBG-1) (Pregnancy-specific glycoprotein 1) (CD66 antigen-like family member F) (Fetal liver non-specific cross-reactive antigen 1/2) (FL-NCA-1/2) (PSG95) (Pregnancy-specific beta-1 glycoprotein C/D) (PS-beta-C/D) (CD antigen CD66f)
1500	HLA-A*24:02_EYLTQAAFF	1264	BHMG1	ENSG00000237452	Basic helix-loop-helix and HMG box domain-containing protein 1
1501	HLA-A*02:07_SIDQIYKKL	1265	SMC1B	ENSG00000077935	Structural maintenance of chromosomes protein 1B (SMC protein 1B) (SMC-1-beta) (SMC-1B)
1502	HLA-A*11:01_IVVDKSDLIPK	1266	TDRD1	ENSG00000095627	Tudor domain-containing protein 1 (Cancer/testis antigen 41.1) (CT41.1)
1503	HLA-A*24:02_NYPETLKFMLI	1267	S14L3	ENSG00000100012	SEC14-like protein 3 (Tocopherol-associated protein 2)

1504	HLA-A*30:02_STLKFIGQY	1268	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
1505	HLA-B*51:01_DAPIIKEI	1269	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1506	HLA-B*51:01_EGNPLLLTV	1270	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1507	HLA-A*02:01_FLEGNPLLLTV	1271	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1508	HLA-A*29:02_GFWSDTILY	1272	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1509	HLA-C*02:02_QEMQNSKENF	1273	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1510	HLA-A*24:02_SYLTGSAGEEL	1274	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1511	HLA-A*24:02_VFADFFNTF	1275	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1512	HLA-C*02:02_SEQMSRTNY	1276	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
1513	HLA-B*44:03_MEFSGENRGY	1277	RBM46	ENSG00000151962	Probable RNA-binding protein 46 (Cancer/testis antigen 68) (CT68) (RNA-binding motif protein 46)
1514	HLA-B*08:01_HPQLRKVTL	1278	S22AD	ENSG00000172940	Solute carrier family 22 member 13 (Organic cation transporter-like 3) (ORCTL-3)
1515	HLA-B*44:03_AEAPLSQRW	1279	CI131	ENSG00000174038	Uncharacterized protein C9orf131
1516	HLA-B*18:01_VEAPVSTF	1280	CI131	ENSG00000174038	Uncharacterized protein C9orf131
1517	HLA-A*01:01_VSEPIADQSNY	1281	CI131	ENSG00000174038	Uncharacterized protein C9orf131
1518	HLA-A*02:07_YLDSFADGL	1282	TEX36	ENSG00000175018	Testis-expressed protein 36
1519	HLA-A*02:01_LLFDKEPINV	1283	HORM2	ENSG00000176635	HORMA domain-containing protein 2
1520	HLA-A*29:02_YFSHHLAVY	1284	FBX39	ENSG00000177294	F-box only protein 39
1521	HLA-B*18:01_SEYQLNDSAAY	1285	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1522	HLA-B*18:01_DDVIISSGY	1286	ACSM4	ENSG00000215009	Acyl-coenzyme A synthetase ACSM4, mitochondrial (EC 6.2.1.2) (Acyl-CoA synthetase medium-chain family member 4)
1523	HLA-A*03:01_AILLQVIAK	1133	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1524	HLA-B*46:01_LVASGLATY	1287	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1525	HLA-B*44:03_SENIDVISL	1288	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1526	HLA-A*29:02_TFPSLFSLY	1289	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1527	HLA-B*18:01_EEITLRENF	1290	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1528	HLA-B*44:03_EEITLRENF	1290	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1529	HLA-B*44:02_EENIETERW	1291	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1530	HLA-B*44:03_EENIETERW	1291	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1531	HLA-B*35:01_NAIDVSEHF	1292	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1532	HLA-B*35:01_NAITLPEEF	1293	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1533	HLA-A*24:02_PYADIIATM	1294	RD21L	ENSG00000244588	Double-strand-break repair protein rad21-like protein 1
1534	HLA-B*18:01_DEKLTVTSL	1295	ESX1	ENSG00000123576	Homeobox protein ESX1 (Extraembryonic, spermatogenesis, homeobox 1) [Cleaved into: Homeobox protein ESX1-N; Homeobox protein ESX1-C]
1535	HLA-B*44:02_EEAANSGYSW	381	PRDM7	ENSG00000126856	Probable histone-lysine N-methyltransferase PRDM7 (EC 2.1.1.43) (PR domain zinc finger protein 7) (PR domain-containing protein 7)
1536	HLA-B*35:01_LPDKVFIKY	1296	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
1537	HLA-A*02:01_AVADTLIGV	1297	GP119	ENSG00000147262	Glucose-dependent insulinotropic receptor (G-protein coupled receptor 119)
1538	HLA-A*11:01_ASLDSITHR	1298	CD045	ENSG00000164123	Uncharacterized protein C4orf45
1539	HLA-A*29:02_YLPGLLYKF	1299	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
1540	HLA-A*30:02_TSLDMTHPY	1300	SP7	ENSG00000170374	Transcription factor Sp7 (Zinc finger protein osterix)
1541	HLA-A*02:07_ALMEVTVYL	470	NAL11	ENSG00000179873	NACHT, LRR and PYD domains-containing protein 11 (Nucleotide-binding oligomerization domain protein 17) (PAAD-and NACHT domain-containing protein 10) (PYRIN-containing APAF1-like protein 6)
1542	HLA-B*35:01_MPQPLNPEL	1259	TR49B	ENSG00000182053	Putative tripartite motif-containing protein 49B (RING finger protein 18B)

1543	HLA-B*18:01_DEHTGIHTM	1301	FAM9A	ENSG00000183304	Protein FAM9A
1544	HLA-A*02:07_MLDALLVHI	1302	TMM89	ENSG00000183396	Transmembrane protein 89
1545	HLA-C*05:01_VADDGVTQY	1188	CNGA2	ENSG00000183862	Cyclic nucleotide-gated olfactory channel (Cyclic nucleotide-gated cation channel 2) (Cyclic nucleotide-gated channel alpha-2) (CNG channel alpha-2) (CNG-2) (CNG2)
1546	HLA-A*11:01_ASSAPTAEK	1303	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1547	HLA-B*18:01_EETQILRDTF	1304	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1548	HLA-B*44:03_EETQILRDTF	1304	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1549	HLA-A*03:01_KVAQVPFTTK	1305	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1550	HLA-A*11:01_STSSYPIAEK	1306	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1551	HLA-B*46:01_VLKDVQRSY	1307	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1552	HLA-A*01:01_VSEAKPSQY	1308	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1553	HLA-A*02:07_LLPSWVPEV	1309	SPT21	ENSG00000187144	Spermatogenesis-associated protein 21
1554	HLA-C*02:02_AESDVTRFL	1212	HYPM	ENSG00000187516	Huntingtin-interacting protein M (Huntingtin yeast partner M)
1555	HLA-A*11:01_STVFDPVFK	1310	RFA4	ENSG00000204086	Replication protein A 30 kDa subunit (RP-A p30) (Replication factor A protein 4) (RF-A protein 4)
1556	HLA-A*29:02_IFSAINPVLYY	1311	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1557	HLA-A*11:01_VTTYPISPK	1312	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1558	HLA-A*29:02_LFLFGVTKY	1313	PSG3	ENSG00000221826	Pregnancy-specific beta-1-glycoprotein 3 (PS-beta-G-3) (PSBG-3) (Pregnancy-specific glycoprotein 3) (Carcinoembryonic antigen SG5)
1559	HLA-B*51:01_LPKLPKPYI	578	PSG3	ENSG00000221826	Pregnancy-specific beta-1-glycoprotein 3 (PS-beta-G-3) (PSBG-3) (Pregnancy-specific glycoprotein 3) (Carcinoembryonic antigen SG5)
1560	HLA-B*51:01_LPTTAQVTI	579	PSG3	ENSG00000221826	Pregnancy-specific beta-1-glycoprotein 3 (PS-beta-G-3) (PSBG-3) (Pregnancy-specific glycoprotein 3) (Carcinoembryonic antigen SG5)
1561	HLA-C*01:02_QVPGGSQEL	1314	ANHX	ENSG00000227059	Anomalous homeobox protein
1562	HLA-A*26:01_SVANSTVAY	615	AP2D	ENSG00000008197	Transcription factor AP-2-delta (AP2-delta) (Activating enhancer-binding protein 2-delta) (Transcription factor AP-2-beta-like 1)
1563	HLA-A*24:02_AYAERLGVTF	1315	RB40L	ENSG00000102128	Ras-related protein Rab-40A-like (Ras-like GTPase)
1564	HLA-A*30:02_GAQGVILVY	1316	RB40L	ENSG00000102128	Ras-related protein Rab-40A-like (Ras-like GTPase)
1565	HLA-B*51:01_HAPGVPKI	1317	RB40L	ENSG00000102128	Ras-related protein Rab-40A-like (Ras-like GTPase)
1566	HLA-C*01:02_NIIESFTEL	1318	RB40L	ENSG00000102128	Ras-related protein Rab-40A-like (Ras-like GTPase)
1567	HLA-B*35:01_QAYAERLGVTF	1319	RB40L	ENSG00000102128	Ras-related protein Rab-40A-like (Ras-like GTPase)
1568	HLA-B*35:01_APANIQVSF	1320	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1569	HLA-B*51:01_DAFSMINV	1321	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1570	HLA-A*26:01_DTKYNITVY	1322	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1571	HLA-A*30:02_GQSPLGDIFNY	1323	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1572	HLA-A*11:01_TVMVSPVAK	1324	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1573	HLA-C*01:02_VSPVAKTGL	1325	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1574	HLA-B*51:01_SAAASVLTV	1326	GP119	ENSG00000147262	Glucose-dependent insulinotropic receptor (G-protein coupled receptor 119)
1575	HLA-A*29:02_AFIIKTIGQLY	1327	BOLL	ENSG00000152430	Protein boule-like
1576	HLA-B*51:01_DAMTAFESI	1328	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1577	HLA-B*44:03_EESSINYTF	1329	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1578	HLA-C*04:01_HFDESTTGSNF	1330	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1579	HLA-A*03:01_KLFPGSPAIYK	1331	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1580	HLA-B*18:01_NEQVVFSH	1332	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1581	HLA-A*11:01_SQYGKMANK	1333	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1582	HLA-A*11:01_SVQGSAPSPRK	1334	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1583	HLA-B*51:01_TAFESIKSV	1335	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1584	HLA-A*11:01_VVVETFANK	1336	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3

1585	HLA-B*44:03_SEIDQGKGY	1337	S4R404	ENSG00000163424	Uncharacterized protein C3orf30
1586	HLA-C*02:02_SEIDQGKGY	1337	S4R404	ENSG00000163424	Uncharacterized protein C3orf30
1587	HLA-A*26:01_EVVVALILQY	1338	S35G3	ENSG00000164729	Solute carrier family 35 member G3 (Acyl-malonyl-condensing enzyme 1) (Transmembrane protein 21A)
1588	HLA-B*51:01_TAYLWIRQI	1339	ACHA9	ENSG00000174343	Neuronal acetylcholine receptor subunit alpha-9 (Nicotinic acetylcholine receptor subunit alpha-9) (NACHR alpha-9)
1589	HLA-A*01:01_SSEDLHVFY	1340	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
1590	HLA-B*46:01_VAHLELATY	1341	FMR1N	ENSG00000176988	Fragile X mental retardation 1 neighbor protein (Cancer/testis antigen 37) (CT37) (Sarcoma antigen NY-SAR-35)
1591	HLA-A*11:01_ATGWGLVSK	1342	PRS38	ENSG00000185888	Serine protease 38 (EC 3.4.21.-) (Marapsin-2)
1592	HLA-A*30:02_GSSSGLSSSY	1343	HORN	ENSG00000197915	Hornerin
1593	HLA-A*29:02_NAGPLNVLY	1344	S4R3Z8	ENSG00000203963	Uncharacterized protein C1orf141 (Fragment)
1594	HLA-B*35:01_NAGPLNVLY	1344	S4R3Z8	ENSG00000203963	Uncharacterized protein C1orf141 (Fragment)
1595	HLA-A*30:02_ATSPPTPGHY	1345	A0A0U1RQF7	ENSG00000263201	HCG1775037
1596	HLA-B*44:03_KEVDPTGHSF	379	MAGAA	ENSG00000124260	Melanoma-associated antigen 10 (Cancer/testis antigen 1.10) (CT1.10) (MAGE-10 antigen)
1597	HLA-B*18:01_DEMGVVGYF	1346	OTOR	ENSG00000125879	Otoraplin (Fibrocyte-derived protein) (Melanoma inhibitory activity-like protein)
1598	HLA-C*01:02_AAPLAAGAL	1347	OCSTP	ENSG00000149635	Osteoclast stimulatory transmembrane protein (OC-STAMP)
1599	HLA-C*02:02_AEQLVKTGW	1348	OCSTP	ENSG00000149635	Osteoclast stimulatory transmembrane protein (OC-STAMP)
1600	HLA-B*44:03_SEGEGKELW	1349	OCSTP	ENSG00000149635	Osteoclast stimulatory transmembrane protein (OC-STAMP)
1601	HLA-A*30:02_RLYQTDPSGTY	1350	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
1602	HLA-A*29:02_WVQENYLEY	75	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
1603	HLA-A*33:01_ELQGPWHTR	1351	SUN3	ENSG00000164744	SUN domain-containing protein 3 (Sad1/unc-84 domain-containing protein 1)
1604	HLA-A*03:01_GIFPKIMPK	1352	SSX3	ENSG00000165584	Protein SSX3 (Cancer/testis antigen 5.3) (CT5.3)
1605	HLA-A*29:02_SVFDEKQQWKF	1353	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
1606	HLA-A*31:01_ASGPPAPAR	798	NGN1	ENSG00000181965	Neurogenin-1 (NGN-1) (Class A basic helix-loop-helix protein 6) (bHLHa6) (Neurogenic basic-helix-loop-helix protein) (Neurogenic differentiation factor 3) (NeuroD3)
1607	HLA-C*02:02_QEGSSGMELSW	644	TEX19	ENSG00000182459	Testis-expressed protein 19
1608	HLA-A*01:01_VSDPAKIAIHY	1354	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
1609	HLA-A*02:01_SLVNLQPEL	1355	FOXE3	ENSG00000186790	Forkhead box protein E3 (Forkhead-related protein FKHL12) (Forkhead-related transcription factor 8) (FREAC-8)
1610	HLA-B*35:01_SPLEVPQSF	1356	MAGBG	ENSG00000189023	Melanoma-associated antigen B16 (MAGE-B16 antigen)
1611	HLA-A*11:01_ATLENLLSH	1044	PRAM9	ENSG00000204501	PRAME family member 9/15
1612	HLA-A*02:07_TLDEYLTYL	1357	PRAM9	ENSG00000204501	PRAME family member 9/15
1613	HLA-B*51:01_DGYYRGIVV	1358	MO2R2	ENSG00000206531	Cell surface glycoprotein CD200 receptor 2 (CD200 cell surface glycoprotein receptor-like 2) (CD200 receptor-like 2) (HuCD200R2) (CD200 cell surface glycoprotein receptor-like a) (CD200RLa) (Cell surface glycoprotein CD200 receptor 1-like) (Cell surface glycoprotein OX2 receptor 2)
1614	HLA-B*51:01_IAPDNVHVI	1359	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1615	HLA-B*08:01_DVVAKTSL	1360	E5RK72	ENSG00000215262	Potassium channel subfamily U member 1
1616	HLA-B*44:03_GEIIIYGPAY	1361	PSG1	ENSG00000231924	Pregnancy-specific beta-1-glycoprotein 1 (PS-beta-G-1) (PSBG-1) (Pregnancy-specific glycoprotein 1) (CD66 antigen-like family member F) (Fetal liver non-specific cross-reactive antigen 1/2) (FL-NCA-1/2) (PSG95) (Pregnancy-specific beta-1 glycoprotein C/D) (PS-beta-C/D) (CD antigen CD66f)

1617	HLA-B*35:01_HPTLGPSAF	1362	TIFAB	ENSG00000255833	TRAF-interacting protein with FHA domain-containing protein B (TIFA-like protein)
1618	HLA-A*33:01_DYRDKSPQNR	1363	ERVV2	ENSG00000268964	Endogenous retrovirus group V member 2 Env polyprotein (HERV-V_19q13.41 provirus ancestral Env polyprotein 2)
1619	HLA-A*02:01_SLLNGFVAV	1364	TSN16	ENSG00000130167	Tetraspanin-16 (Tspan-16) (Tetraspanin TM4-B) (Transmembrane 4 superfamily member 16)
1620	HLA-B*18:01_AEVLAQSF	1365	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1621	HLA-A*26:01_EVFNEDGTVRY	1366	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1622	HLA-A*26:01_EVITSDILHSF	1367	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1623	HLA-A*26:01_EVVQIGTSIF	1368	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1624	HLA-A*11:01_SVLPAEALVLK	1369	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1625	HLA-A*01:01_TSDILHSFLY	1370	PRD12	ENSG00000130711	PR domain zinc finger protein 12 (EC 2.1.1.-) (PR domain-containing protein 12)
1626	HLA-A*02:07_TLADALHTL	596	MSGN1	ENSG00000151379	Mesogenin-1 (Paraxial mesoderm-specific mesogenin1) (pMesogenin1) (pMsgn1)
1627	HLA-A*11:01_RTMVFVETK	1371	DDX4	ENSG00000152670	Probable ATP-dependent RNA helicase DDX4 (EC 3.6.4.13) (DEAD box protein 4) (Vasa homolog)
1628	HLA-B*44:03_REVLPLATF	1372	TERT	ENSG00000164362	Telomerase reverse transcriptase (EC 2.7.7.49) (HEST2) (Telomerase catalytic subunit) (Telomerase-associated protein 2) (TP2)
1629	HLA-A*26:01_ETTGKVIYF	1373	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
1630	HLA-A*03:01_LLFWKPLRY	172	S6A18	ENSG00000164363	Sodium-dependent neutral amino acid transporter B(0)AT3 (Sodium- and chloride-dependent transporter XTRP2) (Solute carrier family 6 member 18) (System B(0) neutral amino acid transporter AT3)
1631	HLA-A*26:01_DSVPLIAQY	1374	CRFM7	ENSG00000166664	CHRNA7-FAM7A fusion protein (CHRNA7-DR1) (D-10)
1632	HLA-B*44:03_AEAALQTLL	1375	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1633	HLA-B*44:03_AEDQGFQFSY	1376	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1634	HLA-B*18:01_DEFVVLAL	1377	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1635	HLA-A*26:01_EAISQIASF	1378	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1636	HLA-A*26:01_EVISMGTSV	1379	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1637	HLA-A*02:07_HLWDPNPKIGV	1380	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1638	HLA-A*02:07_HMDTVVVNL	1381	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1639	HLA-A*02:07_ILDDAIVQRL	1382	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1640	HLA-A*11:01_IVMGDLSTK	1383	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing

					protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1641	HLA-A*01:01_LTDRDVSFY	1384	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1642	HLA-B*18:01_DEIFNTEAM	1385	SL9C1	ENSG00000172139	Sodium/hydrogen exchanger 10 (Na(+)/H(+) exchanger 10) (NHE-10) (Solute carrier family 9 member 10) (Solute carrier family 9 member C1) (Sperm-specific Na(+)/H(+) exchanger) (sNHE)
1643	HLA-B*44:03_SEVEEPLTVW	1386	VCX2	ENSG00000177504	Variable charge X-linked protein 2 (Variable charge protein on X with two repeats) (VCX-2r) (Variably charged protein X-B) (VCX-B)
1644	HLA-A*02:01_LLWERIELYL	1387	GDPD4	ENSG00000178795	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-) (Glycerophosphodiester phosphodiesterase 6) (UgpQ)
1645	HLA-A*11:01_SSQPSPSDPK	1260	VCX1	ENSG00000182583	Variable charge X-linked protein 1 (Variable charge protein on X with ten repeats) (VCX-10r) (Variably charged protein X-B1) (VCX-B1)
1646	HLA-A*33:01_EMYAIYQQR	1388	SAMD7	ENSG00000187033	Sterile alpha motif domain-containing protein 7 (SAM domain-containing protein 7)
1647	HLA-A*03:01_SSYNRGLISK	196	NPSR1	ENSG00000187258	Neuropeptide S receptor (G-protein coupled receptor 154) (G-protein coupled receptor PGR14) (G-protein coupled receptor for asthma susceptibility)
1648	HLA-A*02:01_GLLEISQQL	1389	CS067	ENSG00000188032	UPF0575 protein C19orf67
1649	HLA-A*02:01_VLITAVVEV	1390	RN133	ENSG00000188050	E3 ubiquitin-protein ligase RNF133 (EC 2.3.2.27) (RING finger protein 133) (RING-type E3 ubiquitin transferase RNF133)
1650	HLA-A*02:07_FMDFLQTLL	1391	SG1C1	ENSG00000188076	Secretoglobin family 1C member 1 (Secretoglobin RYD5)
1651	HLA-B*44:03_SESSTILVVRY	316	SPNXD	ENSG00000196406	Sperm protein associated with the nucleus on the X chromosome D (Cancer/testis antigen 11.4) (CT11.4) (Nuclear-associated protein SPAN-Xd) (SPANX-D) (SPANX family member D)
1652	HLA-A*26:01_EAPGLGGTY	1392	ONEC3	ENSG00000205922	One cut domain family member 3 (One cut homeobox 3) (Transcription factor ONECUT-3) (OC-3)
1653	HLA-B*35:01_MPVPGQQSM	1393	AMELY	ENSG00000099721	Amelogenin, Y isoform
1654	HLA-A*02:07_FLEGNPLLLTV	1271	H3BVE8	ENSG00000121446	Regulator of G-protein-signaling protein-like
1655	HLA-C*02:02_AESEGTKAV	1394	H2BWT	ENSG00000123569	Histone H2B type W-T (H2B histone family member W testis-specific)
1656	HLA-C*16:01_AESEGTKAV	1394	H2BWT	ENSG00000123569	Histone H2B type W-T (H2B histone family member W testis-specific)
1657	HLA-A*11:01_RVVPPASNMLK	1395	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1658	HLA-A*01:01_TTDDDITTDHY	1396	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1659	HLA-C*01:02_VVPPASNML	1397	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1660	HLA-B*51:01_YPVSWSSVI	1398	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1661	HLA-A*03:01_STASIFLAY	913	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1662	HLA-B*44:03_AEQLVKTGW	1348	OCSTP	ENSG00000149635	Osteoclast stimulatory transmembrane protein (OC-STAMP)
1663	HLA-A*11:01_ATQNAVKLIDK	1399	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1664	HLA-A*01:01_DTDMKYLLY	1400	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1665	HLA-A*33:01_EYKNVGSER	1401	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1666	HLA-A*01:01_GTEFGDTDMKY	1402	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1667	HLA-B*44:03_TEFGDTDMKY	1403	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1668	HLA-C*02:02_KEVDPAGHSY	1404	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
1669	HLA-A*29:02_IVFSEEFEY	1405	SL9C2	ENSG00000162753	Sodium/hydrogen exchanger 11 (Na(+)/H(+) exchanger 11) (NHE-11) (Solute carrier family 9 member 11) (Solute carrier family 9 member C2)
1670	HLA-B*08:01_DVKMKAVM	1406	PLS2	ENSG00000163746	Phospholipid scramblase 2 (PL scramblase 2) (Ca(2+)-dependent phospholipid scramblase 2)
1671	HLA-A*29:02_YLYPFNIEY	1407	OTOP1	ENSG00000163982	Otopetrin-1

1672	HLA-A*11:01_SSISNPVLPPK	1408	ADAD1	ENSG00000164113	Adenosine deaminase domain-containing protein 1 (Testis nuclear RNA-binding protein)
1673	HLA-B*35:01_FPFTYKGSVY	1409	ESPB1	ENSG00000169393	Epididymal sperm-binding protein 1 (Epididymal secretory protein 12) (hE12)
1674	HLA-A*30:02_STIPGVSAY	249	ZPLD1	ENSG00000170044	Zona pellucida-like domain-containing protein 1 (ZP domain-containing protein 1)
1675	HLA-A*02:01_HLWDPNPKIGV	1380	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1676	HLA-B*18:01_DENGQSASY	1410	ATS20	ENSG00000173157	A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)
1677	HLA-B*44:03_AEVELIDQTL	1411	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1678	HLA-B*35:01_LPIRSSILY	1412	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1679	HLA-A*11:01_STYGIITSR	1413	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1680	HLA-A*31:01_STYGIITSR	1413	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1681	HLA-A*11:01_VVADVSNNK	1414	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1682	HLA-A*11:01_VVADVSSNNK	1415	TMPS7	ENSG00000176040	Transmembrane protease serine 7 (EC 3.4.21.-) (Matriptase-3)
1683	HLA-B*18:01_LELATYEL	1416	FMR1N	ENSG00000176988	Fragile X mental retardation 1 neighbor protein (Cancer/testis antigen 37) (CT37) (Sarcoma antigen NY-SAR-35)
1684	HLA-A*24:02_NYFIDPVTI	554	TR49B	ENSG00000182053	Putative tripartite motif-containing protein 49B (RING finger protein 18B)
1685	HLA-A*29:02_SIFTGFLLY	1417	OTOL1	ENSG00000182447	Otolin-1
1686	HLA-B*18:01_DESLIYSF	1418	TRIML	ENSG00000184108	Probable E3 ubiquitin-protein ligase TRIML1 (EC 2.3.2.27) (RING finger protein 209) (RING-type E3 ubiquitin transferase TRIML1) (Tripartite motif family-like protein 1)
1687	HLA-B*44:03_SEDLKSVKY	1419	TRIML	ENSG00000184108	Probable E3 ubiquitin-protein ligase TRIML1 (EC 2.3.2.27) (RING finger protein 209) (RING-type E3 ubiquitin transferase TRIML1) (Tripartite motif family-like protein 1)
1688	HLA-A*02:07_TLDPATANAYL	1420	TRIML	ENSG00000184108	Probable E3 ubiquitin-protein ligase TRIML1 (EC 2.3.2.27) (RING finger protein 209) (RING-type E3 ubiquitin transferase TRIML1) (Tripartite motif family-like protein 1)
1689	HLA-A*30:02_VLQSEDEQGSY	1421	TRIML	ENSG00000184108	Probable E3 ubiquitin-protein ligase TRIML1 (EC 2.3.2.27) (RING finger protein 209) (RING-type E3 ubiquitin transferase TRIML1) (Tripartite motif family-like protein 1)
1690	HLA-A*03:01_RLYSGTARY	1422	KCNH7	ENSG00000184611	Potassium voltage-gated channel subfamily H member 7 (Ether-a-go-go-related gene potassium channel 3) (ERG-3) (Eag-related protein 3) (Ether-a-go-go-related protein 3) (hERG-3) (Voltage-gated potassium channel subunit Kv11.3)
1691	HLA-A*11:01_VTSGEYSLFQK	1423	OVCH1	ENSG00000187950	Ovochymase-1 (EC 3.4.21.-)
1692	HLA-A*03:01_NTYASTLYK	884	FGF16	ENSG00000196468	Fibroblast growth factor 16 (FGF-16)
1693	HLA-A*03:01_GVHGGILNK	1424	PROF3	ENSG00000196570	Profilin-3 (Profilin III)
1694	HLA-A*11:01_GVHGGILNK	1424	PROF3	ENSG00000196570	Profilin-3 (Profilin III)
1695	HLA-A*30:02_GGLLGPSHSY	1425	DMBX1	ENSG00000197587	Diencephalon/mesencephalon homeobox protein 1 (Orthodenticle homolog 3) (Paired-like homeobox protein DMBX1)
1696	HLA-A*29:02_TVIDVFYQY	1426	HORN	ENSG00000197915	Hornerin
1697	HLA-A*26:01_EYFPKSVSEY	1427	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1698	HLA-B*35:01_LVASGLATY	1287	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1699	HLA-B*44:03_SETSVSDVNSF	1155	TDR15	ENSG00000218819	Tudor domain-containing protein 15
1700	HLA-A*11:01_ASSQSTPVK	1428	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
1701	HLA-A*11:01_GTMSTISPSK	1429	MORC1	ENSG00000114487	MORC family CW-type zinc finger protein 1 (Cancer/testis antigen 33) (CT33)
1702	HLA-B*51:01_TPLKWYQSI	1430	AMELX	ENSG00000125363	Amelogenin, X isoform
1703	HLA-A*02:07_SLPSPGELYAV	1431	RNF17	ENSG00000132972	RING finger protein 17 (Tudor domain-containing protein 4)
1704	HLA-B*44:02_TEDIGSKGY	537	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting

					testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
1705	HLA-C*02:02_TEDIGSKGY	537	RXFP2	ENSG00000133105	Relaxin receptor 2 (G-protein coupled receptor 106) (G-protein coupled receptor affecting testicular descent) (Leucine-rich repeat-containing G-protein coupled receptor 8) (Relaxin family peptide receptor 2)
1706	HLA-A*11:01_GTEQLTITGK	1432	LGSN	ENSG00000146166	Lengsin (Glutamate-ammonia ligase domain-containing protein 1) (Lens glutamine synthase-like)
1707	HLA-A*24:02_LYMQIINFF	1433	STRA8	ENSG00000146857	Stimulated by retinoic acid gene 8 protein homolog
1708	HLA-A*11:01_SGISQVFQR	1434	TRI48	ENSG00000150244	Tripartite motif-containing protein 48 (RING finger protein 101)
1709	HLA-B*51:01_DSLPRLTSV	1435	CNTP5	ENSG00000155052	Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)
1710	HLA-B*44:03_KEVDPAGHSY	1404	MAGA8	ENSG00000156009	Melanoma-associated antigen 8 (Cancer/testis antigen 1.8) (CT1.8) (MAGE-8 antigen)
1711	HLA-C*02:02_AAASLFEVY	1167	OTOP1	ENSG00000163982	Otopetrin-1
1712	HLA-B*46:01_HAKDIIQSF	1436	OTOP1	ENSG00000163982	Otopetrin-1
1713	HLA-B*18:01_DEEQNLVAF	380	PRDM9	ENSG00000164256	Histone-lysine N-methyltransferase PRDM9 (EC 2.1.1.43) (PR domain zinc finger protein 9) (PR domain-containing protein 9)
1714	HLA-B*44:03_EEAANNGYSW	1437	PRDM9	ENSG00000164256	Histone-lysine N-methyltransferase PRDM9 (EC 2.1.1.43) (PR domain zinc finger protein 9) (PR domain-containing protein 9)
1715	HLA-C*02:02_EEAANNGYSW	1437	PRDM9	ENSG00000164256	Histone-lysine N-methyltransferase PRDM9 (EC 2.1.1.43) (PR domain zinc finger protein 9) (PR domain-containing protein 9)
1716	HLA-B*44:03_EEQNLVAFQY	382	PRDM9	ENSG00000164256	Histone-lysine N-methyltransferase PRDM9 (EC 2.1.1.43) (PR domain zinc finger protein 9) (PR domain-containing protein 9)
1717	HLA-C*16:01_AFSDRTNAL	1438	FSHR	ENSG00000170820	Follicle-stimulating hormone receptor (FSH-R) (Follitropin receptor)
1718	HLA-B*35:01_DAAGFFTVF	1439	FSHR	ENSG00000170820	Follicle-stimulating hormone receptor (FSH-R) (Follitropin receptor)
1719	HLA-B*51:01_DAAGFFTV	1440	FSHR	ENSG00000170820	Follicle-stimulating hormone receptor (FSH-R) (Follitropin receptor)
1720	HLA-B*35:01_FPIFGISSY	1441	FSHR	ENSG00000170820	Follicle-stimulating hormone receptor (FSH-R) (Follitropin receptor)
1721	HLA-C*02:02_AEAALQTLL	1375	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1722	HLA-B*35:01_EAISQIASF	1378	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1723	HLA-A*11:01_SVADLTESILK	638	LDH6B	ENSG00000171989	L-lactate dehydrogenase A-like 6B (EC 1.1.1.27)
1724	HLA-A*02:01_TLWEIQNKLKL	1442	LDH6B	ENSG00000171989	L-lactate dehydrogenase A-like 6B (EC 1.1.1.27)
1725	HLA-A*03:01_VVNQGKGMFK	411	CTSRD	ENSG00000174898	Cation channel sperm-associated protein subunit delta (CatSper-delta) (CatSperdelta) (Transmembrane protein 146)
1726	HLA-A*11:01_ASLTTDGSLK	1443	TSYL6	ENSG00000178021	Testis-specific Y-encoded-like protein 6 (TSPY-like protein 6)
1727	HLA-B*51:01_LAIAGMNTI	1444	OTOL1	ENSG00000182447	Otolin-1
1728	HLA-A*29:02_LYLFGVTKY	1445	PSG9	ENSG00000183668	Pregnancy-specific beta-1-glycoprotein 9 (PS-beta-G-9) (PSBG-9) (Pregnancy-specific glycoprotein 9) (PS34) (Pregnancy-specific beta-1 glycoprotein B) (PS-beta-B) (Pregnancy-specific beta-1-glycoprotein 11) (PS-beta-G-11) (PSBG-11) (Pregnancy-specific glycoprotein 11) (Pregnancy-specific glycoprotein 7) (PSG7)
1729	HLA-B*35:01_HPIGGDVAL	1446	PRS38	ENSG00000185888	Serine protease 38 (EC 3.4.21.-) (Marapsin-2)
1730	HLA-B*51:01_FAYIAGHSI	1447	GTR7	ENSG00000197241	Solute carrier family 2, facilitated glucose transporter member 7 (Glucose transporter type 7) (GLUT-7)
1731	HLA-A*02:07_MVDGAVHWL	1448	GTR7	ENSG00000197241	Solute carrier family 2, facilitated glucose transporter member 7 (Glucose transporter type 7) (GLUT-7)
1732	HLA-A*29:02_IVFGDRFDY	1449	CP2AD	ENSG00000197838	Cytochrome P450 2A13 (EC 1.14.14.1) (CYPIIA13)

1733	HLA-B*44:03_EEIFLAKIEKF	1450	X6R7K4	ENSG00000203910	Chromosome 1 open reading frame 146 (Uncharacterized protein C1orf146)
1734	HLA-A*11:01_STEEIFLAK	1451	X6R7K4	ENSG00000203910	Chromosome 1 open reading frame 146 (Uncharacterized protein C1orf146)
1735	HLA-A*24:02_IYSNTLQSI	1452	GNAT3	ENSG00000214415	Guanine nucleotide-binding protein G(t) subunit alpha-3 (Gustducin alpha-3 chain)
1736	HLA-B*18:01_DEKGTIYDY	1453	GPX5	ENSG00000224586	Epididymal secretory glutathione peroxidase (EC 1.11.1.9) (Epididymis-specific glutathione peroxidase-like protein) (EGLP) (Glutathione peroxidase 5) (GPx-5) (GSHPx-5)
1737	HLA-B*18:01_NEYVSFKQY	1454	GPX5	ENSG00000224586	Epididymal secretory glutathione peroxidase (EC 1.11.1.9) (Epididymis-specific glutathione peroxidase-like protein) (EGLP) (Glutathione peroxidase 5) (GPx-5) (GSHPx-5)
1738	HLA-B*44:03_NEYVSFKQY	1454	GPX5	ENSG00000224586	Epididymal secretory glutathione peroxidase (EC 1.11.1.9) (Epididymis-specific glutathione peroxidase-like protein) (EGLP) (Glutathione peroxidase 5) (GPx-5) (GSHPx-5)
1739	HLA-A*11:01_GSGLHQVSK	1455	E9PBZ7	ENSG00000242715	Coiled-coil domain-containing protein 169
1740	HLA-B*44:02_IEAELHISY	254	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
1741	HLA-A*26:01_DTTHPISYY	1456	GGTL2	ENSG00000100121	Gamma-glutamyltransferase light chain 2 (Gamma-glutamyltransferase-like protein 4)
1742	HLA-B*51:01_YAHLTNSSI	1457	TTLL2	ENSG00000120440	Probable tubulin polyglutamylase TTLL2 (EC 6.-.-.-) (Testis-specific protein NYD-TSPG) (Tubulin--tyrosine ligase-like protein 2)
1743	HLA-A*11:01_AQNARIFSK	1458	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1744	HLA-A*02:01_KLVTDLPNV	1459	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1745	HLA-C*16:01_SEKEPGQQY	831	RHXF2	ENSG00000131721	Rhox homeobox family member 2 (Paired-like homeobox protein PEPP-2) (Testis homeobox gene 1)
1746	HLA-A*29:02_HVVSGVFFY	1460	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
1747	HLA-A*02:07_YVPIFVVGV	1461	NMUR2	ENSG00000132911	Neuromedin-U receptor 2 (NMU-R2) (G-protein coupled receptor FM-4) (G-protein coupled receptor TGR-1)
1748	HLA-A*02:07_TVTEKIYYL	695	F71F1	ENSG00000135248	Protein FAM71F1 (Protein FAM137A) (Testis development protein NYD-SP18)
1749	HLA-B*51:01_SAPEIPTI	1462	FNDC7	ENSG00000143107	Fibronectin type III domain-containing protein 7
1750	HLA-B*18:01_DEVQIEVV	1463	X6R6V8	ENSG00000143552	Nuclear pore membrane glycoprotein 210-like
1751	HLA-B*35:01_QPIYQQPAY	1464	BOLL	ENSG00000152430	Protein boule-like
1752	HLA-A*29:02_IFTSATYLY	1465	PANX3	ENSG00000154143	Pannexin-3
1753	HLA-A*30:02_RSHSLVATY	1466	PANX3	ENSG00000154143	Pannexin-3
1754	HLA-A*29:02_YFEFPLLERY	1467	PANX3	ENSG00000154143	Pannexin-3
1755	HLA-A*11:01_GTNIVVLGVEK	1468	PSA7L	ENSG00000154611	Proteasome subunit alpha type-7-like (EC 3.4.25.1)
1756	HLA-A*30:02_AVKSVGEPKY	1469	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1757	HLA-B*18:01_DETESSFAM	1470	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1758	HLA-C*02:02_FASDVRINF	1471	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1759	HLA-C*16:01_FASDVRINF	1471	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1760	HLA-A*03:01_KVIGIVIGK	1472	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1761	HLA-A*11:01_KVIGIVIGK	1472	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1762	HLA-C*04:01_LYDETESSF	1473	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1763	HLA-A*02:07_SLDFKSVFL	1474	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)
1764	HLA-B*51:01_YAYISTLNI	1475	MEIOB	ENSG00000162039	Meiosis-specific with OB domain-containing protein (EC 3.1.-.-)

1765	HLA-B*44:03_DEYGQELGIKW	1476	PRDM9	ENSG00000164256	Histone-lysine N-methyltransferase PRDM9 (EC 2.1.1.43) (PR domain zinc finger protein 9) (PR domain-containing protein 9)
1766	HLA-B*44:03_SEAVSVLHHW	1477	SPT19	ENSG00000166118	Spermatogenesis-associated protein 19, mitochondrial (Spermatogenic cell-specific gene 1 protein) (Spergen-1)
1767	HLA-A*11:01_STLDLANTLQK	1478	MB3L1	ENSG00000170948	Methyl-CpG-binding domain protein 3-like 1 (MBD3-like protein 1)
1768	HLA-B*44:03_QEAAENYRKLF	1479	TRIMM	ENSG00000179046	Probable E3 ubiquitin-protein ligase TRIML2 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase TRIML2) (SPRY domain-containing protein 6) (Tripartite motif family-like protein 2)
1769	HLA-A*24:02_EYLFDTHTL	1480	FTMT	ENSG00000181867	Ferritin, mitochondrial (EC 1.16.3.1)
1770	HLA-A*24:02_VYLSMAYYF	1481	FTMT	ENSG00000181867	Ferritin, mitochondrial (EC 1.16.3.1)
1771	HLA-A*03:01_QTLGIPLTPK	1482	H0YFA1	ENSG00000185958	Protein FAM186A (Fragment)
1772	HLA-A*29:02_LFSPITQQLRY	1483	CS067	ENSG00000188032	UPF0575 protein C19orf67
1773	HLA-A*02:01_ALAPLLMTL	1484	S22AO	ENSG00000197658	Solute carrier family 22 member 24
1774	HLA-A*30:02_AAHPIGLVY	1485	DPRX	ENSG00000204595	Divergent paired-related homeobox
1775	HLA-A*30:02_SVTTYTGSY	530	CD051	ENSG00000237136	Uncharacterized protein C4orf51
1776	HLA-B*44:03_AENGLLEKI	1486	ASIC5	ENSG00000256394	Acid-sensing ion channel 5 (ASIC5) (Amiloride-sensitive cation channel 5) (Human intestine Na(+) channel) (HINaC)
1777	HLA-B*44:03_EEIEYPATISY	1487	ASIC5	ENSG00000256394	Acid-sensing ion channel 5 (ASIC5) (Amiloride-sensitive cation channel 5) (Human intestine Na(+) channel) (HINaC)
1778	HLA-B*18:01_IEYPATISY	1488	ASIC5	ENSG00000256394	Acid-sensing ion channel 5 (ASIC5) (Amiloride-sensitive cation channel 5) (Human intestine Na(+) channel) (HINaC)
1779	HLA-B*18:01_MEFPAVTF	1489	ASIC5	ENSG00000256394	Acid-sensing ion channel 5 (ASIC5) (Amiloride-sensitive cation channel 5) (Human intestine Na(+) channel) (HINaC)
1780	HLA-A*11:01_ASQLHTLIK	1490	DUXA	ENSG00000258873	Double homeobox protein A
1781	HLA-B*44:02_EEQLKILINTF	1491	DUXA	ENSG00000258873	Double homeobox protein A
1782	HLA-A*31:01_RIQIWFQNR	1492	DUXA	ENSG00000258873	Double homeobox protein A
1783	HLA-A*31:01_RVQIWFQNR	1493	DUXA	ENSG00000258873	Double homeobox protein A
1784	HLA-A*11:01_GIADPNQSAK	1251	ADAM7	ENSG00000069206	Disintegrin and metalloproteinase domain-containing protein 7 (ADAM 7) (Sperm maturation-related glycoprotein GP-83)
1785	HLA-A*29:02_GLNQLYFYY	1494	TRPC5	ENSG00000072315	Short transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TRP-5) (hTRP-5) (hTRP5)
1786	HLA-B*35:01_HAISSAGVMY	1495	WNT8B	ENSG00000075290	Protein Wnt-8b
1787	HLA-A*26:01_EVAQSNSAF	1496	SE1L2	ENSG00000101251	Protein sel-1 homolog 2 (Suppressor of lin-12-like protein 2) (Sel-1L2)
1788	HLA-A*02:07_ATDSFHTEL	1497	DKKL1	ENSG00000104901	Dickkopf-like protein 1 (Cancer/testis antigen 34) (CT34) (Protein soggy-1) (SGY-1)
1789	HLA-A*24:02_IYAPPNNRF	1498	GCNT7	ENSG00000124091	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 (EC 2.4.1.-)
1790	HLA-B*51:01_VPAQQPVI	1499	AMELX	ENSG00000125363	Amelogenin, X isoform
1791	HLA-B*18:01_DESTILHL	1500	CCD83	ENSG00000150676	Coiled-coil domain-containing protein 83
1792	HLA-B*44:03_MEGPFFRDY	1501	IZUM2	ENSG00000161652	Izumo sperm-egg fusion protein 2
1793	HLA-B*35:01_DPAVFQLVY	1502	KCNV2	ENSG00000168263	Potassium voltage-gated channel subfamily V member 2 (Voltage-gated potassium channel subunit Kv8.2)
1794	HLA-A*11:01_GSYSNNSTEK	1503	MRO2B	ENSG00000171495	Maestro heat-like repeat-containing protein family member 2B (HEAT repeat-containing protein 7B2) (Sperm PKA-interacting factor) (SPIF)
1795	HLA-A*11:01_ATAQKLKKK	1504	WDR87	ENSG00000171804	WD repeat-containing protein 87 (Testis development protein NYD-SP11)
1796	HLA-A*29:02_GTATLLIVRY	1505	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
1797	HLA-A*11:01_ATAGARSKVK	1506	MAGBA	ENSG00000177689	Melanoma-associated antigen B10 (MAGE-B10 antigen)
1798	HLA-A*11:01_GTNGFQLLR	1049	SG11A	ENSG00000178287	Sperm-associated antigen 11A (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)
1799	HLA-A*02:07_LLPPRTPPYQV	1050	SG11A	ENSG00000178287	Sperm-associated antigen 11A (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)

1800	HLA-B*51:01_VPLGIRNTI	1507	SG11A	ENSG00000178287	Sperm-associated antigen 11A (Human epididymis-specific protein 2) (He2) (Protein EP2) (Sperm antigen HE2)
1801	HLA-B*46:01_ILRPPVEAY	1508	FA71C	ENSG00000180219	Protein FAM71C
1802	HLA-A*02:01_VLSAVTPEL	1509	SAGE1	ENSG00000181433	Sarcoma antigen 1 (Cancer/testis antigen 14) (CT14)
1803	HLA-A*02:07_VVPPWNPQL	1510	ADIG	ENSG00000182035	Adipogenin
1804	HLA-B*44:03_DEYGNTTLHY	1039	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1805	HLA-A*11:01_SQDEILTNK	1511	D7UEQ8	ENSG00000183206	POTE ankyrin domain family member C
1806	HLA-A*01:01_FSDFGLLWY	1512	NALP9	ENSG00000185792	NACHT, LRR and PYD domains-containing protein 9 (Nucleotide-binding oligomerization domain protein 6) (PYRIN and NACHT-containing protein 12)
1807	HLA-B*46:01_NAITGSAF	1513	DCC	ENSG00000187323	Netrin receptor DCC (Colorectal cancer suppressor) (Immunoglobulin superfamily DCC subclass member 1) (Tumor suppressor protein DCC)
1808	HLA-B*46:01_FAFEKDVEM	1116	H9KVA5	ENSG00000187959	Putative cleavage and polyadenylation-specificity factor subunit 4-like protein
1809	HLA-B*44:03_SEYPIIFVY	1514	SPXN3	ENSG00000189252	Sperm protein associated with the nucleus on the X chromosome N3 (Nuclear-associated protein SPAN-Xn3) (SPANX-N3) (SPANX family member N3)
1810	HLA-A*01:01_GSDFGHSSSY	1515	HORN	ENSG00000197915	Hornerin
1811	HLA-B*44:02_EEETLKTLY	1215	Q5VXJ5	ENSG00000198765	Synaptonemal complex protein 1 (Fragment)
1812	HLA-A*26:01_ETPSETPTY	1516	F8W8N9	ENSG00000204930	Protein FAM221B (Fragment)
1813	HLA-A*01:01_ISETPSETPTY	1517	F8W8N9	ENSG00000204930	Protein FAM221B (Fragment)
1814	HLA-B*44:03_SETPSETPTY	1518	F8W8N9	ENSG00000204930	Protein FAM221B (Fragment)
1815	HLA-B*44:03_EEVARFLTYY	1519	1A1L2	ENSG00000205126	Probable inactive 1-aminocyclopropane-1-carboxylate synthase-like protein 2 (ACC synthase-like protein 2)
1816	HLA-A*29:02_STLPTTINY	31	MAGAC	ENSG00000213401	Melanoma-associated antigen 12 (Cancer/testis antigen 1.12) (CT1.12) (MAGE-12 antigen) (MAGE12F antigen)
1817	HLA-B*44:03_SEAPSLPVVF	1520	GRCR1	ENSG00000215203	Glutaredoxin domain-containing cysteine-rich protein 1
1818	HLA-A*30:02_GTGQVSSTY	1521	A0A1B0GTN1	ENSG00000224960	Putative SMEK homolog 3
1819	HLA-A*29:02_HFLFLFLLY	1522	PATE3	ENSG00000236027	Prostate and testis expressed protein 3 (Acrosomal vesicle protein HEL-127) (PATE-like protein DJ) (PATE-DJ)
1820	HLA-B*18:01_MEYLTQAAF	1523	BHMG1	ENSG00000237452	Basic helix-loop-helix and HMG box domain-containing protein 1
1821	HLA-B*27:02_GTGTGIAGITK	253	SYCY2	ENSG00000244476	Syncytin-2 (Endogenous retrovirus group FRD member 1) (Envelope polyprotein) (HERV-FRD) (HERV-FRD_6p24.1 provirus ancestral Env polyprotein) [Cleaved into: Surface protein (SU); Transmembrane protein (TM)]
1822	HLA-B*44:02_VEVGEVKSW	401	RFPLB	ENSG00000251258	Ret finger protein-like 4B (RING finger protein 211)
1823	HLA-A*01:01_WTDGSSYDY	1524	CL19A	ENSG00000261210	C-type lectin domain family 19 member A
1824	HLA-B*44:03_EEFLDGEHW	1525	CALR3	ENSG00000269058	Calreticulin-3 (Calreticulin-2) (Calsperin)
1825	HLA-B*44:03_SEFENIGAIGL	1526	CALR3	ENSG00000269058	Calreticulin-3 (Calreticulin-2) (Calsperin)
1826	HLA-A*02:01_GLSEVISVV	1527	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1827	HLA-B*44:03_IETEFKNDY	886	TRPC7	ENSG00000069018	Short transient receptor potential channel 7 (TrpC7) (Transient receptor protein 7) (TRP-7) (hTRP7)
1828	HLA-A*24:02_IYANISGHL	1528	ADAM2	ENSG00000104755	Disintegrin and metalloproteinase domain-containing protein 2 (ADAM 2) (Cancer/testis antigen 15) (CT15) (Fertilin subunit beta) (PH-30) (PH30) (PH30-beta)
1829	HLA-A*11:01_AVYENELVATR	1529	ZP4	ENSG00000116996	Zona pellucida sperm-binding protein 4 (Zona pellucida glycoprotein 4) (Zp-4) (Zona pellucida protein B) [Cleaved into: Processed zona pellucida sperm-binding protein 4]
1830	HLA-B*44:03_NEIVATIKF	1530	SACA1	ENSG00000118434	Sperm acrosome membrane-associated protein 1 (Sperm acrosomal membrane-associated protein 32)
1831	HLA-A*30:02_AQNARIFSKY	1531	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)

1832	HLA-B*44:03_EEIVNIHNAL	1532	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1833	HLA-A*03:01_RVVPPASNMLK	1395	CRIS1	ENSG00000124812	Cysteine-rich secretory protein 1 (CRISP-1) (AEG-like protein) (ARP) (Acidic epididymal glycoprotein homolog)
1834	HLA-A*03:01_AINLVTKGINK	1533	BAFL	ENSG00000125888	Barrier-to-autointegration factor-like protein (BAF-L) (Barrier-to-autointegration factor 2)
1835	HLA-A*11:01_AINLVTKGINK	1533	BAFL	ENSG00000125888	Barrier-to-autointegration factor-like protein (BAF-L) (Barrier-to-autointegration factor 2)
1836	HLA-A*02:07_WVDGISHEL	1534	BAFL	ENSG00000125888	Barrier-to-autointegration factor-like protein (BAF-L) (Barrier-to-autointegration factor 2)
1837	HLA-A*02:07_KLDQTTMNV	1535	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
1838	HLA-A*29:02_YFFSGPKTY	1536	MMP20	ENSG00000137674	Matrix metalloproteinase-20 (MMP-20) (EC 3.4.24.-) (Enamel metalloproteinase) (Enamelysin)
1839	HLA-A*02:01_TLIETTAEA	1537	NDST4	ENSG00000138653	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 4 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 4) (NDST-4) (N-heparan sulfate sulfotransferase 4) (N-HSST 4) [Includes: Heparan sulfate N-deacetylase 4 (EC 3.-.-.-); Heparan sulfate N-sulfotransferase 4 (EC 2.8.2.-)]
1840	HLA-A*02:01_FLWRGNVVL	1538	TRI43	ENSG00000144015	Tripartite motif-containing protein 43
1841	HLA-B*18:01_QEVITTVY	1539	ZAN	ENSG00000146839	Zonadhesin
1842	HLA-B*44:02_AEQLVKTGW	1348	OCSTP	ENSG00000149635	Osteoclast stimulatory transmembrane protein (OC-STAMP)
1843	HLA-A*11:01_AVDIVSQSK	1540	PO4F2	ENSG00000151615	POU domain, class 4, transcription factor 2 (Brain-specific homeobox/POU domain protein 3B) (Brain-3B) (Brn-3B)
1844	HLA-B*18:01_EESSINYTF	1329	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1845	HLA-A*02:07_KLPVPLESV	1541	J3KNE0	ENSG00000153165	RanBP2-like and GRIP domain-containing protein 3
1846	HLA-B*35:01_TAFGDLEVF	1542	ASZ1	ENSG00000154438	Ankyrin repeat, SAM and basic leucine zipper domain-containing protein 1 (Ankyrin-like protein 1) (Germ cell-specific ankyrin, SAM and basic leucine zipper domain-containing protein)
1847	HLA-A*01:01_KTELETALYY	1543	GG6L2	ENSG00000174450	Golgin subfamily A member 6-like protein 2
1848	HLA-B*18:01_TELETALYY	1544	GG6L2	ENSG00000174450	Golgin subfamily A member 6-like protein 2
1849	HLA-A*26:01_ESIPESSLY	1545	UROL1	ENSG00000177398	Uromodulin-like 1 (Olfactorin)
1850	HLA-A*02:01_ALAESVAQL	1546	A3LT2	ENSG00000184389	Alpha-1,3-galactosyltransferase 2 (EC 2.4.1.87) (Isoglobotriaosylceramide synthase) (iGb3 synthase) (iGb3S)
1851	HLA-B*51:01_LAYLVGQSI	1547	PIWL3	ENSG00000184571	Piwi-like protein 3
1852	HLA-A*29:02_IVLPVWLNY	1548	VHLL	ENSG00000189030	Von Hippel-Lindau-like protein (VHL-like protein) (VLP)
1853	HLA-A*29:02_AAHPIGLVY	1485	DPRX	ENSG00000204595	Divergent paired-related homeobox
1854	HLA-B*35:01_EPLSVTAKY	874	VCX3B	ENSG00000205642	Variable charge X-linked protein 3B (Variably charged protein X-C) (VCX-C)
1855	HLA-A*11:01_ATMGKLASK	1549	LEUTX	ENSG00000213921	Leucine-twenty homeobox
1856	HLA-A*29:02_IITDLSLYY	1550	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1857	HLA-A*31:01_QSQPIGYQR	1551	M4A18	ENSG00000214782	Membrane-spanning 4-domains subfamily A member 18
1858	HLA-A*30:02_KNIALNGEY	1552	GRCR1	ENSG00000215203	Glutaredoxin domain-containing cysteine-rich protein 1
1859	HLA-A*29:02_LFLFGVTKY	1313	PSG11	ENSG00000243130	Pregnancy-specific beta-1-glycoprotein 11 (PS-beta-G-11) (PSBG-11) (Pregnancy-specific glycoprotein 11) (Pregnancy-specific beta-1-glycoprotein 13) (PS-beta-G-13) (PSBG-13) (Pregnancy-specific glycoprotein 13)
1860	HLA-B*51:01_YPKLPMPYI	1553	PSG11	ENSG00000243130	Pregnancy-specific beta-1-glycoprotein 11 (PS-beta-G-11) (PSBG-11) (Pregnancy-specific glycoprotein 11) (Pregnancy-specific beta-1-glycoprotein 13) (PS-beta-G-13) (PSBG-13) (Pregnancy-specific glycoprotein 13)
1861	HLA-A*24:02_VYIPGSNATL	1554	PCDG8	ENSG00000253767	Protocadherin gamma-A8 (PCDH-gamma-A8)
1862	HLA-A*03:01_KVYAENGLLEK	1555	ASIC5	ENSG00000256394	Acid-sensing ion channel 5 (ASIC5) (Amiloride-sensitive cation channel 5) (Human intestine Na(+) channel) (HINaC)

1863	HLA-B*44:03_AEFIESGQY	1556	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1864	HLA-A*11:01_ASTDPNIVRK	1557	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1865	HLA-A*11:01_STDPNIVRKK	1558	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1866	HLA-A*11:01_STDPNIVRK	1559	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1867	HLA-A*03:01_AVSPPASNMLK	1560	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1868	HLA-A*11:01_AVSPPASNMLK	1560	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1869	HLA-B*18:01_DEILDFVY	1561	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1870	HLA-B*51:01_DPTSWSSAI	1562	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1871	HLA-B*35:01_LPAEGKDPAF	1563	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1872	HLA-B*51:01_LPVLFLVTV	1564	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1873	HLA-C*01:02_VSPPASNML	1565	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)
1874	HLA-C*02:02_AEFIESGQY	1556	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1875	HLA-A*03:01_STDPNIVRKK	1558	TAF7L	ENSG00000102387	Transcription initiation factor TFIID subunit 7-like (Cancer/testis antigen 40) (CT40) (RNA polymerase II TBP-associated factor subunit Q) (TATA box-binding protein-associated factor 50 kDa) (Transcription initiation factor TFIID 50 kDa subunit)
1876	HLA-B*44:03_REVTTNAQRW	1566	CRIS2	ENSG00000124490	Cysteine-rich secretory protein 2 (CRISP-2) (Cancer/testis antigen 36) (CT36) (Testis-specific protein TPX-1)

TABLE A (CONT'D)

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Target	**Gene Name**	**Gene ID**	**Peptide**	**SEQ ID NO**	**HLA**

1877	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-A*02:07
1878	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-A*68:02
1879	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-B*38:01
1880	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-B*40:01
1881	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-C*02:02
1882	AFP	ENSG00000081051	AADIIIGHL	1567	HLA-C*05:01
1883	AFP	ENSG00000081051	AATVTKELR	1568	HLA-A*68:01
1884	AFP	ENSG00000081051	AATVTKELR	1568	HLA-C*07:06
1885	AFP	ENSG00000081051	AATVTKEL	1569	HLA-A*32:01
1886	AFP	ENSG00000081051	AATVTKEL	1569	HLA-B*08:01
1887	AFP	ENSG00000081051	AATVTKEL	1569	HLA-B*46:01
1888	AFP	ENSG00000081051	AATVTKEL	1569	HLA-B*58:01
1889	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*01:02
1890	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*03:03
1891	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*03:04
1892	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*05:01
1893	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*12:03
1894	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*14:02
1895	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*16:01
1896	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*16:02
1897	AFP	ENSG00000081051	AATVTKEL	1569	HLA-C*16:04
1898	AFP	ENSG00000081051	ADFSGLLEK	1570	HLA-A*03:01
1899	AFP	ENSG00000081051	ADFSGLLEK	1570	HLA-A*03:02
1900	AFP	ENSG00000081051	ADFSGLLEK	1570	HLA-A*11:01
1901	AFP	ENSG00000081051	ADFSGLLEK	1570	HLA-B*27:02
1902	AFP	ENSG00000081051	ADFSGLLEK	1570	HLA-B*27:05
1903	AFP	ENSG00000081051	ADIIIGHL	1571	HLA-A*30:01
1904	AFP	ENSG00000081051	ADIIIGHL	1571	HLA-B*37:01
1905	AFP	ENSG00000081051	ADIIIGHL	1571	HLA-B*40:02
1906	AFP	ENSG00000081051	ADIIIGHL	1571	HLA-B*44:02
1907	AFP	ENSG00000081051	ADLATIFF	1572	HLA-B*37:01
1908	AFP	ENSG00000081051	AEEGQKLI	1573	HLA-B*44:02
1909	AFP	ENSG00000081051	AEEGQKLI	1573	HLA-B*44:03
1910	AFP	ENSG00000081051	AEEGQKLI	1573	HLA-B*49:01
1911	AFP	ENSG00000081051	AEISLADLATI	1574	HLA-A*30:01
1912	AFP	ENSG00000081051	AEISLADLATI	1574	HLA-B*40:01
1913	AFP	ENSG00000081051	AEISLADLATI	1574	HLA-B*44:02
1914	AFP	ENSG00000081051	AEISLADLATI	1574	HLA-B*44:03
1915	AFP	ENSG00000081051	AEISLADLATI	1574	HLA-B*49:01
1916	AFP	ENSG00000081051	AEISLADLA	1575	HLA-A*30:01
1917	AFP	ENSG00000081051	AEISLADLA	1575	HLA-B*40:01
1918	AFP	ENSG00000081051	AEISLADLA	1575	HLA-B*40:02
1919	AFP	ENSG00000081051	AEISLADLA	1575	HLA-B*49:01
1920	AFP	ENSG00000081051	AEISLADL	1576	HLA-A*30:01
1921	AFP	ENSG00000081051	AEISLADL	1576	HLA-B*37:01
1922	AFP	ENSG00000081051	AEISLADL	1576	HLA-B*40:01
1923	AFP	ENSG00000081051	AEISLADL	1576	HLA-B*44:03
1924	AFP	ENSG00000081051	AEISLADL	1576	HLA-B*49:01
1925	AFP	ENSG00000081051	AENAVECF	1577	HLA-A*30:01
1926	AFP	ENSG00000081051	AENAVECF	1577	HLA-B*18:01
1927	AFP	ENSG00000081051	AENAVECF	1577	HLA-B*27:02
1928	AFP	ENSG00000081051	AENAVECF	1577	HLA-B*37:01
1929	AFP	ENSG00000081051	AENAVECF	1577	HLA-B*44:02
1930	AFP	ENSG00000081051	AENAVECF	1577	HLA-B*44:03
1931	AFP	ENSG00000081051	AENAVECF	1577	HLA-C*16:04
1932	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-A*30:01
1933	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-B*27:02
1934	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-B*40:01
1935	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-B*44:02
1936	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-B*44:03
1937	AFP	ENSG00000081051	AENDEKPEGL	1578	HLA-C*16:04
1938	AFP	ENSG00000081051	AFSDDKFIF	1579	HLA-A*23:01
1939	AFP	ENSG00000081051	AFSDDKFIF	1579	HLA-A*29:02
1940	AFP	ENSG00000081051	ALQTMKQEF	1580	HLA-A*32:01

1941	AFP	ENSG00000081051	ALQTMKQEF	1580	HLA-B*15:01
1942	AFP	ENSG00000081051	ALQTMKQEF	1580	HLA-B*37:01
1943	AFP	ENSG00000081051	ALQTMKQEF	1580	HLA-C*14:02
1944	AFP	ENSG00000081051	ALQTMKQEF	1580	HLA-C*16:01
1945	AFP	ENSG00000081051	APQLTSSELMA	1581	HLA-B*56:01
1946	AFP	ENSG00000081051	APQLTSSELM	1582	HLA-B*07:02
1947	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-B*07:02
1948	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-B*35:01
1949	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-B*35:03
1950	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-B*55:01
1951	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-B*56:01
1952	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-C*01:02
1953	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-C*07:02
1954	AFP	ENSG00000081051	APQLTSSEL	1583	HLA-C*14:02
1955	AFP	ENSG00000081051	APTILLWAA	1584	HLA-B*54:01
1956	AFP	ENSG00000081051	APTILLWAA	1584	HLA-B*55:01
1957	AFP	ENSG00000081051	APTILLWAA	1584	HLA-B*56:01
1958	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-A*03:01
1959	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-A*03:02
1960	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-A*11:01
1961	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-B*13:02
1962	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-B*27:02
1963	AFP	ENSG00000081051	AQFVQEATYK	1585	HLA-B*27:05
1964	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-A*25:01
1965	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-A*26:01
1966	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-A*29:02
1967	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-A*30:02
1968	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-A*32:01
1969	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*13:02
1970	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*15:01
1971	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*15:03
1972	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*18:01
1973	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*27:02
1974	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*27:05
1975	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*35:01
1976	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*37:01
1977	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*39:01
1978	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*44:02
1979	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*44:03
1980	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*46:01
1981	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-B*58:01
1982	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*02:02
1983	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*07:04
1984	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*12:03
1985	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*14:02
1986	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*16:01
1987	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*16:02
1988	AFP	ENSG00000081051	AQFVQEATY	1586	HLA-C*16:04
1989	AFP	ENSG00000081051	AQFVQEAT	1587	HLA-B*13:02
1990	AFP	ENSG00000081051	AQFVQEAT	1587	HLA-B*15:01
1991	AFP	ENSG00000081051	AQGVALQTM	1588	HLA-B*13:02
1992	AFP	ENSG00000081051	AQGVALQTM	1588	HLA-B*15:01
1993	AFP	ENSG00000081051	AQGVALQTM	1588	HLA-B*15:03
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2001	AFP	ENSG00000081051	ASFVHEYSR	1590	HLA-A*31:01
2002	AFP	ENSG00000081051	ASFVHEYSR	1590	HLA-B*57:01
2003	AFP	ENSG00000081051	ASFVHEYSR	1590	HLA-C*07:06
2004	AFP	ENSG00000081051	ATIFFAQFV	1591	HLA-A*68:02

2005	AFP	ENSG00000081051	ATYKEVSKMVK	1592	HLA-A*03:01
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2007	AFP	ENSG00000081051	ATYKEVSKMVK	1592	HLA-A*11:01
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2012	AFP	ENSG00000081051	ATYKEVSKM	1593	HLA-A*25:01
2013	AFP	ENSG00000081051	ATYKEVSKM	1593	HLA-A*26:01
2014	AFP	ENSG00000081051	ATYKEVSKM	1593	HLA-A*31:01
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2017	AFP	ENSG00000081051	ATYKEVSKM	1593	HLA-B*40:02
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2136	AFP	ENSG00000081051	EGAADIIIGHL	1628	HLA-A*68:02
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3063	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-B*37:01
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3065	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-B*40:02
3066	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-B*44:02
3067	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-B*49:01
3068	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-C*05:01
3069	AFP	ENSG00000081051	YEEDRETFM	1897	HLA-C*16:04
3070	AFP	ENSG00000081051	YEEDRETF	1898	HLA-B*18:01
3071	AFP	ENSG00000081051	YEEDRETF	1898	HLA-B*37:01
3072	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-A*01:01
3073	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-A*26:01
3074	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-A*29:02
3075	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-A*30:02
3076	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-B*15:01
3077	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-B*27:02
3078	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-B*35:01
3079	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-B*46:01
3080	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-C*02:02
3081	AFP	ENSG00000081051	YGIASILDSY	1899	HLA-C*16:04
3082	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-B*35:03
3083	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-B*38:01
3084	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-B*39:01
3085	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-B*40:01
3086	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-C*02:02
3087	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-C*03:03
3088	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-C*03:04
3089	AFP	ENSG00000081051	YICSQQDTL	1900	HLA-C*07:04
3090	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*03:02
3091	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*11:01
3092	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*31:01

3093	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*33:01
3094	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*33:03
3095	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-A*68:01
3096	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-B*27:02
3097	AFP	ENSG00000081051	YIQESQALAKR	1901	HLA-C*07:06
3098	AFP	ENSG00000081051	YIQESQALAK	1902	HLA-A*01:01
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3101	AFP	ENSG00000081051	YIQESQALAK	1902	HLA-A*11:01
3102	AFP	ENSG00000081051	YIQESQALAK	1902	HLA-A*68:01
3103	AFP	ENSG00000081051	YIQESQALAK	1902	HLA-B*27:02
3104	AFP	ENSG00000081051	YIQESQALAK	1902	HLA-C*07:06
3105	AFP	ENSG00000081051	YIQESQALA	1903	HLA-A*02:01
3106	AFP	ENSG00000081051	YIQESQAL	1904	HLA-A*30:01
3107	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*08:01
3108	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*15:01
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3110	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*35:03
3111	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*37:01
3112	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*39:01
3113	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*40:01
3114	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*40:02
3115	AFP	ENSG00000081051	YIQESQAL	1904	HLA-B*46:01
3116	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*01:02
3117	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*03:03
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3119	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*05:01
3120	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*07:04
3121	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*14:02
3122	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*16:01
3123	AFP	ENSG00000081051	YIQESQAL	1904	HLA-C*16:02
3124	AFP	ENSG00000081051	YLQNAFLVAY	1905	HLA-A*01:01
3125	AFP	ENSG00000081051	YLQNAFLVAY	1905	HLA-A*29:02
3126	AFP	ENSG00000081051	YLQNAFLVAY	1905	HLA-A*30:02
3127	AFP	ENSG00000081051	YLQNAFLVAY	1905	HLA-B*15:01
3128	AFP	ENSG00000081051	YLQNAFLVAY	1905	HLA-B*46:01
3129	AFP	ENSG00000081051	YLQNAFLVA	1906	HLA-A*02:01
3130	AFP	ENSG00000081051	YLQNAFLVA	1906	HLA-A*02:04
3131	AFP	ENSG00000081051	YLQNAFLVA	1906	HLA-B*54:01
3132	AFP	ENSG00000081051	YLQNAFLV	1907	HLA-A*02:04
3133	AFP	ENSG00000081051	YLQNAFLV	1907	HLA-B*13:02
3134	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-B*13:02
3135	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-B*27:05
3136	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-B*38:01
3137	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-B*39:01
3138	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-B*40:01
3139	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-C*03:03
3140	AFP	ENSG00000081051	YQCTAEISL	1908	HLA-C*07:04
3141	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-B*07:02
3142	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-B*08:01
3143	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-B*40:02
3144	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-B*51:01
3145	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-B*58:01
3146	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*03:03
3147	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*03:04
3148	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*06:02
3149	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*07:01
3150	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*12:03
3151	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*16:01
3152	AFP	ENSG00000081051	YTKKAPQL	1909	HLA-C*16:02
3153	AFP	ENSG00000081051	YYLQNAFLVAY	1910	HLA-A*29:02
3154	AFP	ENSG00000081051	YYLQNAFLV	1911	HLA-A*23:01
3155	AFP	ENSG00000081051	YYLQNAFLV	1911	HLA-A*24:02
3156	AFP	ENSG00000081051	YYLQNAFLV	1911	HLA-A*29:02

3157	AFP	ENSG00000081051	YYLQNAFL	1912	HLA-A*23:01
3158	MART1	ENSG00000120215	AAGIGILTV	1913	HLA-A*02:03
3159	MART1	ENSG00000120215	AAGIGILTV	1913	HLA-B*13:02
3160	MART1	ENSG00000120215	AAGIGILTV	1913	HLA-B*49:01
3161	MART1	ENSG00000120215	AAGIGILTV	1913	HLA-B*51:01
3162	MART1	ENSG00000120215	AAGIGILTV	1913	HLA-C*12:03
3163	MART1	ENSG00000120215	AEEAAGIGIL	1914	HLA-A*30:01
3164	MART1	ENSG00000120215	AEEAAGIGIL	1914	HLA-B*40:01
3165	MART1	ENSG00000120215	AEEAAGIGIL	1914	HLA-B*40:02
3166	MART1	ENSG00000120215	AEEAAGIGIL	1914	HLA-B*44:02
3167	MART1	ENSG00000120215	AEEAAGIGIL	1914	HLA-B*49:01
3168	MART1	ENSG00000120215	AEEAAGIGI	1915	HLA-A*30:01
3169	MART1	ENSG00000120215	AEEAAGIGI	1915	HLA-B*40:01
3170	MART1	ENSG00000120215	AEEAAGIGI	1915	HLA-B*44:02
3171	MART1	ENSG00000120215	AEEAAGIGI	1915	HLA-B*44:03
3172	MART1	ENSG00000120215	AEEAAGIGI	1915	HLA-B*49:01
3173	MART1	ENSG00000120215	AEQSPPPYSP	1916	HLA-B*27:05
3174	MART1	ENSG00000120215	AEQSPPPYSP	1916	HLA-B*40:02
3175	MART1	ENSG00000120215	AEQSPPPYSP	1916	HLA-B*44:02
3176	MART1	ENSG00000120215	AEQSPPPY	1917	HLA-A*30:02
3177	MART1	ENSG00000120215	AEQSPPPY	1917	HLA-B*18:01
3178	MART1	ENSG00000120215	AEQSPPPY	1917	HLA-B*37:01
3179	MART1	ENSG00000120215	AEQSPPPY	1917	HLA-B*44:03
3180	MART1	ENSG00000120215	AGIGILTVI	1918	HLA-A*23:01
3181	MART1	ENSG00000120215	AGIGILTVI	1918	HLA-B*13:02
3182	MART1	ENSG00000120215	AGIGILTVI	1918	HLA-B*49:01
3183	MART1	ENSG00000120215	AGIGILTVI	1918	HLA-C*02:02
3184	MART1	ENSG00000120215	ALMDKSLHVG	1919	HLA-A*02:01
3185	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-A*02:01
3186	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-A*02:03
3187	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-A*02:04
3188	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-A*02:07
3189	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-B*08:01
3190	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-B*13:02
3191	MART1	ENSG00000120215	ALMDKSLHV	1920	HLA-B*55:01
3192	MART1	ENSG00000120215	APPAYEKLSA	1921	HLA-B*54:01
3193	MART1	ENSG00000120215	APPAYEKLSA	1921	HLA-B*56:01
3194	MART1	ENSG00000120215	CPQEGFDHR	1922	HLA-A*33:03
3195	MART1	ENSG00000120215	DAHFIYGYPK	1923	HLA-A*33:01
3196	MART1	ENSG00000120215	DAHFIYGY	1924	HLA-B*18:01
3197	MART1	ENSG00000120215	DAHFIYGY	1924	HLA-B*35:01
3198	MART1	ENSG00000120215	DAHFIYGY	1924	HLA-B*51:01
3199	MART1	ENSG00000120215	DHRDSKVSL	1925	HLA-B*08:01
3200	MART1	ENSG00000120215	DHRDSKVSL	1925	HLA-B*38:01
3201	MART1	ENSG00000120215	DHRDSKVSL	1925	HLA-B*39:01
3202	MART1	ENSG00000120215	DSKVSLQEK	1926	HLA-A*33:01
3203	MART1	ENSG00000120215	DSKVSLQEK	1926	HLA-A*33:03
3204	MART1	ENSG00000120215	DSKVSLQEK	1926	HLA-A*68:01
3205	MART1	ENSG00000120215	DSKVSLQEK	1926	HLA-C*07:06
3206	MART1	ENSG00000120215	EAAGIGILTVI	1927	HLA-A*25:01
3207	MART1	ENSG00000120215	EAAGIGILTVI	1927	HLA-A*26:01
3208	MART1	ENSG00000120215	EAAGIGILTVI	1927	HLA-A*68:01
3209	MART1	ENSG00000120215	EAAGIGILTVI	1927	HLA-A*68:02
3210	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-A*25:01
3211	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-A*26:01
3212	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-A*68:01
3213	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-A*68:02
3214	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-B*51:01
3215	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-B*54:01
3216	MART1	ENSG00000120215	EAAGIGILTV	1928	HLA-C*07:06
3217	MART1	ENSG00000120215	EAAGIGILT	1929	HLA-A*33:03
3218	MART1	ENSG00000120215	EAAGIGILT	1929	HLA-A*68:01
3219	MART1	ENSG00000120215	EAAGIGILT	1929	HLA-A*68:02
3220	MART1	ENSG00000120215	EAAGIGILT	1929	HLA-C*07:06

3221	MART1	ENSG00000120215	EDAHFIYGY	1930	HLA-A*26:01
3222	MART1	ENSG00000120215	EEAAGIGILTV	1931	HLA-A*30:01
3223	MART1	ENSG00000120215	EEAAGIGILTV	1931	HLA-A*68:02
3224	MART1	ENSG00000120215	EEAAGIGILTV	1931	HLA-B*44:02
3225	MART1	ENSG00000120215	EEAAGIGILTV	1931	HLA-B*44:03
3226	MART1	ENSG00000120215	EEAAGIGILTV	1931	HLA-B*49:01
3227	MART1	ENSG00000120215	EEAAGIGIL	1932	HLA-A*30:01
3228	MART1	ENSG00000120215	EEAAGIGIL	1932	HLA-B*38:01
3229	MART1	ENSG00000120215	EEAAGIGIL	1932	HLA-B*40:01
3230	MART1	ENSG00000120215	EEAAGIGIL	1932	HLA-B*44:02
3231	MART1	ENSG00000120215	EEAAGIGIL	1932	HLA-B*44:03
3232	MART1	ENSG00000120215	EEAAGIGI	1933	HLA-B*44:02
3233	MART1	ENSG00000120215	EEAAGIGI	1933	HLA-B*44:03
3234	MART1	ENSG00000120215	EEAAGIGI	1933	HLA-B*49:01
3235	MART1	ENSG00000120215	EPVVPNAPPAY	1934	HLA-A*01:01
3236	MART1	ENSG00000120215	EPVVPNAPPAY	1934	HLA-A*26:01
3237	MART1	ENSG00000120215	EPVVPNAPPAY	1934	HLA-A*30:02
3238	MART1	ENSG00000120215	EPVVPNAPPAY	1934	HLA-B*35:01
3239	MART1	ENSG00000120215	EPVVPNAPPA	1935	HLA-B*54:01
3240	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-B*13:02
3241	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-B*27:05
3242	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-B*38:01
3243	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-B*39:01
3244	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-B*40:02
3245	MART1	ENSG00000120215	EQSPPPYSP	1936	HLA-C*06:02
3246	MART1	ENSG00000120215	GILTVILGV	1937	HLA-A*02:01
3247	MART1	ENSG00000120215	GILTVILGV	1937	HLA-A*02:03
3248	MART1	ENSG00000120215	GILTVILGV	1937	HLA-A*02:04
3249	MART1	ENSG00000120215	GILTVILGV	1937	HLA-A*02:07
3250	MART1	ENSG00000120215	GILTVILGV	1937	HLA-B*13:02
3251	MART1	ENSG00000120215	GTQCALTRR	1938	HLA-A*31:01
3252	MART1	ENSG00000120215	HSYTTAEEA	1939	HLA-B*54:01
3253	MART1	ENSG00000120215	HVGTQCALTR	1940	HLA-A*68:01
3254	MART1	ENSG00000120215	HVGTQCALTR	1940	HLA-C*07:06
3255	MART1	ENSG00000120215	HVGTQCAL	1941	HLA-B*08:01
3256	MART1	ENSG00000120215	HVGTQCAL	1941	HLA-C*01:02
3257	MART1	ENSG00000120215	HVGTQCAL	1941	HLA-C*07:04
3258	MART1	ENSG00000120215	ILTVILGV	1942	HLA-B*13:02
3259	MART1	ENSG00000120215	KLSAEQSPPPY	1943	HLA-A*03:02
3260	MART1	ENSG00000120215	KLSAEQSPPPY	1943	HLA-A*30:02
3261	MART1	ENSG00000120215	KSLHVGTQC	1944	HLA-B*58:01
3262	MART1	ENSG00000120215	LHVGTQCAL	1945	HLA-B*38:01
3263	MART1	ENSG00000120215	LHVGTQCAL	1945	HLA-B*39:01
3264	MART1	ENSG00000120215	LSAEQSPPPY	1946	HLA-A*01:01
3265	MART1	ENSG00000120215	LSAEQSPPPY	1946	HLA-A*26:01
3266	MART1	ENSG00000120215	LSAEQSPPPY	1946	HLA-A*30:02
3267	MART1	ENSG00000120215	MPREDAHFIY	1947	HLA-B*35:01
3268	MART1	ENSG00000120215	MPREDAHFI	1948	HLA-B*51:01
3269	MART1	ENSG00000120215	NAPPAYEKL	1949	HLA-A*02:07
3270	MART1	ENSG00000120215	NAPPAYEKL	1949	HLA-B*35:03
3271	MART1	ENSG00000120215	NAPPAYEKL	1949	HLA-B*51:01
3272	MART1	ENSG00000120215	NAPPAYEKL	1949	HLA-C*01:02
3273	MART1	ENSG00000120215	NAPPAYEKL	1949	HLA-C*05:01
3274	MART1	ENSG00000120215	PVVPNAPPAY	1950	HLA-A*26:01
3275	MART1	ENSG00000120215	PVVPNAPPAY	1950	HLA-A*30:02
3276	MART1	ENSG00000120215	QEKNCEPVV	1951	HLA-B*40:02
3277	MART1	ENSG00000120215	QEKNCEPVV	1951	HLA-B*49:01
3278	MART1	ENSG00000120215	REDAHFIYGY	1952	HLA-B*44:02
3279	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-A*01:01
3280	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-A*30:02
3281	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-A*32:01
3282	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*15:03
3283	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*35:01
3284	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*35:03

3285	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*39:01
3286	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*46:01
3287	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*55:01
3288	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-B*58:01
3289	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*01:02
3290	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*02:02
3291	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*03:03
3292	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*03:04
3293	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*04:01
3294	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*05:01
3295	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*07:04
3296	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*07:06
3297	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*12:03
3298	MART1	ENSG00000120215	SAEQSPPPY	1953	HLA-C*16:02
3299	MART1	ENSG00000120215	SYTTAEEAA	1954	HLA-C*14:02
3300	MART1	ENSG00000120215	SYTTAEEA	1955	HLA-C*14:02
3301	MART1	ENSG00000120215	TAEEAAGIGIL	1956	HLA-B*35:03
3302	MART1	ENSG00000120215	TAEEAAGIGIL	1956	HLA-C*05:01
3303	MART1	ENSG00000120215	TAEEAAGIGI	1957	HLA-C*05:01
3304	MART1	ENSG00000120215	TAEEAAGI	1958	HLA-C*05:01
3305	MART1	ENSG00000120215	TTAEEAAGIGI	1959	HLA-A*26:01
3306	MART1	ENSG00000120215	TTAEEAAGIGI	1959	HLA-A*68:01
3307	MART1	ENSG00000120215	TTAEEAAGIGI	1959	HLA-A*68:02
3308	MART1	ENSG00000120215	VILGVLLLI	1960	HLA-A*02:04
3309	MART1	ENSG00000120215	VILGVLLLI	1960	HLA-A*23:01
3310	MART1	ENSG00000120215	VPNAPPAYEKL	1961	HLA-B*07:02
3311	MART1	ENSG00000120215	VPNAPPAYEKL	1961	HLA-B*35:03
3312	MART1	ENSG00000120215	VPNAPPAYEK	1962	HLA-C*07:06
3313	MART1	ENSG00000120215	VPNAPPAY	1963	HLA-B*35:01
3314	MART1	ENSG00000120215	VVPNAPPAYEK	1964	HLA-A*03:01
3315	MART1	ENSG00000120215	VVPNAPPAYEK	1964	HLA-A*03:02
3316	MART1	ENSG00000120215	VVPNAPPAYEK	1964	HLA-A*11:01
3317	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-A*25:01
3318	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-A*26:01
3319	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-A*29:02
3320	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-A*30:02
3321	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-A*32:01
3322	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-B*15:01
3323	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-B*46:01
3324	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-C*01:02
3325	MART1	ENSG00000120215	VVPNAPPAY	1965	HLA-C*07:04
3326	MART1	ENSG00000120215	YRALMDKSL	1966	HLA-B*27:05
3327	MART1	ENSG00000120215	YRALMDKSL	1966	HLA-C*06:02
3328	MART1	ENSG00000120215	YRALMDKSL	1966	HLA-C*07:02
3329	MAGEA10	ENSG00000124260	ACSSPSVVASL	1967	HLA-A*30:01
3330	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-A*30:01
3331	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-A*30:02
3332	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-B*27:02
3333	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-B*44:02
3334	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-B*44:03
3335	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-B*57:01
3336	MAGEA10	ENSG00000124260	AEILESVIRNY	64	HLA-C*16:04
3337	MAGEA10	ENSG00000124260	AEILESVIRN	1968	HLA-B*44:02
3338	MAGEA10	ENSG00000124260	AEILESVI	1969	HLA-A*30:01
3339	MAGEA10	ENSG00000124260	AEILESVI	1969	HLA-B*40:01
3340	MAGEA10	ENSG00000124260	AEILESVI	1969	HLA-B*44:02
3341	MAGEA10	ENSG00000124260	AEILESVI	1969	HLA-B*44:03
3342	MAGEA10	ENSG00000124260	AEILESVI	1969	HLA-B*49:01
3343	MAGEA10	ENSG00000124260	AEIRKMSLL	1970	HLA-B*37:01
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3346	MAGEA10	ENSG00000124260	AEIRKMSLL	1970	HLA-B*44:02
3347	MAGEA10	ENSG00000124260	AEIRKMSLL	1970	HLA-B*44:03
3348	MAGEA10	ENSG00000124260	AEIRKMSLL	1970	HLA-B*49:01

3349	MAGEA10	ENSG00000124260	AEIRKMSL	1971	HLA-B*37:01
3350	MAGEA10	ENSG00000124260	AEIRKMSL	1971	HLA-B*40:02
3351	MAGEA10	ENSG00000124260	AKVNGSDPRSF	1972	HLA-B*15:03
3352	MAGEA10	ENSG00000124260	ALNMMGLY	1973	HLA-A*30:02
3353	MAGEA10	ENSG00000124260	AMASASSSA	1974	HLA-A*02:03
3354	MAGEA10	ENSG00000124260	AMASASSSA	1974	HLA-A*32:01
3355	MAGEA10	ENSG00000124260	AMASASSSA	1974	HLA-B*55:01
3356	MAGEA10	ENSG00000124260	AMASASSSA	1974	HLA-C*01:02
3357	MAGEA10	ENSG00000124260	AMASASSSA	1974	HLA-C*14:02
3358	MAGEA10	ENSG00000124260	APLAVEEDA	1975	HLA-B*56:01
3359	MAGEA10	ENSG00000124260	AQAPLAVEE	1976	HLA-B*27:05
3360	MAGEA10	ENSG00000124260	AQIACSSPSV	1977	HLA-B*13:02
3361	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-A*25:01
3362	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-A*26:01
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3364	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-A*32:01
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3366	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-B*46:01
3367	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-B*58:01
3368	MAGEA10	ENSG00000124260	ASASSSATGSF	1978	HLA-C*16:04
3369	MAGEA10	ENSG00000124260	ASSSATGSFSY	1979	HLA-A*01:01
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3371	MAGEA10	ENSG00000124260	ASSSATGSFSY	1979	HLA-A*11:01
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3379	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-A*25:01
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3381	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-A*30:02
3382	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-A*32:01
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3384	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-B*15:03
3385	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-B*37:01
3386	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-B*46:01
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3389	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-C*02:02
3390	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-C*03:03
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3392	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-C*05:01
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3394	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-C*16:01
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3396	MAGEA10	ENSG00000124260	ASSSATGSF	1980	HLA-C*16:04
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3399	MAGEA10	ENSG00000124260	ASSSTSTSSSF	1981	HLA-B*58:01
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3406	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-B*58:01
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3408	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*02:02
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3410	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*03:04
3411	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*04:01
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3413	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*07:06
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3416	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*16:01
3417	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*16:02
3418	MAGEA10	ENSG00000124260	ATTDDTTAM	1982	HLA-C*16:04
3419	MAGEA10	ENSG00000124260	DDETPNPPQSA	1983	HLA-B*39:01
3420	MAGEA10	ENSG00000124260	DEKVTDLVQF	1984	HLA-B*18:01
3421	MAGEA10	ENSG00000124260	DEKVTDLVQF	1984	HLA-B*44:02
3422	MAGEA10	ENSG00000124260	DEKVTDLV	1985	HLA-B*18:01
3423	MAGEA10	ENSG00000124260	DEKVTDLV	1985	HLA-B*49:01
3424	MAGEA10	ENSG00000124260	DETPNPPQSA	1986	HLA-B*18:01
3425	MAGEA10	ENSG00000124260	DETPNPPQS	1987	HLA-B*18:01
3426	MAGEA10	ENSG00000124260	DETPNPPQ	1988	HLA-B*18:01
3427	MAGEA10	ENSG00000124260	DGMEHLIY	1989	HLA-B*08:01
3428	MAGEA10	ENSG00000124260	DGMEHLIY	1989	HLA-B*18:01
3429	MAGEA10	ENSG00000124260	DGMEHLIY	1989	HLA-B*35:01
3430	MAGEA10	ENSG00000124260	DGMEHLIY	1989	HLA-C*07:01
3431	MAGEA10	ENSG00000124260	DGMEHLIY	1989	HLA-C*12:03
3432	MAGEA10	ENSG00000124260	DGMLSDVQSM	1990	HLA-B*51:01
3433	MAGEA10	ENSG00000124260	DPTGHSFVL	1991	HLA-B*08:01
3434	MAGEA10	ENSG00000124260	DPTGHSFVL	1991	HLA-B*35:01
3435	MAGEA10	ENSG00000124260	DPTGHSFVL	1991	HLA-B*35:03
3436	MAGEA10	ENSG00000124260	DPTGHSFV	1992	HLA-B*51:01
3437	MAGEA10	ENSG00000124260	DVKEVDPTGH	1993	HLA-A*26:01
3438	MAGEA10	ENSG00000124260	DVKEVDPTGH	1993	HLA-A*33:01
3439	MAGEA10	ENSG00000124260	DVKEVDPTGH	1993	HLA-A*68:01
3440	MAGEA10	ENSG00000124260	EALNMMGLY	1994	HLA-A*01:01
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3442	MAGEA10	ENSG00000124260	EALNMMGLY	1994	HLA-A*26:01
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3444	MAGEA10	ENSG00000124260	EALNMMGLY	1994	HLA-B*35:01
3445	MAGEA10	ENSG00000124260	EALNMMGL	1995	HLA-B*51:01
3446	MAGEA10	ENSG00000124260	EASECMLLV	1996	HLA-A*68:02
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3448	MAGEA10	ENSG00000124260	EDHFPLLF	1997	HLA-C*07:01
3449	MAGEA10	ENSG00000124260	EESPSTLQVL	1998	HLA-A*25:01
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3451	MAGEA10	ENSG00000124260	EESPSTLQVL	1998	HLA-B*27:02
3452	MAGEA10	ENSG00000124260	EESPSTLQVL	1998	HLA-B*38:01
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3457	MAGEA10	ENSG00000124260	EESPSTLQVL	1998	HLA-B*44:03
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3460	MAGEA10	ENSG00000124260	EESPSTLQV	1999	HLA-B*18:01
3461	MAGEA10	ENSG00000124260	EESPSTLQV	1999	HLA-B*37:01
3462	MAGEA10	ENSG00000124260	EESPSTLQV	1999	HLA-B*40:01
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3464	MAGEA10	ENSG00000124260	EESPSTLQV	1999	HLA-B*44:03
3465	MAGEA10	ENSG00000124260	EESPSTLQV	1999	HLA-B*49:01
3466	MAGEA10	ENSG00000124260	EEVIWEAL	2000	HLA-B*18:01
3467	MAGEA10	ENSG00000124260	EGAQAPLAV	2001	HLA-B*13:02
3468	MAGEA10	ENSG00000124260	EGAQAPLAV	2001	HLA-B*51:01
3469	MAGEA10	ENSG00000124260	EHLIYGEPR	2002	HLA-A*33:01
3470	MAGEA10	ENSG00000124260	EHLIYGEPR	2002	HLA-A*33:03
3471	MAGEA10	ENSG00000124260	EIDEKVTDL	2003	HLA-A*02:07
3472	MAGEA10	ENSG00000124260	EIDEKVTDL	2003	HLA-C*05:01
3473	MAGEA10	ENSG00000124260	EILESVIRNY	2004	HLA-A*25:01
3474	MAGEA10	ENSG00000124260	EILESVIRNY	2004	HLA-A*26:01
3475	MAGEA10	ENSG00000124260	EILESVIRNY	2004	HLA-A*29:02
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3477	MAGEA10	ENSG00000124260	EILESVIRNY	2004	HLA-A*33:01
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3479	MAGEA10	ENSG00000124260	EILESVIRNY	2004	HLA-B*44:02
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3482	MAGEA10	ENSG00000124260	EILESVIR	2005	HLA-A*33:03
3483	MAGEA10	ENSG00000124260	EKVTDLVQF	2006	HLA-A*23:01
3484	MAGEA10	ENSG00000124260	EPITKAEIL	2007	HLA-B*07:02
3485	MAGEA10	ENSG00000124260	EPITKAEIL	2007	HLA-B*08:01
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3488	MAGEA10	ENSG00000124260	EPITKAEIL	2007	HLA-C*07:02
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3490	MAGEA10	ENSG00000124260	EPITKAEI	2008	HLA-B*51:01
3491	MAGEA10	ENSG00000124260	ESLPRSEIDEK	2009	HLA-A*33:01
3492	MAGEA10	ENSG00000124260	ESPSTLQVL	2010	HLA-A*25:01
3493	MAGEA10	ENSG00000124260	ESPSTLQVL	2010	HLA-C*01:02
3494	MAGEA10	ENSG00000124260	ETPNPPQSAQI	2011	HLA-A*26:01
3495	MAGEA10	ENSG00000124260	ETPNPPQSAQI	2011	HLA-A*68:02
3496	MAGEA10	ENSG00000124260	ETPNPPQSA	2012	HLA-A*33:03
3497	MAGEA10	ENSG00000124260	EVDPTGHSFVL	2013	HLA-A*01:01
3498	MAGEA10	ENSG00000124260	EVDPTGHSFVL	2013	HLA-A*02:07
3499	MAGEA10	ENSG00000124260	EVDPTGHSFVL	2013	HLA-A*68:02
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3503	MAGEA10	ENSG00000124260	EVDPTGHSFV	2014	HLA-A*01:01
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3506	MAGEA10	ENSG00000124260	EVDPTGHSFV	2014	HLA-C*05:01
3507	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-A*01:01
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3509	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-A*23:01
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3516	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-A*33:01
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3521	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-B*18:01
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3529	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-B*46:01
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3534	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*03:03
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3538	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*07:04
3539	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*07:06
3540	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*14:02

3541	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*16:02
3542	MAGEA10	ENSG00000124260	EVDPTGHSF	2015	HLA-C*16:04
3543	MAGEA10	ENSG00000124260	EVIWEALNMM	2016	HLA-A*25:01
3544	MAGEA10	ENSG00000124260	EVIWEALNMM	2016	HLA-A*26:01
3545	MAGEA10	ENSG00000124260	EVIWEALNM	2017	HLA-A*25:01
3546	MAGEA10	ENSG00000124260	EVIWEALNM	2017	HLA-A*26:01
3547	MAGEA10	ENSG00000124260	FGIDVKEV	2018	HLA-B*51:01
3548	MAGEA10	ENSG00000124260	FGIDVKEV	2018	HLA-C*12:03
3549	MAGEA10	ENSG00000124260	FGIDVKEV	2018	HLA-C*16:02
3550	MAGEA10	ENSG00000124260	FLWGPRAHAEI	2019	HLA-A*02:01
3551	MAGEA10	ENSG00000124260	FLWGPRAHAEI	2019	HLA-A*02:07
3552	MAGEA10	ENSG00000124260	FPLLFSEASEC	2020	HLA-B*54:01
3553	MAGEA10	ENSG00000124260	FPLLFSEAS	2021	HLA-B*54:01
3554	MAGEA10	ENSG00000124260	FPLLFSEA	2022	HLA-B*51:01
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3556	MAGEA10	ENSG00000124260	FPLLFSEA	2022	HLA-B*55:01
3557	MAGEA10	ENSG00000124260	FPLLFSEA	2022	HLA-B*56:01
3558	MAGEA10	ENSG00000124260	FPLWYEEAL	2023	HLA-B*35:01
3559	MAGEA10	ENSG00000124260	FPLWYEEAL	2023	HLA-B*35:03
3560	MAGEA10	ENSG00000124260	FPLWYEEAL	2023	HLA-B*54:01
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3563	MAGEA10	ENSG00000124260	FPSSFPSSSS	2025	HLA-B*56:01
3564	MAGEA10	ENSG00000124260	FPSSFPSSS	2026	HLA-B*54:01
3565	MAGEA10	ENSG00000124260	FPSSFPSSS	2026	HLA-B*56:01
3566	MAGEA10	ENSG00000124260	FPSSFPSS	2027	HLA-B*54:01
3567	MAGEA10	ENSG00000124260	FPSSSSSSS	2028	HLA-B*39:01
3568	MAGEA10	ENSG00000124260	FSEASECML	2029	HLA-C*03:03
3569	MAGEA10	ENSG00000124260	FSEASECML	2029	HLA-C*03:04
3570	MAGEA10	ENSG00000124260	FSEASECML	2029	HLA-C*05:01
3571	MAGEA10	ENSG00000124260	FVLVTSLGLTY	2030	HLA-A*29:02
3572	MAGEA10	ENSG00000124260	GHSFVLVTSL	2031	HLA-B*38:01
3573	MAGEA10	ENSG00000124260	GLYDGMEHLIY	2032	HLA-A*01:01
3574	MAGEA10	ENSG00000124260	GLYDGMEHLIY	2032	HLA-A*03:01
3575	MAGEA10	ENSG00000124260	GLYDGMEHLIY	2032	HLA-A*29:02
3576	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*02:01
3577	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*02:03
3578	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*02:04
3579	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*02:07
3580	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*03:01
3581	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-A*30:01
3582	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-B*13:02
3583	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-B*55:01
3584	MAGEA10	ENSG00000124260	GLYDGMEHLI	2033	HLA-C*06:02
3585	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*02:01
3586	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*02:03
3587	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*02:04
3588	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*02:07
3589	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*03:01
3590	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*30:01
3591	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-A*68:02
3592	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*13:02
3593	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*15:01
3594	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*15:03
3595	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*40:01
3596	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*46:01
3597	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-B*55:01
3598	MAGEA10	ENSG00000124260	GLYDGMEHL	2034	HLA-C*02:02
3599	MAGEA10	ENSG00000124260	GMLSDVQSMPK	2035	HLA-A*03:01
3600	MAGEA10	ENSG00000124260	GMLSDVQSMPK	2035	HLA-A*03:02
3601	MAGEA10	ENSG00000124260	GMLSDVQSMPK	2035	HLA-A*11:01
3602	MAGEA10	ENSG00000124260	GMLSDVQSMPK	2035	HLA-B*27:05
3603	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-A*02:01
3604	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-A*02:04

3605	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-A*23:01
3606	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-A*32:01
3607	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*13:02
3608	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*15:01
3609	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*15:03
3610	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*27:05
3611	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*37:01
3612	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*46:01
3613	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*55:01
3614	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-B*58:01
3615	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-C*01:02
3616	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-C*07:04
3617	MAGEA10	ENSG00000124260	GMLSDVQSM	2036	HLA-C*14:02
3618	MAGEA10	ENSG00000124260	GPRAHAEI	2037	HLA-B*07:02
3619	MAGEA10	ENSG00000124260	GPRAHAEI	2037	HLA-C*07:02
3620	MAGEA10	ENSG00000124260	GSDPARYEFLW	2038	HLA-B*57:01
3621	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-A*01:01
3622	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-A*30:02
3623	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-A*32:01
3624	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-B*15:01
3625	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-B*38:01
3626	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-B*57:01
3627	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-B*58:01
3628	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-C*02:02
3629	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-C*03:04
3630	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-C*05:01
3631	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-C*16:01
3632	MAGEA10	ENSG00000124260	GSDPARYEF	2039	HLA-C*16:04
3633	MAGEA10	ENSG00000124260	GSDPRSFPLWY	2040	HLA-A*01:01
3634	MAGEA10	ENSG00000124260	GSDPRSFPLW	2041	HLA-B*57:01
3635	MAGEA10	ENSG00000124260	GSDPRSFPL	2042	HLA-A*01:01
3636	MAGEA10	ENSG00000124260	GSDPRSFPL	2042	HLA-C*03:04
3637	MAGEA10	ENSG00000124260	GSDPRSFPL	2042	HLA-C*05:01
3638	MAGEA10	ENSG00000124260	HAEIRKMSL	2043	HLA-B*08:01
3639	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-A*68:02
3640	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*08:01
3641	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*15:03
3642	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*18:01
3643	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*35:01
3644	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*40:01
3645	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*40:02
3646	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*46:01
3647	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-B*58:01
3648	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-C*02:02
3649	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-C*03:03
3650	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-C*03:04
3651	MAGEA10	ENSG00000124260	HSFVLVTSL	2044	HLA-C*12:03
3652	MAGEA10	ENSG00000124260	IACSSPSVV	2045	HLA-B*51:01
3653	MAGEA10	ENSG00000124260	IACSSPSVV	2045	HLA-C*12:03
3654	MAGEA10	ENSG00000124260	IACSSPSV	2046	HLA-B*51:01
3655	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-B*35:01
3656	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-B*35:03
3657	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-B*39:01
3658	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-B*55:01
3659	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-C*03:03
3660	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-C*03:04
3661	MAGEA10	ENSG00000124260	IATTDDTTAM	2047	HLA-C*05:01
3662	MAGEA10	ENSG00000124260	IATTDDTTA	2048	HLA-B*35:03
3663	MAGEA10	ENSG00000124260	IDEKVTDL	2049	HLA-B*37:01
3664	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*01:01
3665	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*02:07
3666	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*03:01
3667	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*03:02
3668	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*29:02

3669	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*30:02
3670	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-A*32:01
3671	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*15:01
3672	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*15:03
3673	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*44:02
3674	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*44:03
3675	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*46:01
3676	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*57:01
3677	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-B*58:01
3678	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-C*02:02
3679	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-C*07:04
3680	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-C*16:01
3681	MAGEA10	ENSG00000124260	ILESVIRNY	2050	HLA-C*16:02
3682	MAGEA10	ENSG00000124260	ILILSIVFI	2051	HLA-A*02:01
3683	MAGEA10	ENSG00000124260	ILILSIVFI	2051	HLA-A*02:04
3684	MAGEA10	ENSG00000124260	ILSIVFIEGY	2052	HLA-A*01:01
3685	MAGEA10	ENSG00000124260	IPSTPEEVSA	2053	HLA-B*35:03
3686	MAGEA10	ENSG00000124260	IPSTPEEVSA	2053	HLA-B*54:01
3687	MAGEA10	ENSG00000124260	IPSTPEEVSA	2053	HLA-B*55:01
3688	MAGEA10	ENSG00000124260	IPSTPEEVSA	2053	HLA-B*56:01
3689	MAGEA10	ENSG00000124260	IYGEPRKLL	2054	HLA-A*24:02
3690	MAGEA10	ENSG00000124260	IYGEPRKL	2055	HLA-A*23:01
3691	MAGEA10	ENSG00000124260	IYGEPRKL	2055	HLA-A*24:02
3692	MAGEA10	ENSG00000124260	IYGEPRKL	2055	HLA-C*06:02
3693	MAGEA10	ENSG00000124260	IYGEPRKL	2055	HLA-C*16:01
3694	MAGEA10	ENSG00000124260	KEESPSTLQVL	2056	HLA-A*30:01
3695	MAGEA10	ENSG00000124260	KEESPSTLQVL	2056	HLA-B*40:01
3696	MAGEA10	ENSG00000124260	KEESPSTLQVL	2056	HLA-B*40:02
3697	MAGEA10	ENSG00000124260	KEESPSTLQVL	2056	HLA-B*44:03
3698	MAGEA10	ENSG00000124260	KEESPSTLQVL	2056	HLA-B*49:01
3699	MAGEA10	ENSG00000124260	KEESPSTLQV	2057	HLA-B*40:01
3700	MAGEA10	ENSG00000124260	KEESPSTLQV	2057	HLA-B*49:01
3701	MAGEA10	ENSG00000124260	KEESPSTL	2058	HLA-B*40:01
3702	MAGEA10	ENSG00000124260	KEPITKAEIL	2059	HLA-B*40:01
3703	MAGEA10	ENSG00000124260	KEPITKAEI	2060	HLA-B*37:01
3704	MAGEA10	ENSG00000124260	KEPITKAEI	2060	HLA-B*40:01
3705	MAGEA10	ENSG00000124260	KEPITKAEI	2060	HLA-B*49:01
3706	MAGEA10	ENSG00000124260	KEVDPTGHSFV	2061	HLA-B*49:01
3707	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*23:01
3708	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*24:02
3709	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*25:01
3710	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*30:01
3711	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*30:02
3712	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-A*32:01
3713	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*15:01
3714	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*15:03
3715	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*18:01
3716	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*27:02
3717	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*27:05
3718	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*37:01
3719	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*38:01
3720	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*40:01
3721	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*40:02
3722	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*44:02
3723	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*44:03
3724	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*49:01
3725	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*57:01
3726	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-B*58:01
3727	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-C*02:02
3728	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-C*03:04
3729	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-C*16:01
3730	MAGEA10	ENSG00000124260	KEVDPTGHSF	379	HLA-C*16:04
3731	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-A*03:02
3732	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-A*25:01

3733	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-A*30:02
3734	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-A*32:01
3735	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-B*57:01
3736	MAGEA10	ENSG00000124260	KVNGSDPRSF	2062	HLA-B*58:01
3737	MAGEA10	ENSG00000124260	KVTDLVQFLL	2063	HLA-A*02:04
3738	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*02:01
3739	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*02:03
3740	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*02:04
3741	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*02:07
3742	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*24:02
3743	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*31:01
3744	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*32:01
3745	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-A*68:02
3746	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-B*13:02
3747	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-B*27:05
3748	MAGEA10	ENSG00000124260	KVTDLVQFL	2064	HLA-B*58:01
3749	MAGEA10	ENSG00000124260	KVTDLVQF	2065	HLA-A*32:01
3750	MAGEA10	ENSG00000124260	LEGAQAPLAV	2066	HLA-B*49:01
3751	MAGEA10	ENSG00000124260	LEGAQAPLA	2067	HLA-B*49:01
3752	MAGEA10	ENSG00000124260	LEGAQAPL	2068	HLA-B*18:01
3753	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-B*18:01
3754	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-B*37:01
3755	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-B*44:02
3756	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-B*44:03
3757	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-C*02:02
3758	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-C*16:01
3759	MAGEA10	ENSG00000124260	LESVIRNY	2069	HLA-C*16:04
3760	MAGEA10	ENSG00000124260	LFSEASECM	2070	HLA-C*14:02
3761	MAGEA10	ENSG00000124260	LIPSTPEEV	2071	HLA-A*02:01
3762	MAGEA10	ENSG00000124260	LIPSTPEEV	2071	HLA-A*02:07
3763	MAGEA10	ENSG00000124260	LIYGEPRKL	2072	HLA-A*03:01
3764	MAGEA10	ENSG00000124260	LLFSEASECML	2073	HLA-A*02:01
3765	MAGEA10	ENSG00000124260	LLFSEASEC	2074	HLA-A*02:01
3766	MAGEA10	ENSG00000124260	LQSQSETQGL	2075	HLA-B*27:05
3767	MAGEA10	ENSG00000124260	LQSQSETQGL	2075	HLA-B*38:01
3768	MAGEA10	ENSG00000124260	LQSQSETQGL	2075	HLA-B*39:01
3769	MAGEA10	ENSG00000124260	LQVLPDSESL	2076	HLA-B*39:01
3770	MAGEA10	ENSG00000124260	LSDVQSMPK	2077	HLA-A*01:01
3771	MAGEA10	ENSG00000124260	LSDVQSMPK	2077	HLA-A*03:01
3772	MAGEA10	ENSG00000124260	LSDVQSMPK	2077	HLA-A*03:02
3773	MAGEA10	ENSG00000124260	LSDVQSMPK	2077	HLA-A*11:01
3774	MAGEA10	ENSG00000124260	LSDVQSMPK	2077	HLA-B*27:02
3775	MAGEA10	ENSG00000124260	LSIVFIEGY	2078	HLA-A*01:01
3776	MAGEA10	ENSG00000124260	LSIVFIEGY	2078	HLA-A*30:02
3777	MAGEA10	ENSG00000124260	LSIVFIEGY	2078	HLA-B*46:01
3778	MAGEA10	ENSG00000124260	LSIVFIEGY	2078	HLA-B*57:01
3779	MAGEA10	ENSG00000124260	LTQDWVQENYL	2079	HLA-C*04:01
3780	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-A*01:01
3781	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-A*29:02
3782	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-A*30:02
3783	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-A*32:01
3784	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-B*57:01
3785	MAGEA10	ENSG00000124260	LTQDWVQENY	2080	HLA-B*58:01
3786	MAGEA10	ENSG00000124260	LTYDGMLSDV	2081	HLA-A*02:03
3787	MAGEA10	ENSG00000124260	LTYDGMLSDV	2081	HLA-A*68:02
3788	MAGEA10	ENSG00000124260	LVFGIDVKEV	2082	HLA-A*02:03
3789	MAGEA10	ENSG00000124260	LVFGIDVKEV	2082	HLA-A*68:02
3790	MAGEA10	ENSG00000124260	LVFGIDVK	2083	HLA-B*27:02
3791	MAGEA10	ENSG00000124260	LVQFLLFKY	2084	HLA-A*29:02
3792	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*01:01
3793	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*03:01
3794	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*25:01
3795	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*26:01
3796	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*29:02

3797	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*30:02
3798	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-A*32:01
3799	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*15:01
3800	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*15:03
3801	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*18:01
3802	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*35:01
3803	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*46:01
3804	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-B*58:01
3805	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*02:02
3806	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*07:04
3807	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*14:02
3808	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*16:01
3809	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*16:02
3810	MAGEA10	ENSG00000124260	LVTSLGLTY	2085	HLA-C*16:04
3811	MAGEA10	ENSG00000124260	LYDGMEHLIY	2086	HLA-A*29:02
3812	MAGEA10	ENSG00000124260	LYDGMEHLIY	2086	HLA-C*07:01
3813	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-A*02:07
3814	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-A*23:01
3815	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-A*24:02
3816	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-B*35:01
3817	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-B*35:03
3818	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-B*38:01
3819	MAGEA10	ENSG00000124260	LYDGMEHLI	2087	HLA-C*04:01
3820	MAGEA10	ENSG00000124260	LYDGMEHL	2088	HLA-C*04:01
3821	MAGEA10	ENSG00000124260	MASASSSAT	2089	HLA-C*03:04
3822	MAGEA10	ENSG00000124260	MASASSSA	2090	HLA-B*54:01
3823	MAGEA10	ENSG00000124260	MEHLIYGEP	2091	HLA-B*40:02
3824	MAGEA10	ENSG00000124260	MLLVFGIDV	2092	HLA-A*02:01
3825	MAGEA10	ENSG00000124260	MLLVFGIDV	2092	HLA-A*02:04
3826	MAGEA10	ENSG00000124260	MLSDVQSMPKT	2093	HLA-C*06:02
3827	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-A*01:01
3828	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-A*03:01
3829	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-A*03:02
3830	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-A*11:01
3831	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-A*68:01
3832	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-B*27:02
3833	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-B*27:05
3834	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-C*04:01
3835	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-C*06:02
3836	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-C*07:01
3837	MAGEA10	ENSG00000124260	MLSDVQSMPK	2094	HLA-C*07:06
3838	MAGEA10	ENSG00000124260	MLSDVQSM	2095	HLA-B*37:01
3839	MAGEA10	ENSG00000124260	MPEEDLQSQ	2096	HLA-B*35:01
3840	MAGEA10	ENSG00000124260	MPEEDLQSQ	2096	HLA-B*35:03
3841	MAGEA10	ENSG00000124260	MPEEDLQSQ	2096	HLA-B*55:01
3842	MAGEA10	ENSG00000124260	MPEEDLQSQ	2096	HLA-C*03:03
3843	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*07:02
3844	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*08:01
3845	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*35:01
3846	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*35:03
3847	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*51:01
3848	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-B*54:01
3849	MAGEA10	ENSG00000124260	MPKTGILIL	2097	HLA-C*07:02
3850	MAGEA10	ENSG00000124260	MPKTGILI	2098	HLA-B*08:01
3851	MAGEA10	ENSG00000124260	MPKTGILI	2098	HLA-B*51:01
3852	MAGEA10	ENSG00000124260	MPKTGILI	2098	HLA-B*54:01
3853	MAGEA10	ENSG00000124260	NGSDPRSFPL	2099	HLA-C*16:01
3854	MAGEA10	ENSG00000124260	NGSDPRSF	2100	HLA-C*16:01
3855	MAGEA10	ENSG00000124260	NPPQSAQI	2101	HLA-B*51:01
3856	MAGEA10	ENSG00000124260	NYEDHFPLLF	2102	HLA-A*24:02
3857	MAGEA10	ENSG00000124260	NYEDHFPLLF	2102	HLA-A*29:02
3858	MAGEA10	ENSG00000124260	NYEDHFPLL	2103	HLA-A*23:01
3859	MAGEA10	ENSG00000124260	NYEDHFPLL	2103	HLA-A*24:02
3860	MAGEA10	ENSG00000124260	PDSESLPR	2104	HLA-B*27:02

3861	MAGEA10	ENSG00000124260	PLIPSTPEEV	2105	HLA-A*02:03
3862	MAGEA10	ENSG00000124260	QDWVQENYL	2106	HLA-A*30:01
3863	MAGEA10	ENSG00000124260	QIACSSPSV	2107	HLA-A*02:01
3864	MAGEA10	ENSG00000124260	QKEESPSTL	2108	HLA-B*39:01
3865	MAGEA10	ENSG00000124260	QMKEPITKA	2109	HLA-A*02:03
3866	MAGEA10	ENSG00000124260	QMKEPITKA	2109	HLA-B*55:01
3867	MAGEA10	ENSG00000124260	QSDEGSSSQK	2110	HLA-A*01:01
3868	MAGEA10	ENSG00000124260	QSDEGSSSQ	2111	HLA-C*05:01
3869	MAGEA10	ENSG00000124260	QSMPKTGIL	2112	HLA-B*08:01
3870	MAGEA10	ENSG00000124260	QSMPKTGIL	2112	HLA-B*58:01
3871	MAGEA10	ENSG00000124260	QSMPKTGI	2113	HLA-B*08:01
3872	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*03:01
3873	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*11:01
3874	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*31:01
3875	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*33:01
3876	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*33:03
3877	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-A*68:01
3878	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-B*27:02
3879	MAGEA10	ENSG00000124260	QVLPDSESLPR	2114	HLA-C*07:06
3880	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-B*15:01
3881	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-B*35:01
3882	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-B*35:03
3883	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-B*38:01
3884	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-B*39:01
3885	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-C*01:02
3886	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-C*03:03
3887	MAGEA10	ENSG00000124260	QVLPDSESL	2115	HLA-C*03:04
3888	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-A*01:01
3889	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-A*25:01
3890	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-A*26:01
3891	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-A*29:02
3892	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-A*30:02
3893	MAGEA10	ENSG00000124260	QVPGSDPARY	2116	HLA-C*07:04
3894	MAGEA10	ENSG00000124260	RIATTDDTTAM	2117	HLA-B*15:01
3895	MAGEA10	ENSG00000124260	RNYEDHFPLLF	2118	HLA-B*57:01
3896	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-A*29:02
3897	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-A*30:02
3898	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-A*32:01
3899	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-B*15:01
3900	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-B*15:03
3901	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-B*57:01
3902	MAGEA10	ENSG00000124260	RQVPGSDPARY	65	HLA-B*58:01
3903	MAGEA10	ENSG00000124260	SASSSATGSF	2119	HLA-A*25:01
3904	MAGEA10	ENSG00000124260	SASSSATGSF	2119	HLA-A*26:01
3905	MAGEA10	ENSG00000124260	SASSSATGSF	2119	HLA-A*30:02
3906	MAGEA10	ENSG00000124260	SASSSATGSF	2119	HLA-B*07:02
3907	MAGEA10	ENSG00000124260	SASSSATGSF	2119	HLA-C*03:04
3908	MAGEA10	ENSG00000124260	SATGSFSYP	2120	HLA-C*16:02
3909	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-A*30:02
3910	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-B*15:01
3911	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-B*15:03
3912	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-B*35:01
3913	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-B*39:01
3914	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-B*58:01
3915	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-C*16:01
3916	MAGEA10	ENSG00000124260	SATGSFSY	2121	HLA-C*16:02
3917	MAGEA10	ENSG00000124260	SDPARYEF	2122	HLA-B*37:01
3918	MAGEA10	ENSG00000124260	SDPRSFPLW	2123	HLA-A*24:02
3919	MAGEA10	ENSG00000124260	SDVQSMPK	2124	HLA-C*06:02
3920	MAGEA10	ENSG00000124260	SEASECMLLV	2125	HLA-B*49:01
3921	MAGEA10	ENSG00000124260	SEASECMLL	2126	HLA-A*30:01
3922	MAGEA10	ENSG00000124260	SEASECMLL	2126	HLA-B*40:01
3923	MAGEA10	ENSG00000124260	SEASECMLL	2126	HLA-B*44:03
3924	MAGEA10	ENSG00000124260	SEASECMLL	2126	HLA-B*49:01

3925	MAGEA10	ENSG00000124260	SECMLLVF	2127	HLA-B*18:01
3926	MAGEA10	ENSG00000124260	SEIDEKVTDLV	2128	HLA-B*49:01
3927	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-A*30:01
3928	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-B*40:01
3929	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-B*40:02
3930	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-B*44:02
3931	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-B*44:03
3932	MAGEA10	ENSG00000124260	SEIDEKVTDL	2129	HLA-B*49:01
3933	MAGEA10	ENSG00000124260	SESLPRSEI	2130	HLA-B*37:01
3934	MAGEA10	ENSG00000124260	SESLPRSEI	2130	HLA-B*40:01
3935	MAGEA10	ENSG00000124260	SESLPRSEI	2130	HLA-B*44:02
3936	MAGEA10	ENSG00000124260	SESLPRSEI	2130	HLA-B*44:03
3937	MAGEA10	ENSG00000124260	SESLPRSEI	2130	HLA-B*49:01
3938	MAGEA10	ENSG00000124260	SFVLVTSL	2131	HLA-A*23:01
3939	MAGEA10	ENSG00000124260	SFVLVTSL	2131	HLA-C*14:02
3940	MAGEA10	ENSG00000124260	SIVFIEGY	2132	HLA-B*15:01
3941	MAGEA10	ENSG00000124260	SLLKFLAKV	2133	HLA-A*02:01
3942	MAGEA10	ENSG00000124260	SLLKFLAKV	2133	HLA-A*02:03
3943	MAGEA10	ENSG00000124260	SLLKFLAKV	2133	HLA-A*02:04
3944	MAGEA10	ENSG00000124260	SLLKFLAKV	2133	HLA-A*02:07
3945	MAGEA10	ENSG00000124260	SLLKFLAK	2134	HLA-A*03:01
3946	MAGEA10	ENSG00000124260	SPSTLQVL	2135	HLA-B*07:02
3947	MAGEA10	ENSG00000124260	SPSVVASLPL	2136	HLA-B*07:02
3948	MAGEA10	ENSG00000124260	SPSVVASLPL	2136	HLA-C*07:02
3949	MAGEA10	ENSG00000124260	SPSVVASL	2137	HLA-B*07:02
3950	MAGEA10	ENSG00000124260	SPSVVASL	2137	HLA-B*08:01
3951	MAGEA10	ENSG00000124260	SPSVVASL	2137	HLA-B*37:01
3952	MAGEA10	ENSG00000124260	SPSVVASL	2137	HLA-B*56:01
3953	MAGEA10	ENSG00000124260	SPSVVASL	2137	HLA-C*07:02
3954	MAGEA10	ENSG00000124260	SQKEESPSTL	2138	HLA-B*15:01
3955	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*01:01
3956	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*11:01
3957	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*25:01
3958	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*26:01
3959	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*29:02
3960	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*30:02
3961	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-A*32:01
3962	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*15:01
3963	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*15:03
3964	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*27:05
3965	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*35:01
3966	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*46:01
3967	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-B*58:01
3968	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*02:02
3969	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*07:01
3970	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*07:06
3971	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*16:01
3972	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*16:02
3973	MAGEA10	ENSG00000124260	SSATGSFSY	2139	HLA-C*16:04
3974	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-A*02:07
3975	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-A*24:02
3976	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-A*25:01
3977	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-A*26:01
3978	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-B*46:01
3979	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-B*58:01
3980	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-C*01:02
3981	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-C*03:03
3982	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-C*03:04
3983	MAGEA10	ENSG00000124260	SSPSVVASL	66	HLA-C*14:02
3984	MAGEA10	ENSG00000124260	SSSATGSFSY	2140	HLA-A*01:01
3985	MAGEA10	ENSG00000124260	SSSATGSFSY	2140	HLA-A*29:02
3986	MAGEA10	ENSG00000124260	SSSATGSFSY	2140	HLA-A*30:02
3987	MAGEA10	ENSG00000124260	SSSATGSF	2141	HLA-C*05:01
3988	MAGEA10	ENSG00000124260	SSSFPSSF	2142	HLA-B*37:01

3989	MAGEA10	ENSG00000124260	SSSSSSCY	2143	HLA-A*30:02
3990	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-A*01:01
3991	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-A*26:01
3992	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-A*30:02
3993	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-B*15:01
3994	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-B*15:03
3995	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-C*07:04
3996	MAGEA10	ENSG00000124260	SSSSSSSCY	2144	HLA-C*16:01
3997	MAGEA10	ENSG00000124260	SSSSSSSSCY	2145	HLA-A*30:02
3998	MAGEA10	ENSG00000124260	SSSSSSSSSCY	2146	HLA-A*30:02
3999	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-A*25:01
4000	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-A*26:01
4001	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-A*30:02
4002	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-A*32:01
4003	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-B*15:01
4004	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-B*15:03
4005	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-B*46:01
4006	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-B*58:01
4007	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*02:02
4008	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*03:03
4009	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*03:04
4010	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*14:02
4011	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*16:01
4012	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*16:02
4013	MAGEA10	ENSG00000124260	SSTSTSSSF	2147	HLA-C*16:04
4014	MAGEA10	ENSG00000124260	STSSSFPSSF	2148	HLA-A*25:01
4015	MAGEA10	ENSG00000124260	STSSSFPSSF	2148	HLA-A*26:01
4016	MAGEA10	ENSG00000124260	STSTSSSF	2149	HLA-C*05:01
4017	MAGEA10	ENSG00000124260	TAMASASSSA	2150	HLA-B*54:01
4018	MAGEA10	ENSG00000124260	TAMASASSSA	2150	HLA-B*56:01
4019	MAGEA10	ENSG00000124260	TDLVQFLL	2151	HLA-B*37:01
4020	MAGEA10	ENSG00000124260	TKAEILESV	2152	HLA-A*68:02
4021	MAGEA10	ENSG00000124260	TPEEVIWEAL	2153	HLA-B*35:03
4022	MAGEA10	ENSG00000124260	TPEEVIWEA	2154	HLA-B*35:03
4023	MAGEA10	ENSG00000124260	TPEEVIWEA	2154	HLA-B*54:01
4024	MAGEA10	ENSG00000124260	TPEEVIWEA	2154	HLA-B*56:01
4025	MAGEA10	ENSG00000124260	TPNPPQSAQIA	2155	HLA-B*54:01
4026	MAGEA10	ENSG00000124260	TPNPPQSAQIA	2155	HLA-B*56:01
4027	MAGEA10	ENSG00000124260	TPNPPQSAQI	2156	HLA-B*07:02
4028	MAGEA10	ENSG00000124260	TPNPPQSAQI	2156	HLA-B*51:01
4029	MAGEA10	ENSG00000124260	TPNPPQSAQI	2156	HLA-B*56:01
4030	MAGEA10	ENSG00000124260	TPNPPQSAQI	2156	HLA-C*07:02
4031	MAGEA10	ENSG00000124260	TPNPPQSA	2157	HLA-B*56:01
4032	MAGEA10	ENSG00000124260	TQDWVQENYL	2158	HLA-B*38:01
4033	MAGEA10	ENSG00000124260	TQDWVQENYL	2158	HLA-C*05:01
4034	MAGEA10	ENSG00000124260	TQDWVQENY	2159	HLA-A*01:01
4035	MAGEA10	ENSG00000124260	TQDWVQENY	2159	HLA-A*30:02
4036	MAGEA10	ENSG00000124260	TQDWVQENY	2159	HLA-B*15:01
4037	MAGEA10	ENSG00000124260	TQDWVQENY	2159	HLA-B*38:01
4038	MAGEA10	ENSG00000124260	TQGLEGAQAPL	2160	HLA-B*27:05
4039	MAGEA10	ENSG00000124260	TQGLEGAQAPL	2160	HLA-B*38:01
4040	MAGEA10	ENSG00000124260	TQGLEGAQAPL	2160	HLA-B*39:01
4041	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-A*25:01
4042	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-A*26:01
4043	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-A*30:02
4044	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-A*32:01
4045	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-B*37:01
4046	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-C*02:02
4047	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-C*16:01
4048	MAGEA10	ENSG00000124260	TSSSFPSSF	2161	HLA-C*16:04
4049	MAGEA10	ENSG00000124260	TTDDTTAMA	2162	HLA-A*01:01
4050	MAGEA10	ENSG00000124260	TTDDTTAMA	2162	HLA-C*05:01
4051	MAGEA10	ENSG00000124260	TTDDTTAM	2163	HLA-B*35:03
4052	MAGEA10	ENSG00000124260	TTDDTTAM	2163	HLA-C*04:01

4053	MAGEA10	ENSG00000124260	TTDDTTAM	2163	HLA-C*05:01
4054	MAGEA10	ENSG00000124260	TTDDTTAM	2163	HLA-C*07:04
4055	MAGEA10	ENSG00000124260	TYDGMLSDVQS	2164	HLA-C*04:01
4056	MAGEA10	ENSG00000124260	TYDGMLSDV	226	HLA-B*35:01
4057	MAGEA10	ENSG00000124260	TYDGMLSDV	226	HLA-B*35:03
4058	MAGEA10	ENSG00000124260	TYDGMLSDV	226	HLA-C*04:01
4059	MAGEA10	ENSG00000124260	TYDGMLSDV	226	HLA-C*05:01
4060	MAGEA10	ENSG00000124260	TYDGMLSDV	226	HLA-C*07:04
4061	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-B*37:01
4062	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-C*01:02
4063	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-C*04:01
4064	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-C*07:01
4065	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-C*14:02
4066	MAGEA10	ENSG00000124260	VDPTGHSF	2165	HLA-C*16:01
4067	MAGEA10	ENSG00000124260	VEEDASSSTST	2166	HLA-A*30:01
4068	MAGEA10	ENSG00000124260	VKEVDPTGHSF	2167	HLA-B*15:03
4069	MAGEA10	ENSG00000124260	VLPDSESLPRS	2168	HLA-A*02:07
4070	MAGEA10	ENSG00000124260	VLPDSESL	2169	HLA-C*01:02
4071	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*01:01
4072	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*23:01
4073	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*25:01
4074	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*26:01
4075	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*29:02
4076	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*30:02
4077	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-A*32:01
4078	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-B*15:01
4079	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-B*15:03
4080	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-B*46:01
4081	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-B*58:01
4082	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-C*02:02
4083	MAGEA10	ENSG00000124260	VLVTSLGLTY	2170	HLA-C*07:04
4084	MAGEA10	ENSG00000124260	VNGSDPRSF	2171	HLA-C*16:01
4085	MAGEA10	ENSG00000124260	VPGSDPARYEF	2172	HLA-B*35:01
4086	MAGEA10	ENSG00000124260	VPGSDPARYEF	2172	HLA-B*55:01
4087	MAGEA10	ENSG00000124260	VPGSDPARY	2173	HLA-A*30:02
4088	MAGEA10	ENSG00000124260	VPGSDPARY	2173	HLA-B*35:01
4089	MAGEA10	ENSG00000124260	VPGSDPARY	2173	HLA-B*55:01
4090	MAGEA10	ENSG00000124260	VPGSDPARY	2173	HLA-C*03:03
4091	MAGEA10	ENSG00000124260	VQENYLEY	2174	HLA-A*01:01
4092	MAGEA10	ENSG00000124260	VQENYLEY	2174	HLA-B*39:01
4093	MAGEA10	ENSG00000124260	VQSMPKTGI	2175	HLA-A*32:01
4094	MAGEA10	ENSG00000124260	VQSMPKTGI	2175	HLA-B*13:02
4095	MAGEA10	ENSG00000124260	VQSMPKTGI	2175	HLA-B*38:01
4096	MAGEA10	ENSG00000124260	VQSMPKTGI	2175	HLA-C*06:02
4097	MAGEA10	ENSG00000124260	VQSMPKTGI	2175	HLA-C*07:04
4098	MAGEA10	ENSG00000124260	VTDLVQFLLF	2176	HLA-A*01:01
4099	MAGEA10	ENSG00000124260	VTDLVQFLL	2177	HLA-A*01:01
4100	MAGEA10	ENSG00000124260	VTDLVQFLL	2177	HLA-A*02:07
4101	MAGEA10	ENSG00000124260	VTDLVQFL	2178	HLA-A*01:01
4102	MAGEA10	ENSG00000124260	VTDLVQFL	2178	HLA-C*04:01
4103	MAGEA10	ENSG00000124260	VTDLVQFL	2178	HLA-C*05:01
4104	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-A*01:01
4105	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-A*29:02
4106	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-A*32:01
4107	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-B*15:01
4108	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-B*46:01
4109	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-B*58:01
4110	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-C*03:04
4111	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-C*14:02
4112	MAGEA10	ENSG00000124260	VTSLGLTY	2179	HLA-C*16:01
4113	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-A*01:01
4114	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-A*25:01
4115	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-A*26:01
4116	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-A*29:02

4117	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-A*30:02
4118	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-B*15:01
4119	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-B*35:01
4120	MAGEA10	ENSG00000124260	WVQENYLEY	75	HLA-C*07:04
4121	MAGEA10	ENSG00000124260	YDGMEHLI	2180	HLA-B*38:01
4122	MAGEA10	ENSG00000124260	YDGMEHLI	2180	HLA-C*07:01
4123	MAGEA10	ENSG00000124260	YDGMEHLI	2180	HLA-C*07:04
4124	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-A*01:01
4125	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-A*02:07
4126	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-A*24:02
4127	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-A*29:02
4128	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-B*18:01
4129	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-B*44:02
4130	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-B*44:03
4131	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-B*49:01
4132	MAGEA10	ENSG00000124260	YEDHFPLLF	2181	HLA-B*57:01
4133	MAGEA10	ENSG00000124260	YEDHFPLL	2182	HLA-B*18:01
4134	MAGEA10	ENSG00000124260	YEDHFPLL	2182	HLA-B*49:01
4135	MAGEA10	ENSG00000124260	YEFLWGPRA	2183	HLA-A*02:04
4136	MAGEA10	ENSG00000124260	YPLIPSTPEEV	2184	HLA-A*68:02
4137	MAGEA10	ENSG00000124260	YPLIPSTPEEV	2184	HLA-B*51:01
4138	MAGEA10	ENSG00000124260	YPLIPSTPEEV	2184	HLA-B*54:01
4139	MAGEA10	ENSG00000124260	YPLIPSTPEEV	2184	HLA-B*56:01
4140	MAGEA10	ENSG00000124260	YQMKEPITKA	2185	HLA-A*02:03
4141	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-A*03:01
4142	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-A*03:02
4143	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-A*11:01
4144	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-B*13:02
4145	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-B*27:05
4146	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-B*38:01
4147	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-C*02:02
4148	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-C*03:03
4149	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-C*03:04
4150	MAGEA10	ENSG00000124260	YQMKEPITK	2186	HLA-C*07:04
4151	MAGEA10	ENSG00000124260	YRQVPGSDPAR	2187	HLA-B*27:05
4152	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*07:02
4153	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*15:01
4154	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*35:03
4155	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*39:01
4156	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*40:01
4157	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*46:01
4158	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-B*58:01
4159	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*01:02
4160	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*02:02
4161	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*03:03
4162	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*03:04
4163	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*07:02
4164	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*12:03
4165	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*14:02
4166	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*16:01
4167	MAGEA4	ENSG00000147381	AAVSSSSPL	2188	HLA-C*16:04
4168	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-A*30:02
4169	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-B*27:02
4170	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-B*44:02
4171	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-B*44:03
4172	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-B*57:01
4173	MAGEA4	ENSG00000147381	AEMLERVIKNY	9	HLA-C*16:04
4174	MAGEA4	ENSG00000147381	AEMLERVIKN	2189	HLA-B*44:02
4175	MAGEA4	ENSG00000147381	AEMLERVI	2190	HLA-B*37:01
4176	MAGEA4	ENSG00000147381	AEMLERVI	2190	HLA-B*44:02
4177	MAGEA4	ENSG00000147381	AEMLERVI	2190	HLA-B*44:03
4178	MAGEA4	ENSG00000147381	AEMLERVI	2190	HLA-B*49:01
4179	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-A*30:01
4180	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*07:02

4181	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*18:01
4182	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*27:02
4183	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*37:01
4184	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*40:01
4185	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*40:02
4186	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*44:02
4187	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*44:03
4188	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-B*49:01
4189	MAGEA4	ENSG00000147381	AESLFREAL	2191	HLA-C*16:04
4190	MAGEA4	ENSG00000147381	AESLFREA	2192	HLA-B*37:01
4191	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-A*30:01
4192	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*18:01
4193	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*27:02
4194	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*27:05
4195	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*37:01
4196	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*40:01
4197	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*40:02
4198	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*44:02
4199	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*44:03
4200	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-B*49:01
4201	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*02:02
4202	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*07:04
4203	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*12:03
4204	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*16:01
4205	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*16:02
4206	MAGEA4	ENSG00000147381	AETSYVKVL	10	HLA-C*16:04
4207	MAGEA4	ENSG00000147381	AETSYVKV	2193	HLA-A*30:01
4208	MAGEA4	ENSG00000147381	AETSYVKV	2193	HLA-B*37:01
4209	MAGEA4	ENSG00000147381	AETSYVKV	2193	HLA-B*49:01
4210	MAGEA4	ENSG00000147381	AKELVTKAEM	2194	HLA-B*15:03
4211	MAGEA4	ENSG00000147381	AKELVTKAEM	2194	HLA-C*04:01
4212	MAGEA4	ENSG00000147381	ALAETSYVKVL	2195	HLA-A*02:03
4213	MAGEA4	ENSG00000147381	ALAETSYVKVL	2195	HLA-A*02:04
4214	MAGEA4	ENSG00000147381	ALAETSYVKV	2196	HLA-A*02:01
4215	MAGEA4	ENSG00000147381	ALAETSYVKV	2196	HLA-A*02:03
4216	MAGEA4	ENSG00000147381	ALAETSYVKV	2196	HLA-A*02:04
4217	MAGEA4	ENSG00000147381	ALAETSYVKV	2196	HLA-A*02:07
4218	MAGEA4	ENSG00000147381	ALAETSYVKV	2196	HLA-B*55:01
4219	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*01:01
4220	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*03:01
4221	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*03:02
4222	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*11:01
4223	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*29:02
4224	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-A*68:01
4225	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-B*13:02
4226	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-B*27:02
4227	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-B*27:05
4228	MAGEA4	ENSG00000147381	ALAETSYVK	162	HLA-C*07:06
4229	MAGEA4	ENSG00000147381	ALAETSYV	2197	HLA-A*02:01
4230	MAGEA4	ENSG00000147381	ALAETSYV	2197	HLA-A*02:03
4231	MAGEA4	ENSG00000147381	ALAETSYV	2197	HLA-B*55:01
4232	MAGEA4	ENSG00000147381	ALGLVGAQA	2198	HLA-A*02:01
4233	MAGEA4	ENSG00000147381	ALGLVGAQA	2198	HLA-A*02:03
4234	MAGEA4	ENSG00000147381	ALGLVGAQA	2198	HLA-B*56:01
4235	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-A*02:01
4236	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-A*02:03
4237	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-A*02:04
4238	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-A*02:07
4239	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-B*13:02
4240	MAGEA4	ENSG00000147381	ALLEEEEGV	11	HLA-B*55:01
4241	MAGEA4	ENSG00000147381	ALPTTISFTCW	2199	HLA-A*02:07
4242	MAGEA4	ENSG00000147381	ALPTTISFTCW	2199	HLA-A*24:02
4243	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-A*23:01
4244	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-B*15:01

4245	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-B*37:01
4246	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-B*46:01
4247	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-C*01:02
4248	MAGEA4	ENSG00000147381	ALPTTISF	2200	HLA-C*14:02
4249	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-A*02:01
4250	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-A*02:03
4251	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-A*02:04
4252	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-A*02:07
4253	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-B*55:01
4254	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-C*01:02
4255	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-C*16:01
4256	MAGEA4	ENSG00000147381	ALSNKVDEL	2201	HLA-C*16:02
4257	MAGEA4	ENSG00000147381	APTTEEQEAAV	2202	HLA-B*56:01
4258	MAGEA4	ENSG00000147381	APTTEEQEA	2203	HLA-B*35:03
4259	MAGEA4	ENSG00000147381	APTTEEQEA	2203	HLA-B*55:01
4260	MAGEA4	ENSG00000147381	APTTEEQEA	2203	HLA-B*56:01
4261	MAGEA4	ENSG00000147381	AQAPTTEEQEA	2204	HLA-B*27:05
4262	MAGEA4	ENSG00000147381	AQAPTTEEQ	2205	HLA-B*13:02
4263	MAGEA4	ENSG00000147381	AQAPTTEEQ	2205	HLA-B*15:01
4264	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-A*01:01
4265	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-B*46:01
4266	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-B*57:01
4267	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-B*58:01
4268	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-C*01:02
4269	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-C*04:01
4270	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-C*16:01
4271	MAGEA4	ENSG00000147381	ASALPTTISF	2206	HLA-C*16:04
4272	MAGEA4	ENSG00000147381	ASESLKMIF	2207	HLA-A*01:01
4273	MAGEA4	ENSG00000147381	ASESLKMIF	2207	HLA-B*57:01
4274	MAGEA4	ENSG00000147381	ASESLKMIF	2207	HLA-B*58:01
4275	MAGEA4	ENSG00000147381	ASESLKMIF	2207	HLA-C*12:03
4276	MAGEA4	ENSG00000147381	ASNTYTLVT	2208	HLA-A*11:01
4277	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*02:01
4278	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*02:03
4279	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*02:07
4280	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*03:02
4281	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*26:01
4282	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-A*32:01
4283	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-B*13:02
4284	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-B*27:05
4285	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-B*39:01
4286	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-B*55:01
4287	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-C*02:02
4288	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-C*06:02
4289	MAGEA4	ENSG00000147381	AVSSSSPLV	2209	HLA-C*16:02
4290	MAGEA4	ENSG00000147381	AVSSSSPL	2210	HLA-C*05:01
4291	MAGEA4	ENSG00000147381	AYPSLREAALL	2211	HLA-A*24:02
4292	MAGEA4	ENSG00000147381	AYPSLREAAL	2212	HLA-A*24:02
4293	MAGEA4	ENSG00000147381	AYPSLREAAL	2212	HLA-C*01:02
4294	MAGEA4	ENSG00000147381	AYPSLREAAL	2212	HLA-C*14:02
4295	MAGEA4	ENSG00000147381	DAESLFREA	2213	HLA-B*51:01
4296	MAGEA4	ENSG00000147381	DAESLFREA	2213	HLA-B*54:01
4297	MAGEA4	ENSG00000147381	DELAHFLLRKY	2214	HLA-B*44:02
4298	MAGEA4	ENSG00000147381	DELAHFLLR	2215	HLA-A*33:01
4299	MAGEA4	ENSG00000147381	DELAHFLL	2216	HLA-B*18:01
4300	MAGEA4	ENSG00000147381	DELAHFLL	2216	HLA-B*37:01
4301	MAGEA4	ENSG00000147381	DELAHFLL	2216	HLA-B*40:02
4302	MAGEA4	ENSG00000147381	DELAHFLL	2216	HLA-B*44:02
4303	MAGEA4	ENSG00000147381	DGLLGNNQI	2217	HLA-B*51:01
4304	MAGEA4	ENSG00000147381	DGREHTVY	2218	HLA-B*08:01
4305	MAGEA4	ENSG00000147381	DGREHTVY	2218	HLA-B*18:01
4306	MAGEA4	ENSG00000147381	DPASNTYTLV	2219	HLA-A*68:01
4307	MAGEA4	ENSG00000147381	DPASNTYTLV	2219	HLA-B*51:01
4308	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-A*23:01

4309	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-A*68:01
4310	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*07:02
4311	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*35:01
4312	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*35:03
4313	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*38:01
4314	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*39:01
4315	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*51:01
4316	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*55:01
4317	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-B*56:01
4318	MAGEA4	ENSG00000147381	DPASNTYTL	2220	HLA-C*07:02
4319	MAGEA4	ENSG00000147381	DVKEVDPASN	2221	HLA-A*25:01
4320	MAGEA4	ENSG00000147381	DVKEVDPASN	2221	HLA-A*26:01
4321	MAGEA4	ENSG00000147381	DVKEVDPASN	2221	HLA-A*33:01
4322	MAGEA4	ENSG00000147381	DVKEVDPASN	2221	HLA-A*68:01
4323	MAGEA4	ENSG00000147381	EALGLVGAQA	2222	HLA-A*33:03
4324	MAGEA4	ENSG00000147381	EALGLVGAQA	2222	HLA-B*54:01
4325	MAGEA4	ENSG00000147381	EALGLVGAQA	2222	HLA-C*07:06
4326	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-A*26:01
4327	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-A*33:01
4328	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-A*33:03
4329	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-C*04:01
4330	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-C*07:01
4331	MAGEA4	ENSG00000147381	EALGLVGAQ	2223	HLA-C*12:03
4332	MAGEA4	ENSG00000147381	EALGLVGA	2224	HLA-B*54:01
4333	MAGEA4	ENSG00000147381	EAQEEALGL	2225	HLA-B*35:03
4334	MAGEA4	ENSG00000147381	EAQEEALGL	2225	HLA-C*07:06
4335	MAGEA4	ENSG00000147381	EEALGLVGAQA	2226	HLA-B*44:03
4336	MAGEA4	ENSG00000147381	EEALGLVGA	2227	HLA-A*30:01
4337	MAGEA4	ENSG00000147381	EEALGLVGA	2227	HLA-B*18:01
4338	MAGEA4	ENSG00000147381	EEALGLVGA	2227	HLA-B*40:02
4339	MAGEA4	ENSG00000147381	EEALGLVGA	2227	HLA-B*49:01
4340	MAGEA4	ENSG00000147381	EEEGPSTSPDA	2228	HLA-B*39:01
4341	MAGEA4	ENSG00000147381	EEEGPSTSP	2229	HLA-B*39:01
4342	MAGEA4	ENSG00000147381	EEIWEELGV	2230	HLA-B*49:01
4343	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-A*25:01
4344	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-A*26:01
4345	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-A*30:02
4346	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*15:03
4347	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*18:01
4348	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*27:02
4349	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*40:01
4350	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*44:02
4351	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-B*44:03
4352	MAGEA4	ENSG00000147381	EELGVMGVY	98	HLA-C*16:04
4353	MAGEA4	ENSG00000147381	EELGVMGV	2231	HLA-B*18:01
4354	MAGEA4	ENSG00000147381	EELGVMGV	2231	HLA-B*37:01
4355	MAGEA4	ENSG00000147381	EELGVMGV	2231	HLA-B*40:02
4356	MAGEA4	ENSG00000147381	EELGVMGV	2231	HLA-B*49:01
4357	MAGEA4	ENSG00000147381	EEVPAAESA	2232	HLA-A*30:01
4358	MAGEA4	ENSG00000147381	EEVPAAESA	2232	HLA-B*18:01
4359	MAGEA4	ENSG00000147381	EEVPAAESA	2232	HLA-B*40:01
4360	MAGEA4	ENSG00000147381	EEVPAAESA	2232	HLA-B*40:02
4361	MAGEA4	ENSG00000147381	EEVPAAESA	2232	HLA-B*49:01
4362	MAGEA4	ENSG00000147381	EHTVYGEPR	2233	HLA-A*33:01
4363	MAGEA4	ENSG00000147381	EHTVYGEPR	2233	HLA-A*33:03
4364	MAGEA4	ENSG00000147381	EHVVRVNAR	2234	HLA-A*33:03
4365	MAGEA4	ENSG00000147381	EIWEELGVMGV	2235	HLA-A*68:02
4366	MAGEA4	ENSG00000147381	ELGVMGVY	2236	HLA-A*25:01
4367	MAGEA4	ENSG00000147381	ELGVMGVY	2236	HLA-A*26:01
4368	MAGEA4	ENSG00000147381	ELGVMGVY	2236	HLA-B*15:01
4369	MAGEA4	ENSG00000147381	ELGVMGVY	2236	HLA-C*07:01
4370	MAGEA4	ENSG00000147381	ELGVMGVY	2236	HLA-C*07:04
4371	MAGEA4	ENSG00000147381	ELVTKAEMLER	2237	HLA-A*33:01
4372	MAGEA4	ENSG00000147381	ELVTKAEML	2238	HLA-A*25:01

4373	MAGEA4	ENSG00000147381	ELVTKAEML	2238	HLA-A*26:01
4374	MAGEA4	ENSG00000147381	ELVTKAEML	2238	HLA-B*08:01
4375	MAGEA4	ENSG00000147381	ELVTKAEM	2239	HLA-B*08:01
4376	MAGEA4	ENSG00000147381	EMLERVIKNY	2240	HLA-A*25:01
4377	MAGEA4	ENSG00000147381	EMLERVIKNY	2240	HLA-B*44:02
4378	MAGEA4	ENSG00000147381	ESAGPPQSP	2241	HLA-B*39:01
4379	MAGEA4	ENSG00000147381	ESLFREALSNK	2242	HLA-A*33:01
4380	MAGEA4	ENSG00000147381	ESLFREAL	2243	HLA-B*08:01
4381	MAGEA4	ENSG00000147381	ETSYVKVLEHV	2244	HLA-A*68:02
4382	MAGEA4	ENSG00000147381	ETSYVKVLEH	2245	HLA-A*68:01
4383	MAGEA4	ENSG00000147381	ETSYVKVLE	2246	HLA-A*68:02
4384	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*01:01
4385	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*02:07
4386	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*25:01
4387	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*26:01
4388	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*33:03
4389	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*68:01
4390	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-A*68:02
4391	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-B*27:05
4392	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-B*35:03
4393	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-B*38:01
4394	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-B*39:01
4395	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-B*40:01
4396	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-C*05:01
4397	MAGEA4	ENSG00000147381	EVDPASNTYTL	2247	HLA-C*07:06
4398	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*01:01
4399	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*25:01
4400	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*26:01
4401	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*29:02
4402	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*30:02
4403	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*32:01
4404	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*33:03
4405	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-A*68:01
4406	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*15:01
4407	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*15:03
4408	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*18:01
4409	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*35:01
4410	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*38:01
4411	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*39:01
4412	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*44:03
4413	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*46:01
4414	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*55:01
4415	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-B*58:01
4416	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*02:02
4417	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*03:03
4418	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*05:01
4419	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*07:04
4420	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*07:06
4421	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*12:03
4422	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*16:02
4423	MAGEA4	ENSG00000147381	EVDPASNTY	12	HLA-C*16:04
4424	MAGEA4	ENSG00000147381	EVPAAESAGP	2248	HLA-A*26:01
4425	MAGEA4	ENSG00000147381	EYRQVPGSNP	2249	HLA-A*33:03
4426	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-B*46:01
4427	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-B*49:01
4428	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-B*51:01
4429	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-C*02:02
4430	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-C*03:04
4431	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-C*12:03
4432	MAGEA4	ENSG00000147381	FGIDVKEV	2018	HLA-C*16:02
4433	MAGEA4	ENSG00000147381	FGKASESLK	2250	HLA-C*07:02
4434	MAGEA4	ENSG00000147381	FGKASESL	2251	HLA-B*46:01
4435	MAGEA4	ENSG00000147381	FGKASESL	2251	HLA-C*03:04
4436	MAGEA4	ENSG00000147381	FGKASESL	2251	HLA-C*14:02

4437	MAGEA4	ENSG00000147381	FLWGPRALAET	199	HLA-A*02:01
4438	MAGEA4	ENSG00000147381	FLWGPRALAET	199	HLA-A*02:03
4439	MAGEA4	ENSG00000147381	FLWGPRALAET	199	HLA-A*02:04
4440	MAGEA4	ENSG00000147381	FLWGPRALAET	199	HLA-A*02:07
4441	MAGEA4	ENSG00000147381	FLWGPRALA	2252	HLA-A*02:01
4442	MAGEA4	ENSG00000147381	FLWGPRAL	2253	HLA-A*02:04
4443	MAGEA4	ENSG00000147381	FPKTGLLII	2254	HLA-B*51:01
4444	MAGEA4	ENSG00000147381	FPKTGLLII	2254	HLA-B*54:01
4445	MAGEA4	ENSG00000147381	FPKTGLLI	2255	HLA-B*51:01
4446	MAGEA4	ENSG00000147381	FPVIFGKAS	2256	HLA-B*54:01
4447	MAGEA4	ENSG00000147381	FPVIFGKA	2257	HLA-B*54:01
4448	MAGEA4	ENSG00000147381	FPVIFGKA	2257	HLA-B*55:01
4449	MAGEA4	ENSG00000147381	FPVIFGKA	2257	HLA-B*56:01
4450	MAGEA4	ENSG00000147381	FREALSNKV	2258	HLA-C*06:02
4451	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-B*13:02
4452	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-B*15:03
4453	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-B*49:01
4454	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-B*51:01
4455	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-B*58:01
4456	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-C*02:02
4457	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-C*12:03
4458	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-C*16:02
4459	MAGEA4	ENSG00000147381	GASALPTTI	2259	HLA-C*16:04
4460	MAGEA4	ENSG00000147381	GKASESLKM	2260	HLA-B*15:03
4461	MAGEA4	ENSG00000147381	GLLGNNQIFPK	2261	HLA-A*03:01
4462	MAGEA4	ENSG00000147381	GLLGNNQIFPK	2261	HLA-A*03:02
4463	MAGEA4	ENSG00000147381	GLLGNNQIFPK	2261	HLA-A*11:01
4464	MAGEA4	ENSG00000147381	GLLGNNQIFPK	2261	HLA-A*31:01
4465	MAGEA4	ENSG00000147381	GLLGNNQIF	2262	HLA-B*15:01
4466	MAGEA4	ENSG00000147381	GLLIIVLGTI	2263	HLA-A*02:04
4467	MAGEA4	ENSG00000147381	GPPQSPQGASA	2264	HLA-B*56:01
4468	MAGEA4	ENSG00000147381	GPRALAETSYV	2265	HLA-C*07:02
4469	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-A*30:02
4470	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-B*07:02
4471	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-B*15:01
4472	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-B*15:03
4473	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-B*35:01
4474	MAGEA4	ENSG00000147381	GPRALAETSY	2266	HLA-B*55:01
4475	MAGEA4	ENSG00000147381	GSNPARYEFLW	2267	HLA-B*57:01
4476	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-A*23:01
4477	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-A*29:02
4478	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-A*30:02
4479	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-A*31:01
4480	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-A*32:01
4481	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-B*15:01
4482	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-B*15:03
4483	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-B*46:01
4484	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-B*57:01
4485	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-B*58:01
4486	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-C*02:02
4487	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-C*16:01
4488	MAGEA4	ENSG00000147381	GSNPARYEF	2268	HLA-C*16:04
4489	MAGEA4	ENSG00000147381	GTLEEVPAA	2269	HLA-A*02:01
4490	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-A*03:02
4491	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-A*11:01
4492	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-A*31:01
4493	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-A*33:03
4494	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-A*68:01
4495	MAGEA4	ENSG00000147381	GVMGVYDGR	2270	HLA-C*07:06
4496	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*01:01
4497	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*03:01
4498	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*03:02
4499	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*11:01
4500	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*25:01

4501	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*26:01
4502	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*29:02
4503	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*30:02
4504	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-A*32:01
4505	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*15:01
4506	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*15:03
4507	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*27:05
4508	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*35:01
4509	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*46:01
4510	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*55:01
4511	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-B*58:01
4512	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-C*02:02
4513	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-C*07:04
4514	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-C*12:03
4515	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-C*16:01
4516	MAGEA4	ENSG00000147381	GVYDGREHTVY	2271	HLA-C*16:04
4517	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*02:01
4518	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*02:03
4519	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*02:04
4520	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*02:07
4521	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*03:01
4522	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*25:01
4523	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*26:01
4524	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*30:01
4525	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*32:01
4526	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-A*68:02
4527	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*13:02
4528	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*15:01
4529	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*27:05
4530	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*37:01
4531	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*40:02
4532	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*46:01
4533	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*49:01
4534	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*51:01
4535	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*55:01
4536	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*56:01
4537	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-B*58:01
4538	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*01:02
4539	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*02:02
4540	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*03:03
4541	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*03:04
4542	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*06:02
4543	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*07:02
4544	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*12:03
4545	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*16:02
4546	MAGEA4	ENSG00000147381	GVYDGREHTV	2272	HLA-C*16:04
4547	MAGEA4	ENSG00000147381	HTVYGEPR	2273	HLA-A*68:01
4548	MAGEA4	ENSG00000147381	HVVRVNARV	2274	HLA-A*68:02
4549	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-B*54:01
4550	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-C*01:02
4551	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-C*03:03
4552	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-C*03:04
4553	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-C*05:01
4554	MAGEA4	ENSG00000147381	IAMEGDSA	2275	HLA-C*14:02
4555	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-B*07:02
4556	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-B*35:03
4557	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-B*46:01
4558	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*01:02
4559	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*02:02
4560	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*03:03
4561	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*03:04
4562	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*16:01
4563	MAGEA4	ENSG00000147381	IAYPSLREAAL	2276	HLA-C*16:02
4564	MAGEA4	ENSG00000147381	IAYPSLREAA	2277	HLA-B*54:01

4565	MAGEA4	ENSG00000147381	IAYPSLREAA	2277	HLA-B*56:01
4566	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-A*02:01
4567	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-A*02:03
4568	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*08:01
4569	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*46:01
4570	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*51:01
4571	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*54:01
4572	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*55:01
4573	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*56:01
4574	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*57:01
4575	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-B*58:01
4576	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*02:02
4577	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*03:03
4578	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*03:04
4579	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*06:02
4580	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*12:03
4581	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*16:01
4582	MAGEA4	ENSG00000147381	IAYPSLREA	2278	HLA-C*16:02
4583	MAGEA4	ENSG00000147381	IFGKASESL	2279	HLA-C*01:02
4584	MAGEA4	ENSG00000147381	IFGKASESL	2279	HLA-C*14:02
4585	MAGEA4	ENSG00000147381	IFPKTGLLII	2280	HLA-A*24:02
4586	MAGEA4	ENSG00000147381	IFPKTGLLI	2281	HLA-A*23:01
4587	MAGEA4	ENSG00000147381	IFPKTGLLI	2281	HLA-A*24:02
4588	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*08:01
4589	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*15:01
4590	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*35:01
4591	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*35:03
4592	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*39:01
4593	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-B*46:01
4594	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-C*01:02
4595	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-C*03:03
4596	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-C*03:04
4597	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-C*07:04
4598	MAGEA4	ENSG00000147381	IIVLGTIAM	2282	HLA-C*14:02
4599	MAGEA4	ENSG00000147381	IVLGTIAMEG	2283	HLA-C*04:01
4600	MAGEA4	ENSG00000147381	IVLGTIAM	2284	HLA-A*23:01
4601	MAGEA4	ENSG00000147381	IVLGTIAM	2284	HLA-B*46:01
4602	MAGEA4	ENSG00000147381	IVLGTIAM	2284	HLA-C*01:02
4603	MAGEA4	ENSG00000147381	IVLGTIAM	2284	HLA-C*03:03
4604	MAGEA4	ENSG00000147381	IVLGTIAM	2284	HLA-C*14:02
4605	MAGEA4	ENSG00000147381	KAEMLERVI	2285	HLA-C*16:02
4606	MAGEA4	ENSG00000147381	KASESLKMIF	2286	HLA-B*57:01
4607	MAGEA4	ENSG00000147381	KASESLKMI	2287	HLA-C*16:02
4608	MAGEA4	ENSG00000147381	KASESLKM	2288	HLA-B*37:01
4609	MAGEA4	ENSG00000147381	KASESLKM	2288	HLA-B*58:01
4610	MAGEA4	ENSG00000147381	KASESLKM	2288	HLA-C*03:04
4611	MAGEA4	ENSG00000147381	KASESLKM	2288	HLA-C*16:01
4612	MAGEA4	ENSG00000147381	KASESLKM	2288	HLA-C*16:02
4613	MAGEA4	ENSG00000147381	KELVTKAEML	2289	HLA-A*30:01
4614	MAGEA4	ENSG00000147381	KELVTKAEML	2289	HLA-B*40:01
4615	MAGEA4	ENSG00000147381	KELVTKAEML	2289	HLA-B*40:02
4616	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-A*30:01
4617	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*18:01
4618	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*37:01
4619	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*40:01
4620	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*40:02
4621	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*44:02
4622	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*44:03
4623	MAGEA4	ENSG00000147381	KELVTKAEM	2290	HLA-B*49:01
4624	MAGEA4	ENSG00000147381	KEVDPASNTYT	2291	HLA-B*40:01
4625	MAGEA4	ENSG00000147381	KEVDPASNTYT	2291	HLA-B*49:01
4626	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*25:01
4627	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*26:01
4628	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*29:02

4629	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*30:01
4630	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*30:02
4631	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-A*32:01
4632	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*15:01
4633	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*15:03
4634	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*18:01
4635	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*27:02
4636	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*27:05
4637	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*37:01
4638	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*39:01
4639	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*40:01
4640	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*40:02
4641	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*44:02
4642	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*44:03
4643	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*46:01
4644	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*49:01
4645	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*57:01
4646	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-B*58:01
4647	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*02:02
4648	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*12:03
4649	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*14:02
4650	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*16:01
4651	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*16:02
4652	MAGEA4	ENSG00000147381	KEVDPASNTY	19	HLA-C*16:04
4653	MAGEA4	ENSG00000147381	KEVDPASNT	2292	HLA-B*40:01
4654	MAGEA4	ENSG00000147381	KEVDPASNT	2292	HLA-B*49:01
4655	MAGEA4	ENSG00000147381	KMIFGIDVKEV	2293	HLA-A*02:01
4656	MAGEA4	ENSG00000147381	KVDELAHFLLR	2294	HLA-A*02:07
4657	MAGEA4	ENSG00000147381	KVDELAHFLLR	2294	HLA-A*03:01
4658	MAGEA4	ENSG00000147381	KVDELAHFLLR	2294	HLA-A*31:01
4659	MAGEA4	ENSG00000147381	KVDELAHFLL	16	HLA-A*02:01
4660	MAGEA4	ENSG00000147381	KVDELAHFLL	16	HLA-A*02:04
4661	MAGEA4	ENSG00000147381	KVDELAHFLL	16	HLA-A*02:07
4662	MAGEA4	ENSG00000147381	KVDELAHFLL	16	HLA-A*31:01
4663	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*02:01
4664	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*02:04
4665	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*02:07
4666	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*03:02
4667	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*31:01
4668	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-A*68:02
4669	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-B*13:02
4670	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-B*38:01
4671	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-B*58:01
4672	MAGEA4	ENSG00000147381	KVDELAHFL	13	HLA-C*05:01
4673	MAGEA4	ENSG00000147381	KVDELAHF	2295	HLA-C*05:01
4674	MAGEA4	ENSG00000147381	KVLEHVVRVNA	2296	HLA-A*31:01
4675	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*02:01
4676	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*02:03
4677	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*02:04
4678	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*02:07
4679	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*03:01
4680	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*03:02
4681	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*31:01
4682	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-A*68:02
4683	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-B*13:02
4684	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-B*37:01
4685	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-B*55:01
4686	MAGEA4	ENSG00000147381	KVLEHVVRV	2297	HLA-C*02:02
4687	MAGEA4	ENSG00000147381	KVLEHVVR	2298	HLA-A*31:01
4688	MAGEA4	ENSG00000147381	LAETSYVKV	2299	HLA-C*05:01
4689	MAGEA4	ENSG00000147381	LAETSYVK	2300	HLA-B*27:02
4690	MAGEA4	ENSG00000147381	LAHFLLRKY	2301	HLA-A*29:02
4691	MAGEA4	ENSG00000147381	LEHVVRVNA	2302	HLA-B*40:02
4692	MAGEA4	ENSG00000147381	LERVIKNY	2303	HLA-B*18:01

4693	MAGEA4	ENSG00000147381	LGNNQIFPK	2304	HLA-A*03:02
4694	MAGEA4	ENSG00000147381	LGNNQIFPK	2304	HLA-A*11:01
4695	MAGEA4	ENSG00000147381	LGNNQIFPK	2304	HLA-B*27:02
4696	MAGEA4	ENSG00000147381	LGNNQIFPK	2304	HLA-C*07:06
4697	MAGEA4	ENSG00000147381	LGVMGVYDGR	2305	HLA-B*27:02
4698	MAGEA4	ENSG00000147381	LIIVLGTIAM	2306	HLA-B*46:01
4699	MAGEA4	ENSG00000147381	LLGNNQIFPK	2307	HLA-A*03:01
4700	MAGEA4	ENSG00000147381	LLGNNQIFPK	2307	HLA-A*03:02
4701	MAGEA4	ENSG00000147381	LLGNNQIFPK	2307	HLA-B*27:02
4702	MAGEA4	ENSG00000147381	LLIIVLGTI	2308	HLA-A*02:03
4703	MAGEA4	ENSG00000147381	LPTTISFTCW	2309	HLA-B*35:01
4704	MAGEA4	ENSG00000147381	LPTTISFTCW	2309	HLA-B*51:01
4705	MAGEA4	ENSG00000147381	LPTTISFTCW	2309	HLA-B*54:01
4706	MAGEA4	ENSG00000147381	LPTTISFTC	2310	HLA-B*35:03
4707	MAGEA4	ENSG00000147381	LPTTISFTC	2310	HLA-B*54:01
4708	MAGEA4	ENSG00000147381	LPTTISFTC	2310	HLA-B*56:01
4709	MAGEA4	ENSG00000147381	LSNKVDELAHF	2311	HLA-B*57:01
4710	MAGEA4	ENSG00000147381	LSYDGLLGNN	2312	HLA-C*06:02
4711	MAGEA4	ENSG00000147381	LSYDGLLGNN	2312	HLA-C*12:03
4712	MAGEA4	ENSG00000147381	LTQDWVQENYL	2079	HLA-C*04:01
4713	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-A*01:01
4714	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-A*29:02
4715	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-A*30:02
4716	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-A*32:01
4717	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-B*57:01
4718	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-B*58:01
4719	MAGEA4	ENSG00000147381	LTQDWVQENY	2080	HLA-C*07:01
4720	MAGEA4	ENSG00000147381	LVPGTLEEV	2313	HLA-A*02:01
4721	MAGEA4	ENSG00000147381	LVPGTLEEV	2313	HLA-A*02:07
4722	MAGEA4	ENSG00000147381	LVTCLGLSY	2314	HLA-A*01:01
4723	MAGEA4	ENSG00000147381	LVTCLGLSY	2314	HLA-A*26:01
4724	MAGEA4	ENSG00000147381	LVTCLGLSY	2314	HLA-A*29:02
4725	MAGEA4	ENSG00000147381	LVTCLGLSY	2314	HLA-A*30:02
4726	MAGEA4	ENSG00000147381	MIFGIDVKEV	2315	HLA-A*02:01
4727	MAGEA4	ENSG00000147381	MIFGIDVKEV	2315	HLA-A*02:03
4728	MAGEA4	ENSG00000147381	MIFGIDVKEV	2315	HLA-A*02:04
4729	MAGEA4	ENSG00000147381	MIFGIDVKEV	2315	HLA-A*02:07
4730	MAGEA4	ENSG00000147381	MIFGIDVKEV	2315	HLA-A*68:02
4731	MAGEA4	ENSG00000147381	MLERVIKNY	2316	HLA-A*01:01
4732	MAGEA4	ENSG00000147381	MLERVIKNY	2316	HLA-A*29:02
4733	MAGEA4	ENSG00000147381	MLERVIKNY	2316	HLA-A*30:02
4734	MAGEA4	ENSG00000147381	MLERVIKNY	2316	HLA-B*44:02
4735	MAGEA4	ENSG00000147381	NARVRIAY	2317	HLA-C*16:01
4736	MAGEA4	ENSG00000147381	NKVDELAHF	2318	HLA-A*23:01
4737	MAGEA4	ENSG00000147381	NKVDELAHF	2318	HLA-B*15:03
4738	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*13:02
4739	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*15:01
4740	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*15:03
4741	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*27:05
4742	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*38:01
4743	MAGEA4	ENSG00000147381	NQIFPKTGL	2319	HLA-B*39:01
4744	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-A*23:01
4745	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-A*25:01
4746	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-A*26:01
4747	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-A*68:01
4748	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-A*68:02
4749	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-B*18:01
4750	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-B*39:01
4751	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-C*06:02
4752	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-C*07:06
4753	MAGEA4	ENSG00000147381	NTYTLVTCL	2320	HLA-C*12:03
4754	MAGEA4	ENSG00000147381	NYKRCFPVI	2321	HLA-A*24:02
4755	MAGEA4	ENSG00000147381	PASNTYTL	2322	HLA-B*07:02
4756	MAGEA4	ENSG00000147381	PASNTYTL	2322	HLA-C*07:02

4757	MAGEA4	ENSG00000147381	PDAESLFR	2323	HLA-B*27:02
4758	MAGEA4	ENSG00000147381	PLVPGTLEEV	2324	HLA-A*02:01
4759	MAGEA4	ENSG00000147381	PLVPGTLEEV	2324	HLA-A*02:03
4760	MAGEA4	ENSG00000147381	PRALAETSY	2325	HLA-B*15:03
4761	MAGEA4	ENSG00000147381	PRALAETSY	2325	HLA-B*27:02
4762	MAGEA4	ENSG00000147381	PRALAETSY	2325	HLA-C*07:01
4763	MAGEA4	ENSG00000147381	PRALAETSY	2325	HLA-C*07:04
4764	MAGEA4	ENSG00000147381	PTTISFTCW	2326	HLA-B*57:01
4765	MAGEA4	ENSG00000147381	QDWVQENYL	2106	HLA-A*30:01
4766	MAGEA4	ENSG00000147381	QDWVQENYL	2106	HLA-B*37:01
4767	MAGEA4	ENSG00000147381	QDWVQENY	2327	HLA-B*18:01
4768	MAGEA4	ENSG00000147381	QEAAVSSSSPL	2328	HLA-A*30:01
4769	MAGEA4	ENSG00000147381	QEAAVSSSSPL	2328	HLA-B*40:01
4770	MAGEA4	ENSG00000147381	QEEALGLVGA	2329	HLA-A*30:01
4771	MAGEA4	ENSG00000147381	QEEALGLVGA	2329	HLA-B*40:02
4772	MAGEA4	ENSG00000147381	QEEALGLVGA	2329	HLA-B*49:01
4773	MAGEA4	ENSG00000147381	QEEALGLV	2330	HLA-B*49:01
4774	MAGEA4	ENSG00000147381	QIFPKTGLLII	2331	HLA-A*02:01
4775	MAGEA4	ENSG00000147381	QIFPKTGLLII	2331	HLA-A*02:03
4776	MAGEA4	ENSG00000147381	QIFPKTGLLII	2331	HLA-A*02:04
4777	MAGEA4	ENSG00000147381	QIFPKTGLL	2332	HLA-A*02:03
4778	MAGEA4	ENSG00000147381	QIFPKTGLL	2332	HLA-A*03:01
4779	MAGEA4	ENSG00000147381	QIFPKTGL	2333	HLA-B*08:01
4780	MAGEA4	ENSG00000147381	QSPQGASAL	127	HLA-C*01:02
4781	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*01:01
4782	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*25:01
4783	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*26:01
4784	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*29:02
4785	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*30:02
4786	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*32:01
4787	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-A*68:01
4788	MAGEA4	ENSG00000147381	QVPGSNPARY	2334	HLA-C*07:04
4789	MAGEA4	ENSG00000147381	QVPGSNPAR	2335	HLA-A*68:01
4790	MAGEA4	ENSG00000147381	RAKELVTKA	2336	HLA-B*54:01
4791	MAGEA4	ENSG00000147381	RAKELVTKA	2336	HLA-B*55:01
4792	MAGEA4	ENSG00000147381	RALAETSYVK	2337	HLA-A*03:02
4793	MAGEA4	ENSG00000147381	RALAETSYVK	2337	HLA-B*27:02
4794	MAGEA4	ENSG00000147381	RCFPVIFGK	2338	HLA-A*03:01
4795	MAGEA4	ENSG00000147381	RCFPVIFGK	2338	HLA-A*03:02
4796	MAGEA4	ENSG00000147381	RCFPVIFGK	2338	HLA-A*11:01
4797	MAGEA4	ENSG00000147381	RCFPVIFGK	2338	HLA-A*31:01
4798	MAGEA4	ENSG00000147381	RCFPVIFGK	2338	HLA-B*57:01
4799	MAGEA4	ENSG00000147381	REALSNKVDEL	2339	HLA-A*30:01
4800	MAGEA4	ENSG00000147381	REALSNKVDEL	2339	HLA-B*40:01
4801	MAGEA4	ENSG00000147381	REALSNKV	2340	HLA-B*37:01
4802	MAGEA4	ENSG00000147381	REALSNKV	2340	HLA-B*49:01
4803	MAGEA4	ENSG00000147381	RIAYPSLREA	2341	HLA-A*02:03
4804	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-A*29:02
4805	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-A*30:02
4806	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-A*32:01
4807	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-B*15:01
4808	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-B*15:03
4809	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-B*44:03
4810	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-B*57:01
4811	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-B*58:01
4812	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-C*02:02
4813	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-C*07:04
4814	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-C*16:02
4815	MAGEA4	ENSG00000147381	RQVPGSNPARY	14	HLA-C*16:04
4816	MAGEA4	ENSG00000147381	RQVPGSNPAR	2342	HLA-A*31:01
4817	MAGEA4	ENSG00000147381	RVIKNYKR	2343	HLA-A*31:01
4818	MAGEA4	ENSG00000147381	RVNARVRIAY	2344	HLA-A*32:01
4819	MAGEA4	ENSG00000147381	RVRIAYPSLR	2345	HLA-A*03:01
4820	MAGEA4	ENSG00000147381	RVRIAYPSLR	2345	HLA-A*31:01

4821	MAGEA4	ENSG00000147381	RVRIAYPSL	2346	HLA-B*07:02
4822	MAGEA4	ENSG00000147381	SAGPPQSPQGA	2347	HLA-C*12:03
4823	MAGEA4	ENSG00000147381	SAGPPQSPQ	2348	HLA-C*03:03
4824	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*02:01
4825	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*02:04
4826	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*02:07
4827	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*11:01
4828	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*23:01
4829	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*24:02
4830	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*25:01
4831	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*26:01
4832	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*29:02
4833	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*30:01
4834	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*30:02
4835	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*31:01
4836	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*32:01
4837	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*33:01
4838	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*33:03
4839	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-A*68:01
4840	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*07:02
4841	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*08:01
4842	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*15:01
4843	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*15:03
4844	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*18:01
4845	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*27:02
4846	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*35:01
4847	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*35:03
4848	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*37:01
4849	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*38:01
4850	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*39:01
4851	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*44:02
4852	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*44:03
4853	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*46:01
4854	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*51:01
4855	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*54:01
4856	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*55:01
4857	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*56:01
4858	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*57:01
4859	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-B*58:01
4860	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*01:02
4861	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*02:02
4862	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*03:03
4863	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*03:04
4864	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*04:01
4865	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*05:01
4866	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*07:02
4867	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*07:04
4868	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*07:06
4869	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*12:03
4870	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*14:02
4871	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*16:01
4872	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*16:02
4873	MAGEA4	ENSG00000147381	SALPTTISF	15	HLA-C*16:04
4874	MAGEA4	ENSG00000147381	SEEEIWEEL	2349	HLA-A*30:01
4875	MAGEA4	ENSG00000147381	SEEEIWEEL	2349	HLA-B*40:01
4876	MAGEA4	ENSG00000147381	SESLKMIF	2350	HLA-B*18:01
4877	MAGEA4	ENSG00000147381	SESLKMIF	2350	HLA-B*37:01
4878	MAGEA4	ENSG00000147381	SESLKMIF	2350	HLA-B*44:02
4879	MAGEA4	ENSG00000147381	SESLKMIF	2350	HLA-B*44:03
4880	MAGEA4	ENSG00000147381	SLFREALSNK	2351	HLA-A*03:01
4881	MAGEA4	ENSG00000147381	SLFREALSNK	2351	HLA-A*03:02
4882	MAGEA4	ENSG00000147381	SPDAESLFREA	2352	HLA-B*54:01
4883	MAGEA4	ENSG00000147381	SPDAESLFREA	2352	HLA-B*55:01
4884	MAGEA4	ENSG00000147381	SPDAESLFREA	2352	HLA-B*56:01

4885	MAGEA4	ENSG00000147381	SPDAESLF	2353	HLA-B*55:01
4886	MAGEA4	ENSG00000147381	SPDAESLF	2353	HLA-C*05:01
4887	MAGEA4	ENSG00000147381	SPLVPGTLEEV	2354	HLA-B*56:01
4888	MAGEA4	ENSG00000147381	SPLVPGTL	2355	HLA-B*07:02
4889	MAGEA4	ENSG00000147381	SPLVPGTL	2355	HLA-B*08:01
4890	MAGEA4	ENSG00000147381	SPLVPGTL	2355	HLA-C*07:02
4891	MAGEA4	ENSG00000147381	SPQGASAL	2356	HLA-B*07:02
4892	MAGEA4	ENSG00000147381	SPQGASAL	2356	HLA-C*07:02
4893	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-B*07:02
4894	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-B*46:01
4895	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-B*58:01
4896	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-C*01:02
4897	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-C*03:04
4898	MAGEA4	ENSG00000147381	SSPLVPGTL	2357	HLA-C*07:02
4899	MAGEA4	ENSG00000147381	STSPDAESLFR	2358	HLA-A*11:01
4900	MAGEA4	ENSG00000147381	STSPDAESLFR	2358	HLA-A*68:01
4901	MAGEA4	ENSG00000147381	STSPDAESLFR	2358	HLA-C*07:06
4902	MAGEA4	ENSG00000147381	SYDGLLGNNQI	2359	HLA-A*23:01
4903	MAGEA4	ENSG00000147381	SYDGLLGNNQI	2359	HLA-A*24:02
4904	MAGEA4	ENSG00000147381	SYDGLLGNNQI	2359	HLA-B*35:03
4905	MAGEA4	ENSG00000147381	SYDGLLGNNQI	2359	HLA-B*38:01
4906	MAGEA4	ENSG00000147381	SYDGLLGNNQI	2359	HLA-C*04:01
4907	MAGEA4	ENSG00000147381	SYDGLLGNN	2360	HLA-C*04:01
4908	MAGEA4	ENSG00000147381	SYVKVLEHV	2361	HLA-A*23:01
4909	MAGEA4	ENSG00000147381	SYVKVLEHV	2361	HLA-A*24:02
4910	MAGEA4	ENSG00000147381	TLVTCLGLSY	2362	HLA-A*29:02
4911	MAGEA4	ENSG00000147381	TQDWVQENYL	2158	HLA-B*38:01
4912	MAGEA4	ENSG00000147381	TQDWVQENYL	2158	HLA-C*05:01
4913	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-A*01:01
4914	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-A*30:02
4915	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-B*15:01
4916	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-B*15:03
4917	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-B*38:01
4918	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-B*39:01
4919	MAGEA4	ENSG00000147381	TQDWVQENY	2159	HLA-C*05:01
4920	MAGEA4	ENSG00000147381	TSPDAESLFR	2363	HLA-A*68:01
4921	MAGEA4	ENSG00000147381	TSPDAESLFR	2363	HLA-B*27:02
4922	MAGEA4	ENSG00000147381	TSPDAESLF	2364	HLA-C*01:02
4923	MAGEA4	ENSG00000147381	TSPDAESLF	2364	HLA-C*05:01
4924	MAGEA4	ENSG00000147381	TSPDAESL	2365	HLA-C*01:02
4925	MAGEA4	ENSG00000147381	TSYVKVLEHV	2366	HLA-A*68:02
4926	MAGEA4	ENSG00000147381	TSYVKVLEH	2367	HLA-A*03:01
4927	MAGEA4	ENSG00000147381	TSYVKVLEH	2367	HLA-A*11:01
4928	MAGEA4	ENSG00000147381	TSYVKVLEH	2367	HLA-C*02:02
4929	MAGEA4	ENSG00000147381	TSYVKVLEH	2367	HLA-C*07:06
4930	MAGEA4	ENSG00000147381	TSYVKVLEH	2367	HLA-C*12:03
4931	MAGEA4	ENSG00000147381	TTEEQEAAV	2368	HLA-C*05:01
4932	MAGEA4	ENSG00000147381	TTISFTCWR	2369	HLA-A*31:01
4933	MAGEA4	ENSG00000147381	TTISFTCW	2370	HLA-A*25:01
4934	MAGEA4	ENSG00000147381	TTISFTCW	2370	HLA-B*57:01
4935	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-A*02:03
4936	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-A*03:01
4937	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-A*68:02
4938	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-C*02:02
4939	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-C*03:04
4940	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-C*06:02
4941	MAGEA4	ENSG00000147381	TVYGEPRKL	2371	HLA-C*12:03
4942	MAGEA4	ENSG00000147381	TYTLVTCL	2372	HLA-A*23:01
4943	MAGEA4	ENSG00000147381	TYTLVTCL	2372	HLA-A*24:02
4944	MAGEA4	ENSG00000147381	TYTLVTCL	2372	HLA-C*14:02
4945	MAGEA4	ENSG00000147381	VDELAHFL	2373	HLA-B*37:01
4946	MAGEA4	ENSG00000147381	VDELAHFL	2373	HLA-B*40:02
4947	MAGEA4	ENSG00000147381	VDELAHFL	2373	HLA-C*07:04
4948	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-B*15:03

4949	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-B*37:01
4950	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-B*39:01
4951	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*01:02
4952	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*04:01
4953	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*07:01
4954	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*12:03
4955	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*14:02
4956	MAGEA4	ENSG00000147381	VDPASNTY	2374	HLA-C*16:02
4957	MAGEA4	ENSG00000147381	VEAQEEALGLV	2375	HLA-B*49:01
4958	MAGEA4	ENSG00000147381	VEAQEEALGL	2376	HLA-A*30:01
4959	MAGEA4	ENSG00000147381	VEAQEEALGL	2376	HLA-B*40:01
4960	MAGEA4	ENSG00000147381	VEAQEEAL	2377	HLA-A*30:01
4961	MAGEA4	ENSG00000147381	VEAQEEAL	2377	HLA-B*40:01
4962	MAGEA4	ENSG00000147381	VIFGKASESLK	2378	HLA-A*03:01
4963	MAGEA4	ENSG00000147381	VIFGKASESLK	2378	HLA-A*03:02
4964	MAGEA4	ENSG00000147381	VIFGKASESLK	2378	HLA-A*11:01
4965	MAGEA4	ENSG00000147381	VIFGKASESL	2379	HLA-C*01:02
4966	MAGEA4	ENSG00000147381	VKEVDPASNTY	2380	HLA-B*15:03
4967	MAGEA4	ENSG00000147381	VNARVRIAY	2381	HLA-A*32:01
4968	MAGEA4	ENSG00000147381	VNARVRIAY	2381	HLA-C*16:01
4969	MAGEA4	ENSG00000147381	VPGSNPARYEF	2382	HLA-B*35:01
4970	MAGEA4	ENSG00000147381	VPGSNPARY	2383	HLA-A*29:02
4971	MAGEA4	ENSG00000147381	VPGSNPARY	2383	HLA-A*30:02
4972	MAGEA4	ENSG00000147381	VPGSNPARY	2383	HLA-B*35:01
4973	MAGEA4	ENSG00000147381	VPGSNPARY	2383	HLA-B*55:01
4974	MAGEA4	ENSG00000147381	VPGTLEEV	2384	HLA-B*56:01
4975	MAGEA4	ENSG00000147381	VQENYLEY	2174	HLA-A*01:01
4976	MAGEA4	ENSG00000147381	VQENYLEY	2174	HLA-B*15:01
4977	MAGEA4	ENSG00000147381	VQENYLEY	2174	HLA-B*15:03
4978	MAGEA4	ENSG00000147381	VQENYLEY	2174	HLA-B*39:01
4979	MAGEA4	ENSG00000147381	VQENYLEY	2174	HLA-C*07:01
4980	MAGEA4	ENSG00000147381	VRIAYPSLR	2385	HLA-B*27:05
4981	MAGEA4	ENSG00000147381	VTCLGLSY	2386	HLA-A*01:01
4982	MAGEA4	ENSG00000147381	VTCLGLSY	2386	HLA-C*07:01
4983	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*03:01
4984	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*11:01
4985	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*31:01
4986	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*33:01
4987	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*33:03
4988	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-A*68:01
4989	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-B*57:01
4990	MAGEA4	ENSG00000147381	VTKAEMLER	2387	HLA-C*07:06
4991	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-A*24:02
4992	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-A*29:02
4993	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-B*35:01
4994	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-B*55:01
4995	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-C*04:01
4996	MAGEA4	ENSG00000147381	VYDGREHTVY	2388	HLA-C*07:01
4997	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-A*02:01
4998	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-A*02:07
4999	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-A*23:01
5000	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-A*24:02
5001	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-A*32:01
5002	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*08:01
5003	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*35:01
5004	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*35:03
5005	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*38:01
5006	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*51:01
5007	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-B*55:01
5008	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*01:02
5009	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*03:04
5010	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*04:01
5011	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*05:01
5012	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*14:02

5013	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*16:01
5014	MAGEA4	ENSG00000147381	VYDGREHTV	2389	HLA-C*16:02
5015	MAGEA4	ENSG00000147381	VYGEPRKLL	2390	HLA-A*23:01
5016	MAGEA4	ENSG00000147381	VYGEPRKLL	2390	HLA-A*24:02
5017	MAGEA4	ENSG00000147381	VYGEPRKL	2391	HLA-A*23:01
5018	MAGEA4	ENSG00000147381	VYGEPRKL	2391	HLA-A*24:02
5019	MAGEA4	ENSG00000147381	WEELGVMGV	2392	HLA-B*40:02
5020	MAGEA4	ENSG00000147381	WEELGVMGV	2392	HLA-B*49:01
5021	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*01:01
5022	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*03:01
5023	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*25:01
5024	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*26:01
5025	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*29:02
5026	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-A*30:02
5027	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-B*15:01
5028	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-B*35:01
5029	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-B*46:01
5030	MAGEA4	ENSG00000147381	WVQENYLEY	75	HLA-C*07:04
5031	MAGEA4	ENSG00000147381	YDGLLGNNQIF	2393	HLA-C*07:01
5032	MAGEA4	ENSG00000147381	YDGREHTVY	2394	HLA-A*01:01
5033	MAGEA4	ENSG00000147381	YDGREHTVY	2394	HLA-A*29:02
5034	MAGEA4	ENSG00000147381	YDGREHTVY	2394	HLA-C*07:01
5035	MAGEA4	ENSG00000147381	YDGREHTV	2395	HLA-C*06:02
5036	MAGEA4	ENSG00000147381	YDGREHTV	2395	HLA-C*07:01
5037	MAGEA4	ENSG00000147381	YDGREHTV	2395	HLA-C*07:04
5038	MAGEA4	ENSG00000147381	YEFLWGPRA	2183	HLA-A*02:04
5039	MAGEA4	ENSG00000147381	YPSLREAALL	2396	HLA-B*07:02
5040	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*07:02
5041	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*08:01
5042	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*35:01
5043	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*35:03
5044	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*37:01
5045	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*39:01
5046	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*40:01
5047	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*51:01
5048	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*54:01
5049	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*55:01
5050	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-B*56:01
5051	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*01:02
5052	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*03:03
5053	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*03:04
5054	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*07:02
5055	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*14:02
5056	MAGEA4	ENSG00000147381	YPSLREAAL	2397	HLA-C*16:01
5057	MAGEA4	ENSG00000147381	YPSLREAA	2398	HLA-B*54:01
5058	MAGEA4	ENSG00000147381	YPSLREAA	2398	HLA-B*55:01
5059	MAGEA4	ENSG00000147381	YPSLREAA	2398	HLA-B*56:01
5060	MAGEA4	ENSG00000147381	YRAKELVTK	2399	HLA-B*27:02
5061	MAGEA4	ENSG00000147381	YRAKELVTK	2399	HLA-B*27:05
5062	MAGEA4	ENSG00000147381	YRAKELVTK	2399	HLA-C*06:02
5063	MAGEA4	ENSG00000147381	YRQVPGSNPAR	2400	HLA-B*27:05
5064	MAGEA4	ENSG00000147381	YRQVPGSNP	2401	HLA-B*27:05
5065	MAGEA4	ENSG00000147381	YVKVLEHVVR	2402	HLA-A*31:01
5066	MAGEA4	ENSG00000147381	YVKVLEHVVR	2402	HLA-A*33:01
5067	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*02:01
5068	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*02:03
5069	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*02:04
5070	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*02:07
5071	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*24:02
5072	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*30:01
5073	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*32:01
5074	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-A*68:02
5075	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-B*08:01
5076	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-B*13:02

5077	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-B*40:02
5078	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-B*51:01
5079	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-B*54:01
5080	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*02:02
5081	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*04:01
5082	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*07:01
5083	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*07:04
5084	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*12:03
5085	MAGEA4	ENSG00000147381	YVKVLEHVV	2403	HLA-C*16:02
5086	MAGEA4	ENSG00000147381	YVKVLEHV	2404	HLA-A*02:03
5087	MAGEA4	ENSG00000147381	YVKVLEHV	2404	HLA-B*08:01
5088	MAGEA4	ENSG00000147381	YVKVLEHV	2404	HLA-B*54:01
5089	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-A*01:01
5090	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-A*02:07
5091	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-B*07:02
5092	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-B*08:01
5093	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-B*38:01
5094	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-B*40:01
5095	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-B*58:01
5096	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*01:02
5097	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*03:03
5098	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*03:04
5099	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*05:01
5100	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*07:02
5101	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*16:01
5102	NY-ESO1	ENSG00000184033	AADHRQLQL	2405	HLA-C*16:02
5103	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-A*30:01
5104	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-B*37:01
5105	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-B*38:01
5106	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-B*44:02
5107	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-B*44:03
5108	NY-ESO1	ENSG00000184033	ADGPGGPGI	2406	HLA-B*49:01
5109	NY-ESO1	ENSG00000184033	ADHRQLQL	2407	HLA-A*30:01
5110	NY-ESO1	ENSG00000184033	ADHRQLQL	2407	HLA-B*37:01
5111	NY-ESO1	ENSG00000184033	ADHRQLQL	2407	HLA-B*40:02
5112	NY-ESO1	ENSG00000184033	ADHRQLQL	2407	HLA-C*06:02
5113	NY-ESO1	ENSG00000184033	ADHRQLQL	2407	HLA-C*07:04
5114	NY-ESO1	ENSG00000184033	AEGRGTGGST	2408	HLA-B*40:01
5115	NY-ESO1	ENSG00000184033	AGAARASGPGG	2409	HLA-C*04:01
5116	NY-ESO1	ENSG00000184033	AGAARASGP	2410	HLA-A*32:01
5117	NY-ESO1	ENSG00000184033	AGAARASGP	2410	HLA-C*07:04
5118	NY-ESO1	ENSG00000184033	AGAARASGP	2410	HLA-C*16:01
5119	NY-ESO1	ENSG00000184033	AGAARASGP	2410	HLA-C*16:02
5120	NY-ESO1	ENSG00000184033	AGATGGRGP	2411	HLA-C*16:01
5121	NY-ESO1	ENSG00000184033	AMPFATPMEA	2412	HLA-A*02:01
5122	NY-ESO1	ENSG00000184033	AMPFATPMEA	2412	HLA-A*02:03
5123	NY-ESO1	ENSG00000184033	AMPFATPMEA	2412	HLA-A*02:07
5124	NY-ESO1	ENSG00000184033	AMPFATPM	2413	HLA-C*01:02
5125	NY-ESO1	ENSG00000184033	APPLPVPGVLL	2414	HLA-B*07:02
5126	NY-ESO1	ENSG00000184033	APPLPVPGVL	2415	HLA-B*07:02
5127	NY-ESO1	ENSG00000184033	APPLPVPGVL	2415	HLA-B*56:01
5128	NY-ESO1	ENSG00000184033	APPLPVPGVL	2415	HLA-C*07:02
5129	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-A*02:07
5130	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*07:02
5131	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*13:02
5132	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*37:01
5133	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*51:01
5134	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*54:01
5135	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*55:01
5136	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-B*56:01
5137	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-C*04:01
5138	NY-ESO1	ENSG00000184033	APPLPVPGV	2416	HLA-C*07:02
5139	NY-ESO1	ENSG00000184033	APRGPHGGAAS	2417	HLA-B*07:02
5140	NY-ESO1	ENSG00000184033	APRGPHGGAAS	2417	HLA-C*07:02

5141	NY-ESO1	ENSG00000184033	APRGPHGGAA	2418	HLA-B*07:02
5142	NY-ESO1	ENSG00000184033	APRGPHGGAA	2418	HLA-B*54:01
5143	NY-ESO1	ENSG00000184033	APRGPHGGAA	2418	HLA-B*55:01
5144	NY-ESO1	ENSG00000184033	APRGPHGGAA	2418	HLA-B*56:01
5145	NY-ESO1	ENSG00000184033	APRGPHGGAA	2418	HLA-C*07:02
5146	NY-ESO1	ENSG00000184033	APRGPHGGA	2419	HLA-B*07:02
5147	NY-ESO1	ENSG00000184033	APRGPHGGA	2419	HLA-B*54:01
5148	NY-ESO1	ENSG00000184033	APRGPHGGA	2419	HLA-B*55:01
5149	NY-ESO1	ENSG00000184033	APRGPHGGA	2419	HLA-B*56:01
5150	NY-ESO1	ENSG00000184033	APRGPHGGA	2419	HLA-C*07:02
5151	NY-ESO1	ENSG00000184033	AQDAPPLPVPG	2420	HLA-B*27:05
5152	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*01:01
5153	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*02:01
5154	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*02:03
5155	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*02:07
5156	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*03:01
5157	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*11:01
5158	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-A*30:01
5159	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*13:02
5160	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*27:05
5161	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*37:01
5162	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*38:01
5163	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*39:01
5164	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*49:01
5165	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-B*55:01
5166	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-C*02:02
5167	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-C*03:03
5168	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-C*03:04
5169	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-C*05:01
5170	NY-ESO1	ENSG00000184033	AQDAPPLPV	2421	HLA-C*06:02
5171	NY-ESO1	ENSG00000184033	AQPPSGQRR	2422	HLA-A*31:01
5172	NY-ESO1	ENSG00000184033	AQPPSGQRR	2422	HLA-A*32:01
5173	NY-ESO1	ENSG00000184033	AQPPSGQRR	2422	HLA-B*27:05
5174	NY-ESO1	ENSG00000184033	AQPPSGQRR	2422	HLA-C*06:02
5175	NY-ESO1	ENSG00000184033	AQPPSGQRR	2422	HLA-C*07:02
5176	NY-ESO1	ENSG00000184033	ARASGPGGGAP	2423	HLA-B*27:05
5177	NY-ESO1	ENSG00000184033	ARASGPGGGAP	2423	HLA-B*39:01
5178	NY-ESO1	ENSG00000184033	ARASGPGGGA	2424	HLA-B*27:05
5179	NY-ESO1	ENSG00000184033	ARGPESRLLEF	2425	HLA-C*16:04
5180	NY-ESO1	ENSG00000184033	ARGPESRLL	2426	HLA-B*07:02
5181	NY-ESO1	ENSG00000184033	ARGPESRLL	2426	HLA-B*27:05
5182	NY-ESO1	ENSG00000184033	ARGPESRLL	2426	HLA-C*06:02
5183	NY-ESO1	ENSG00000184033	ARGPESRLL	2426	HLA-C*07:01
5184	NY-ESO1	ENSG00000184033	ARGPESRLL	2426	HLA-C*07:02
5185	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*01:01
5186	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*03:02
5187	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*11:01
5188	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*30:02
5189	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*31:01
5190	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*33:01
5191	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*33:03
5192	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-A*68:01
5193	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-B*27:05
5194	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-C*01:02
5195	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-C*07:04
5196	NY-ESO1	ENSG00000184033	ASGPGGGAPR	2427	HLA-C*07:06
5197	NY-ESO1	ENSG00000184033	ATPMEAELARR	2428	HLA-A*11:01
5198	NY-ESO1	ENSG00000184033	ATPMEAELAR	2429	HLA-C*07:06
5199	NY-ESO1	ENSG00000184033	ATPMEAEL	2430	HLA-C*01:02
5200	NY-ESO1	ENSG00000184033	DADGPGGPGI	2431	HLA-B*38:01
5201	NY-ESO1	ENSG00000184033	DADGPGGPGI	2431	HLA-B*51:01
5202	NY-ESO1	ENSG00000184033	DADGPGGPGI	2431	HLA-C*05:01
5203	NY-ESO1	ENSG00000184033	DAPPLPVPGV	2432	HLA-A*26:01
5204	NY-ESO1	ENSG00000184033	DAPPLPVPGV	2432	HLA-B*51:01

5205	NY-ESO1	ENSG00000184033	DAPPLPVP	2433	HLA-B*51:01
5206	NY-ESO1	ENSG00000184033	DGPGGPGI	2434	HLA-B*51:01
5207	NY-ESO1	ENSG00000184033	DHRQLQLSI	2435	HLA-B*51:01
5208	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-B*07:02
5209	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-B*08:01
5210	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-C*01:02
5211	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-C*03:03
5212	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-C*03:04
5213	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-C*07:02
5214	NY-ESO1	ENSG00000184033	EAELARRSL	2436	HLA-C*16:01
5215	NY-ESO1	ENSG00000184033	EFTVSGNIL	2437	HLA-C*14:02
5216	NY-ESO1	ENSG00000184033	EFYLAMPF	2438	HLA-C*07:01
5217	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-A*02:01
5218	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-A*23:01
5219	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-A*30:01
5220	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-A*32:01
5221	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-A*68:02
5222	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*13:02
5223	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*15:03
5224	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*27:05
5225	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*35:01
5226	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*35:03
5227	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*38:01
5228	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*39:01
5229	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*40:01
5230	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*46:01
5231	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*51:01
5232	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*54:01
5233	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*55:01
5234	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-B*58:01
5235	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*01:02
5236	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*02:02
5237	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*03:03
5238	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*03:04
5239	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*04:01
5240	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*05:01
5241	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*07:04
5242	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*07:06
5243	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*12:03
5244	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*14:02
5245	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*16:01
5246	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*16:02
5247	NY-ESO1	ENSG00000184033	FATPMEAEL	2439	HLA-C*16:04
5248	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*01:01
5249	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*02:03
5250	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*02:04
5251	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*31:01
5252	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*33:01
5253	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*33:03
5254	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*68:01
5255	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-A*68:02
5256	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-B*27:05
5257	NY-ESO1	ENSG00000184033	FLAQPPSGQRR	2440	HLA-C*07:02
5258	NY-ESO1	ENSG00000184033	FLAQPPSGQR	2441	HLA-A*68:01
5259	NY-ESO1	ENSG00000184033	FLAQPPSGQ	2442	HLA-A*02:03
5260	NY-ESO1	ENSG00000184033	FLAQPPSGQ	2442	HLA-A*32:01
5261	NY-ESO1	ENSG00000184033	FLPVFLAQP	2443	HLA-A*02:07
5262	NY-ESO1	ENSG00000184033	FTVSGNILTIR	2444	HLA-A*33:03
5263	NY-ESO1	ENSG00000184033	FTVSGNILTIR	2444	HLA-A*68:01
5264	NY-ESO1	ENSG00000184033	FTVSGNILTIR	2444	HLA-A*68:02
5265	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-A*02:03
5266	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-A*23:01
5267	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-A*25:01
5268	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-A*26:01

5269	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-A*68:02
5270	NY-ESO1	ENSG00000184033	FTVSGNILTI	2445	HLA-C*02:02
5271	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-B*39:01
5272	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-B*46:01
5273	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-C*02:02
5274	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-C*03:03
5275	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-C*03:04
5276	NY-ESO1	ENSG00000184033	FTVSGNIL	2446	HLA-C*14:02
5277	NY-ESO1	ENSG00000184033	GARGPESRL	2447	HLA-B*07:02
5278	NY-ESO1	ENSG00000184033	GARGPESRL	2447	HLA-C*07:02
5279	NY-ESO1	ENSG00000184033	GATGGRGP	2448	HLA-C*16:02
5280	NY-ESO1	ENSG00000184033	GEAGATGGRGP	2449	HLA-C*06:02
5281	NY-ESO1	ENSG00000184033	GEAGATGGRGP	2449	HLA-C*16:04
5282	NY-ESO1	ENSG00000184033	GPESRLLEF	2450	HLA-B*07:02
5283	NY-ESO1	ENSG00000184033	GPESRLLEF	2450	HLA-B*08:01
5284	NY-ESO1	ENSG00000184033	GPESRLLEF	2450	HLA-B*35:01
5285	NY-ESO1	ENSG00000184033	GPESRLLEF	2450	HLA-B*55:01
5286	NY-ESO1	ENSG00000184033	GPESRLLEF	2450	HLA-C*07:02
5287	NY-ESO1	ENSG00000184033	GPGGGAPRGP	2451	HLA-C*07:02
5288	NY-ESO1	ENSG00000184033	GPHGGAASGL	2452	HLA-B*07:02
5289	NY-ESO1	ENSG00000184033	GPHGGAASGL	2452	HLA-C*07:02
5290	NY-ESO1	ENSG00000184033	GPRGAGAARAS	2453	HLA-B*07:02
5291	NY-ESO1	ENSG00000184033	GPRGAGAARA	2454	HLA-B*07:02
5292	NY-ESO1	ENSG00000184033	GPRGAGAARA	2454	HLA-B*56:01
5293	NY-ESO1	ENSG00000184033	GPRGAGAARA	2454	HLA-C*07:02
5294	NY-ESO1	ENSG00000184033	GPRGAGAAR	2455	HLA-A*33:03
5295	NY-ESO1	ENSG00000184033	GPRGAGAAR	2455	HLA-B*07:02
5296	NY-ESO1	ENSG00000184033	GPRGAGAAR	2455	HLA-C*07:02
5297	NY-ESO1	ENSG00000184033	GRGPRGAGAAR	2456	HLA-B*27:05
5298	NY-ESO1	ENSG00000184033	GVLLKEFTV	2457	HLA-A*02:01
5299	NY-ESO1	ENSG00000184033	GVLLKEFTV	2457	HLA-A*02:04
5300	NY-ESO1	ENSG00000184033	GVLLKEFTV	2457	HLA-B*13:02
5301	NY-ESO1	ENSG00000184033	HGGAASGL	2458	HLA-C*07:04
5302	NY-ESO1	ENSG00000184033	ILTIRLTAA	2459	HLA-A*02:01
5303	NY-ESO1	ENSG00000184033	ILTIRLTAA	2459	HLA-A*02:03
5304	NY-ESO1	ENSG00000184033	ILTIRLTAA	2459	HLA-A*02:04
5305	NY-ESO1	ENSG00000184033	ILTIRLTAA	2459	HLA-B*08:01
5306	NY-ESO1	ENSG00000184033	ILTIRLTAA	2459	HLA-B*55:01
5307	NY-ESO1	ENSG00000184033	IPDGPGGNA	2460	HLA-B*07:02
5308	NY-ESO1	ENSG00000184033	IPDGPGGNA	2460	HLA-B*55:01
5309	NY-ESO1	ENSG00000184033	IPDGPGGNA	2460	HLA-B*56:01
5310	NY-ESO1	ENSG00000184033	IPDGPGGNA	2460	HLA-C*05:01
5311	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-A*30:01
5312	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*27:05
5313	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*37:01
5314	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*40:01
5315	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*40:02
5316	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*44:02
5317	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*44:03
5318	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-B*49:01
5319	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-C*12:03
5320	NY-ESO1	ENSG00000184033	KEFTVSGNIL	2461	HLA-C*16:04
5321	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-A*30:01
5322	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*13:02
5323	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*37:01
5324	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*40:01
5325	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*40:02
5326	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*44:02
5327	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*44:03
5328	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-B*49:01
5329	NY-ESO1	ENSG00000184033	KEFTVSGNI	2462	HLA-C*16:04
5330	NY-ESO1	ENSG00000184033	LAMPFATPMEA	2463	HLA-B*54:01
5331	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-A*11:01
5332	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-A*23:01

5333	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-A*24:02
5334	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-A*26:01
5335	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*07:02
5336	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*08:01
5337	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*15:01
5338	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*15:03
5339	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*18:01
5340	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*35:01
5341	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*35:03
5342	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*37:01
5343	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*39:01
5344	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*40:02
5345	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*46:01
5346	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*51:01
5347	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*54:01
5348	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*56:01
5349	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*57:01
5350	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-B*58:01
5351	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*01:02
5352	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*02:02
5353	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*03:03
5354	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*03:04
5355	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*04:01
5356	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*05:01
5357	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*06:02
5358	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*07:01
5359	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*07:04
5360	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*07:06
5361	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*12:03
5362	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*14:02
5363	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*16:01
5364	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*16:02
5365	NY-ESO1	ENSG00000184033	LAMPFATPM	2464	HLA-C*16:04
5366	NY-ESO1	ENSG00000184033	LAQDAPPLPV	2465	HLA-B*56:01
5367	NY-ESO1	ENSG00000184033	LAQDAPPLPV	2465	HLA-C*03:03
5368	NY-ESO1	ENSG00000184033	LAQDAPPLPV	2465	HLA-C*03:04
5369	NY-ESO1	ENSG00000184033	LAQDAPPLPV	2465	HLA-C*16:04
5370	NY-ESO1	ENSG00000184033	LAQDAPPL	2466	HLA-C*03:03
5371	NY-ESO1	ENSG00000184033	LAQDAPPL	2466	HLA-C*03:04
5372	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*03:02
5373	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*11:01
5374	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*31:01
5375	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*33:01
5376	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*33:03
5377	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-A*68:01
5378	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-B*27:05
5379	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-B*57:01
5380	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-B*58:01
5381	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-C*06:02
5382	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-C*07:01
5383	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-C*07:02
5384	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-C*07:06
5385	NY-ESO1	ENSG00000184033	LAQPPSGQRR	2467	HLA-C*16:02
5386	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*03:02
5387	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*11:01
5388	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*31:01
5389	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*33:01
5390	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*33:03
5391	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-A*68:01
5392	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-B*27:05
5393	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-C*07:06
5394	NY-ESO1	ENSG00000184033	LAQPPSGQR	2468	HLA-C*16:02
5395	NY-ESO1	ENSG00000184033	LPVFLAQPPSG	2469	HLA-B*54:01
5396	NY-ESO1	ENSG00000184033	LPVFLAQPPS	2470	HLA-B*54:01

5397	NY-ESO1	ENSG00000184033	LPVFLAQPP	2471	HLA-B*54:01
5398	NY-ESO1	ENSG00000184033	LPVPGVLLKEF	2472	HLA-B*35:01
5399	NY-ESO1	ENSG00000184033	LPVPGVLLK	2473	HLA-B*51:01
5400	NY-ESO1	ENSG00000184033	LPVPGVLL	2474	HLA-B*35:01
5401	NY-ESO1	ENSG00000184033	LPVPGVLL	2474	HLA-B*35:03
5402	NY-ESO1	ENSG00000184033	LPVPGVLL	2474	HLA-B*51:01
5403	NY-ESO1	ENSG00000184033	LPVPGVLL	2474	HLA-B*56:01
5404	NY-ESO1	ENSG00000184033	LQLSISSCL	2475	HLA-B*27:05
5405	NY-ESO1	ENSG00000184033	LTAADHRQL	2476	HLA-C*03:04
5406	NY-ESO1	ENSG00000184033	LTAADHRQL	2476	HLA-C*06:02
5407	NY-ESO1	ENSG00000184033	LTAADHRQL	2476	HLA-C*12:03
5408	NY-ESO1	ENSG00000184033	LTAADHRQL	2476	HLA-C*16:01
5409	NY-ESO1	ENSG00000184033	LTAADHRQL	2476	HLA-C*16:02
5410	NY-ESO1	ENSG00000184033	MEAELARRSL	2477	HLA-A*30:01
5411	NY-ESO1	ENSG00000184033	MEAELARRSL	2477	HLA-B*40:02
5412	NY-ESO1	ENSG00000184033	MEAELARRSL	2477	HLA-B*44:02
5413	NY-ESO1	ENSG00000184033	MEAELARRSL	2477	HLA-B*44:03
5414	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-A*68:02
5415	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*07:02
5416	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*35:01
5417	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*35:03
5418	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*51:01
5419	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*54:01
5420	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*55:01
5421	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-B*56:01
5422	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-C*03:03
5423	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-C*04:01
5424	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-C*07:01
5425	NY-ESO1	ENSG00000184033	MPFATPMEAEL	2478	HLA-C*07:06
5426	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-A*02:01
5427	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-A*02:03
5428	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*07:02
5429	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*08:01
5430	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*35:01
5431	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*35:03
5432	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*51:01
5433	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*54:01
5434	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*55:01
5435	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-B*56:01
5436	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*02:02
5437	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*03:03
5438	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*04:01
5439	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*06:02
5440	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*07:02
5441	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*12:03
5442	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*14:02
5443	NY-ESO1	ENSG00000184033	MPFATPMEA	2479	HLA-C*16:04
5444	NY-ESO1	ENSG00000184033	MPFATPME	2480	HLA-B*54:01
5445	NY-ESO1	ENSG00000184033	NILTIRLTAA	2481	HLA-A*02:03
5446	NY-ESO1	ENSG00000184033	NILTIRLTA	2482	HLA-B*54:01
5447	NY-ESO1	ENSG00000184033	NILTIRLTA	2482	HLA-C*16:01
5448	NY-ESO1	ENSG00000184033	PFATPMEAEL	2483	HLA-C*07:02
5449	NY-ESO1	ENSG00000184033	PGGGAPRGP	2484	HLA-C*07:02
5450	NY-ESO1	ENSG00000184033	PLPVPGVLL	2485	HLA-A*24:02
5451	NY-ESO1	ENSG00000184033	PPLPVPGVL	2486	HLA-B*07:02
5452	NY-ESO1	ENSG00000184033	QDAPPLPVPG	2487	HLA-C*04:01
5453	NY-ESO1	ENSG00000184033	QDAPPLPVPG	2487	HLA-C*06:02
5454	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-B*27:05
5455	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-B*40:02
5456	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*04:01
5457	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*06:02
5458	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*07:01
5459	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*07:02
5460	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*07:04

5461	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*12:03
5462	NY-ESO1	ENSG00000184033	QDAPPLPVP	2488	HLA-C*16:02
5463	NY-ESO1	ENSG00000184033	QDAPPLPV	2489	HLA-B*37:01
5464	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-A*31:01
5465	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-A*33:01
5466	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-A*33:03
5467	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-A*68:01
5468	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-B*27:05
5469	NY-ESO1	ENSG00000184033	RASGPGGGAPR	2490	HLA-C*07:06
5470	NY-ESO1	ENSG00000184033	RGAGAARASGP	2491	HLA-A*32:01
5471	NY-ESO1	ENSG00000184033	RGPESRLLEF	2492	HLA-A*02:07
5472	NY-ESO1	ENSG00000184033	RGPESRLLEF	2492	HLA-A*24:02
5473	NY-ESO1	ENSG00000184033	RGPHGGAASGL	2493	HLA-C*01:02
5474	NY-ESO1	ENSG00000184033	RGPRGAGAAR	2494	HLA-A*31:01
5475	NY-ESO1	ENSG00000184033	RLLEFYLAM	2495	HLA-A*02:04
5476	NY-ESO1	ENSG00000184033	RLLEFYLAM	2495	HLA-A*02:07
5477	NY-ESO1	ENSG00000184033	SGNILTIRL	2496	HLA-A*02:04
5478	NY-ESO1	ENSG00000184033	SGNILTIRL	2496	HLA-C*07:02
5479	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-B*07:02
5480	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-C*04:01
5481	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-C*06:02
5482	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-C*07:01
5483	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-C*07:02
5484	NY-ESO1	ENSG00000184033	SGPGGGAPRGP	2497	HLA-C*16:02
5485	NY-ESO1	ENSG00000184033	SGPGGGAPR	2498	HLA-A*68:01
5486	NY-ESO1	ENSG00000184033	SGPGGGAPR	2498	HLA-C*01:02
5487	NY-ESO1	ENSG00000184033	SGPGGGAPR	2498	HLA-C*07:06
5488	NY-ESO1	ENSG00000184033	SGPGGGAP	2499	HLA-C*01:02
5489	NY-ESO1	ENSG00000184033	SISSCLQQL	2500	HLA-A*02:04
5490	NY-ESO1	ENSG00000184033	SISSCLQQL	2500	HLA-A*24:02
5491	NY-ESO1	ENSG00000184033	SISSCLQQL	2500	HLA-A*68:02
5492	NY-ESO1	ENSG00000184033	SISSCLQQL	2500	HLA-C*07:04
5493	NY-ESO1	ENSG00000184033	SLAQDAPPLPV	2501	HLA-A*02:01
5494	NY-ESO1	ENSG00000184033	SLAQDAPPLPV	2501	HLA-A*02:03
5495	NY-ESO1	ENSG00000184033	SLAQDAPPL	2502	HLA-A*02:01
5496	NY-ESO1	ENSG00000184033	SLAQDAPPL	2502	HLA-A*02:04
5497	NY-ESO1	ENSG00000184033	SLAQDAPPL	2502	HLA-B*35:03
5498	NY-ESO1	ENSG00000184033	SLAQDAPPL	2502	HLA-C*01:02
5499	NY-ESO1	ENSG00000184033	SLLMWITQC	2503	HLA-A*02:01
5500	NY-ESO1	ENSG00000184033	SLLMWITQC	2503	HLA-A*02:04
5501	NY-ESO1	ENSG00000184033	TAADHRQLQL	2504	HLA-A*30:01
5502	NY-ESO1	ENSG00000184033	TAADHRQLQL	2504	HLA-B*07:02
5503	NY-ESO1	ENSG00000184033	TAADHRQLQL	2504	HLA-C*07:02
5504	NY-ESO1	ENSG00000184033	TAADHRQLQL	2504	HLA-C*16:01
5505	NY-ESO1	ENSG00000184033	TAADHRQLQL	2504	HLA-C*16:02
5506	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-B*07:02
5507	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-B*08:01
5508	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-B*35:03
5509	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*03:03
5510	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*03:04
5511	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*06:02
5512	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*12:03
5513	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*16:01
5514	NY-ESO1	ENSG00000184033	TAADHRQL	2505	HLA-C*16:02
5515	NY-ESO1	ENSG00000184033	TPMEAELARR	2506	HLA-A*33:03
5516	NY-ESO1	ENSG00000184033	TPMEAELARR	2506	HLA-A*68:01
5517	NY-ESO1	ENSG00000184033	TPMEAELARR	2506	HLA-C*07:06
5518	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-A*33:03
5519	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-A*68:01
5520	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-B*35:01
5521	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-B*35:03
5522	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-B*54:01
5523	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-B*55:01
5524	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-B*56:01

5525	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-C*03:03
5526	NY-ESO1	ENSG00000184033	TPMEAELAR	2507	HLA-C*07:06
5527	NY-ESO1	ENSG00000184033	TPMEAELA	2508	HLA-B*56:01
5528	NY-ESO1	ENSG00000184033	TVSGNILTIRL	2509	HLA-A*68:02
5529	NY-ESO1	ENSG00000184033	TVSGNILTIR	2510	HLA-A*31:01
5530	NY-ESO1	ENSG00000184033	TVSGNILTIR	2510	HLA-A*33:03
5531	NY-ESO1	ENSG00000184033	TVSGNILTIR	2510	HLA-A*68:01
5532	NY-ESO1	ENSG00000184033	TVSGNILTIR	2510	HLA-A*68:02
5533	NY-ESO1	ENSG00000184033	TVSGNILTIR	2510	HLA-C*07:06
5534	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*02:01
5535	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*02:03
5536	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*02:04
5537	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*02:07
5538	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*03:01
5539	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*11:01
5540	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*23:01
5541	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*25:01
5542	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*26:01
5543	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*30:01
5544	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*32:01
5545	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*68:01
5546	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-A*68:02
5547	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*13:02
5548	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*27:05
5549	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*35:01
5550	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*35:03
5551	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*38:01
5552	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*39:01
5553	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*40:02
5554	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*49:01
5555	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*51:01
5556	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*55:01
5557	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-B*58:01
5558	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*02:02
5559	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*03:04
5560	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*04:01
5561	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*06:02
5562	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*07:04
5563	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*07:06
5564	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*12:03
5565	NY-ESO1	ENSG00000184033	TVSGNILTI	2511	HLA-C*16:02
5566	NY-ESO1	ENSG00000184033	VLLKEFTV	2512	HLA-A*02:01
5567	NY-ESO1	ENSG00000184033	VLLKEFTV	2512	HLA-A*02:04
5568	NY-ESO1	ENSG00000184033	VSGNILTIR	2513	HLA-A*31:01
5569	NY-ESO1	ENSG00000184033	VSGNILTIR	2513	HLA-A*33:03
5570	NY-ESO1	ENSG00000184033	VSGNILTIR	2513	HLA-A*68:01
5571	NY-ESO1	ENSG00000184033	VSGNILTIR	2513	HLA-C*07:06
5572	NY-ESO1	ENSG00000184033	VSGNILTI	2514	HLA-A*23:01
5573	NY-ESO1	ENSG00000184033	VSGNILTI	2514	HLA-B*13:02
5574	NY-ESO1	ENSG00000184033	VSGNILTI	2514	HLA-B*51:01
5575	NY-ESO1	ENSG00000184033	VSGNILTI	2514	HLA-B*58:01
5576	NY-ESO1	ENSG00000184033	YLAMPFATPM	2515	HLA-C*07:01
5577	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-A*25:01
5578	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-B*27:02
5579	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-B*44:02
5580	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-B*44:03
5581	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-B*58:01
5582	WT1	ENSG00000184937	AAGSSSSVKW	2516	HLA-C*16:04
5583	WT1	ENSG00000184937	AAGSSSSVK	2517	HLA-A*03:02
5584	WT1	ENSG00000184937	AAQFPNHSFK	2518	HLA-A*03:01
5585	WT1	ENSG00000184937	AAQFPNHSFK	2518	HLA-A*03:02
5586	WT1	ENSG00000184937	AAQFPNHSFK	2518	HLA-A*11:01
5587	WT1	ENSG00000184937	AAQFPNHSFK	2518	HLA-B*27:02
5588	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-A*23:01

5589	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-A*24:02
5590	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-A*30:02
5591	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-A*32:01
5592	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*07:02
5593	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*15:01
5594	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*15:03
5595	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*35:01
5596	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*37:01
5597	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*39:01
5598	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*44:02
5599	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*46:01
5600	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*57:01
5601	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-B*58:01
5602	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*01:02
5603	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*02:02
5604	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*03:03
5605	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*03:04
5606	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*05:01
5607	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*07:04
5608	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*12:03
5609	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*14:02
5610	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*16:01
5611	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*16:02
5612	WT1	ENSG00000184937	AAQFPNHSF	2519	HLA-C*16:04
5613	WT1	ENSG00000184937	AEPHEEQCL	2520	HLA-B*40:01
5614	WT1	ENSG00000184937	AEPHEEQCL	2520	HLA-B*44:03
5615	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-A*32:01
5616	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-B*27:02
5617	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-B*44:02
5618	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-B*44:03
5619	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-B*58:01
5620	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-C*12:03
5621	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-C*16:01
5622	WT1	ENSG00000184937	AGSSSSVKW	2521	HLA-C*16:04
5623	WT1	ENSG00000184937	AIRNQGYSTV	2522	HLA-A*02:03
5624	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*02:01
5625	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*02:03
5626	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*02:04
5627	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*02:07
5628	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*03:01
5629	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*03:02
5630	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*23:01
5631	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*24:02
5632	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*25:01
5633	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*29:02
5634	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*30:01
5635	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*31:01
5636	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-A*32:01
5637	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*07:02
5638	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*13:02
5639	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*15:01
5640	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*15:03
5641	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*37:01
5642	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*40:01
5643	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*40:02
5644	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*46:01
5645	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*55:01
5646	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-B*58:01
5647	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*01:02
5648	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*02:02
5649	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*03:03
5650	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*03:04
5651	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*07:04
5652	WT1	ENSG00000184937	ALLPAVPSL	2523	HLA-C*14:02

5653	WT1	ENSG00000184937	ALPVSGAAQW	2524	HLA-A*25:01
5654	WT1	ENSG00000184937	ALPVSGAAQ	2525	HLA-C*01:02
5655	WT1	ENSG00000184937	APPGASAYGSL	2526	HLA-B*07:02
5656	WT1	ENSG00000184937	APPGASAYGSL	2526	HLA-C*01:02
5657	WT1	ENSG00000184937	APPGASAYGSL	2526	HLA-C*07:02
5658	WT1	ENSG00000184937	APPPAPPPPP	2527	HLA-C*04:01
5659	WT1	ENSG00000184937	APPPAPPPP	2528	HLA-C*04:01
5660	WT1	ENSG00000184937	APPPPPPPPP	2529	HLA-C*04:01
5661	WT1	ENSG00000184937	APPPPPPPP	2530	HLA-B*56:01
5662	WT1	ENSG00000184937	APPPPPPPP	2530	HLA-C*04:01
5663	WT1	ENSG00000184937	APTLVRSASET	2531	HLA-B*07:02
5664	WT1	ENSG00000184937	APTLVRSAS	2532	HLA-B*56:01
5665	WT1	ENSG00000184937	APTLVRSA	2533	HLA-B*07:02
5666	WT1	ENSG00000184937	APTLVRSA	2533	HLA-B*54:01
5667	WT1	ENSG00000184937	APTLVRSA	2533	HLA-B*55:01
5668	WT1	ENSG00000184937	APTLVRSA	2533	HLA-B*56:01
5669	WT1	ENSG00000184937	APVLDFAPPGA	2534	HLA-B*56:01
5670	WT1	ENSG00000184937	APVLDFAPPG	2535	HLA-B*56:01
5671	WT1	ENSG00000184937	APVLDFAPP	2536	HLA-B*56:01
5672	WT1	ENSG00000184937	APYLPSCL	2537	HLA-B*07:02
5673	WT1	ENSG00000184937	APYLPSCL	2537	HLA-B*08:01
5674	WT1	ENSG00000184937	APYLPSCL	2537	HLA-B*56:01
5675	WT1	ENSG00000184937	AQFPNHSFK	2538	HLA-A*03:01
5676	WT1	ENSG00000184937	AQFPNHSFK	2538	HLA-A*03:02
5677	WT1	ENSG00000184937	AQFPNHSFK	2538	HLA-A*11:01
5678	WT1	ENSG00000184937	AQFPNHSFK	2538	HLA-A*31:01
5679	WT1	ENSG00000184937	AQFPNHSFK	2538	HLA-B*27:05
5680	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-A*23:01
5681	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-A*30:02
5682	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-A*32:01
5683	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*13:02
5684	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*15:01
5685	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*15:03
5686	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*27:05
5687	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*37:01
5688	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*39:01
5689	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*44:02
5690	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*46:01
5691	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*57:01
5692	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-B*58:01
5693	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-C*02:02
5694	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-C*14:02
5695	WT1	ENSG00000184937	AQFPNHSF	2539	HLA-C*16:04
5696	WT1	ENSG00000184937	AQWAPVLDF	2540	HLA-B*13:02
5697	WT1	ENSG00000184937	AQWAPVLDF	2540	HLA-B*15:01
5698	WT1	ENSG00000184937	AQWAPVLDF	2540	HLA-B*15:03
5699	WT1	ENSG00000184937	ARSDELVRH	2541	HLA-B*27:05
5700	WT1	ENSG00000184937	ASETSEKRPF	2542	HLA-C*16:01
5701	WT1	ENSG00000184937	ASSGQARMF	2543	HLA-A*32:01
5702	WT1	ENSG00000184937	ASSGQARMF	2543	HLA-B*58:01
5703	WT1	ENSG00000184937	ASSGQARMF	2543	HLA-C*02:02
5704	WT1	ENSG00000184937	ASSGQARMF	2543	HLA-C*16:01
5705	WT1	ENSG00000184937	ASSGQARMF	2543	HLA-C*16:02
5706	WT1	ENSG00000184937	CALPVSGAAQW	2544	HLA-B*57:01
5707	WT1	ENSG00000184937	CALPVSGAAQW	2544	HLA-B*58:01
5708	WT1	ENSG00000184937	CALPVSGAA	2545	HLA-B*56:01
5709	WT1	ENSG00000184937	DELVRHHNM	2546	HLA-B*08:01
5710	WT1	ENSG00000184937	DELVRHHNM	2546	HLA-B*37:01
5711	WT1	ENSG00000184937	DFAPPGASAY	2547	HLA-A*25:01
5712	WT1	ENSG00000184937	DFAPPGASAY	2547	HLA-A*26:01
5713	WT1	ENSG00000184937	DFAPPGASAY	2547	HLA-A*29:02
5714	WT1	ENSG00000184937	DFAPPGASAY	2547	HLA-A*30:02
5715	WT1	ENSG00000184937	DFAPPGASAY	2547	HLA-C*14:02
5716	WT1	ENSG00000184937	DFAPPGASA	2548	HLA-C*14:02

5717	WT1	ENSG00000184937	DHLKTHTR	2549	HLA-A*33:01
5718	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-B*07:02
5719	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-B*08:01
5720	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-B*35:01
5721	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-B*35:03
5722	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-B*51:01
5723	WT1	ENSG00000184937	DPMGQQGSL	2550	HLA-C*07:02
5724	WT1	ENSG00000184937	DVRDLNALL	2551	HLA-A*25:01
5725	WT1	ENSG00000184937	DVRDLNALL	2551	HLA-A*26:01
5726	WT1	ENSG00000184937	DVRDLNALL	2551	HLA-A*33:01
5727	WT1	ENSG00000184937	DVRDLNAL	2552	HLA-B*08:01
5728	WT1	ENSG00000184937	DVRRVPGV	2553	HLA-B*51:01
5729	WT1	ENSG00000184937	EEQCLSAF	2554	HLA-B*18:01
5730	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-A*26:01
5731	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-A*30:02
5732	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-B*44:02
5733	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-B*44:03
5734	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-C*04:01
5735	WT1	ENSG00000184937	EGQSNHSTGY	2555	HLA-C*07:01
5736	WT1	ENSG00000184937	EQQYSVPPPVY	2556	HLA-A*30:02
5737	WT1	ENSG00000184937	ESQPAIRNQGY	2557	HLA-A*01:01
5738	WT1	ENSG00000184937	ESQPAIRNQGY	2557	HLA-A*25:01
5739	WT1	ENSG00000184937	ESQPAIRNQGY	2557	HLA-A*26:01
5740	WT1	ENSG00000184937	ESQPAIRNQGY	2557	HLA-A*30:02
5741	WT1	ENSG00000184937	ESQPAIRNQGY	2557	HLA-B*44:02
5742	WT1	ENSG00000184937	ETSEKRPFM	2558	HLA-A*26:01
5743	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*01:01
5744	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*25:01
5745	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*26:01
5746	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*29:02
5747	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*30:02
5748	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-A*32:01
5749	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*15:01
5750	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*15:03
5751	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*35:01
5752	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*39:01
5753	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*46:01
5754	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*51:01
5755	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*55:01
5756	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-B*58:01
5757	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*01:02
5758	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*02:02
5759	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*03:03
5760	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*03:04
5761	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*05:01
5762	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*07:04
5763	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*12:03
5764	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*14:02
5765	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*16:01
5766	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*16:02
5767	WT1	ENSG00000184937	FAPPGASAY	2559	HLA-C*16:04
5768	WT1	ENSG00000184937	FGPPPPSQA	2560	HLA-A*02:01
5769	WT1	ENSG00000184937	FGPPPPSQA	2560	HLA-A*02:07
5770	WT1	ENSG00000184937	FPNAPYLPSCL	2561	HLA-B*35:03
5771	WT1	ENSG00000184937	FPNAPYLPSC	2562	HLA-B*54:01
5772	WT1	ENSG00000184937	FPNAPYLPSC	2562	HLA-B*56:01
5773	WT1	ENSG00000184937	FPNAPYLPS	2563	HLA-B*54:01
5774	WT1	ENSG00000184937	FPNAPYLP	2564	HLA-B*54:01
5775	WT1	ENSG00000184937	FTGTAGACRY	2565	HLA-A*01:01
5776	WT1	ENSG00000184937	FTGTAGACRY	2565	HLA-A*29:02
5777	WT1	ENSG00000184937	FTGTAGACRY	2565	HLA-A*30:02
5778	WT1	ENSG00000184937	FTGTAGACR	2566	HLA-A*68:01
5779	WT1	ENSG00000184937	FTGTAGACR	2566	HLA-C*07:06
5780	WT1	ENSG00000184937	FTGTAGAC	2567	HLA-C*12:03

5781	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-A*25:01
5782	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-A*26:01
5783	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-A*29:02
5784	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-B*46:01
5785	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-B*57:01
5786	WT1	ENSG00000184937	FTVHFSGQF	2568	HLA-C*02:02
5787	WT1	ENSG00000184937	GAAQWAPVL	2569	HLA-C*03:03
5788	WT1	ENSG00000184937	GAAQWAPVL	2569	HLA-C*03:04
5789	WT1	ENSG00000184937	GATLKGVAA	2570	HLA-B*54:01
5790	WT1	ENSG00000184937	GATLKGVAA	2570	HLA-B*56:01
5791	WT1	ENSG00000184937	GATLKGVAA	2570	HLA-C*03:04
5792	WT1	ENSG00000184937	GATLKGVAA	2570	HLA-C*16:01
5793	WT1	ENSG00000184937	GATLKGVA	2571	HLA-C*16:01
5794	WT1	ENSG00000184937	GEKPYQCDF	2572	HLA-A*30:01
5795	WT1	ENSG00000184937	GEKPYQCDF	2572	HLA-B*37:01
5796	WT1	ENSG00000184937	GEKPYQCDF	2572	HLA-B*44:02
5797	WT1	ENSG00000184937	GEKPYQCDF	2572	HLA-B*44:03
5798	WT1	ENSG00000184937	GEKPYQCDF	2572	HLA-C*16:04
5799	WT1	ENSG00000184937	GPAPPPAPP	2573	HLA-B*56:01
5800	WT1	ENSG00000184937	GPFGPPPPSQA	2574	HLA-B*54:01
5801	WT1	ENSG00000184937	GPFGPPPPSQA	2574	HLA-B*55:01
5802	WT1	ENSG00000184937	GPFGPPPPSQA	2574	HLA-B*56:01
5803	WT1	ENSG00000184937	GPFGPPPPSQ	2575	HLA-B*54:01
5804	WT1	ENSG00000184937	GPFGPPPPS	2576	HLA-B*54:01
5805	WT1	ENSG00000184937	GPFGPPPPS	2576	HLA-B*56:01
5806	WT1	ENSG00000184937	GPFGPPPP	2577	HLA-B*56:01
5807	WT1	ENSG00000184937	GQARMFPNAPY	2578	HLA-A*30:02
5808	WT1	ENSG00000184937	GQARMFPNAPY	2578	HLA-B*15:01
5809	WT1	ENSG00000184937	GQFTGTAGACR	2579	HLA-A*31:01
5810	WT1	ENSG00000184937	GQFTGTAGACR	2579	HLA-B*13:02
5811	WT1	ENSG00000184937	GQFTGTAGACR	2579	HLA-B*27:05
5812	WT1	ENSG00000184937	GQFTGTAGACR	2579	HLA-C*07:06
5813	WT1	ENSG00000184937	GQFTGTAGAC	2580	HLA-B*13:02
5814	WT1	ENSG00000184937	GQFTGTAGAC	2580	HLA-B*15:01
5815	WT1	ENSG00000184937	GQFTGTAGAC	2580	HLA-B*15:03
5816	WT1	ENSG00000184937	GQFTGTAGAC	2580	HLA-B*27:05
5817	WT1	ENSG00000184937	GQFTGTAGAC	2580	HLA-C*16:04
5818	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-A*02:01
5819	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-A*02:03
5820	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-A*32:01
5821	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-B*13:02
5822	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-B*15:01
5823	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-B*15:03
5824	WT1	ENSG00000184937	GQFTGTAGA	2581	HLA-B*27:05
5825	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-A*30:02
5826	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-B*15:01
5827	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-B*15:03
5828	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-B*27:05
5829	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-B*39:01
5830	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-C*07:04
5831	WT1	ENSG00000184937	GQQGSLGEQQY	2582	HLA-C*16:04
5832	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-A*26:01
5833	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-A*29:02
5834	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-A*30:02
5835	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-A*32:01
5836	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*13:02
5837	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*15:01
5838	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*15:03
5839	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*27:02
5840	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*27:05
5841	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*39:01
5842	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*44:03
5843	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-B*46:01
5844	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-C*02:02

5845	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-C*07:04
5846	WT1	ENSG00000184937	GQSNHSTGY	2583	HLA-C*16:04
5847	WT1	ENSG00000184937	GSLGGPAPPP	2584	HLA-A*11:01
5848	WT1	ENSG00000184937	GSLGGPAPPP	2584	HLA-C*06:02
5849	WT1	ENSG00000184937	GSLGGPAPPP	2584	HLA-C*07:02
5850	WT1	ENSG00000184937	GSQALLLRTPY	2585	HLA-A*30:02
5851	WT1	ENSG00000184937	GSSSSVKW	2586	HLA-A*32:01
5852	WT1	ENSG00000184937	GSSSSVKW	2586	HLA-B*57:01
5853	WT1	ENSG00000184937	GSSSSVKW	2586	HLA-B*58:01
5854	WT1	ENSG00000184937	GTAGACRY	2587	HLA-A*30:02
5855	WT1	ENSG00000184937	GVAAGSSSSVK	2588	HLA-A*03:01
5856	WT1	ENSG00000184937	GVAAGSSSSVK	2588	HLA-A*03:02
5857	WT1	ENSG00000184937	GVAAGSSSSVK	2588	HLA-A*11:01
5858	WT1	ENSG00000184937	GVAAGSSSSV	2589	HLA-A*02:03
5859	WT1	ENSG00000184937	GVAAGSSSSV	2589	HLA-B*13:02
5860	WT1	ENSG00000184937	GVAPTLVRSA	2590	HLA-B*56:01
5861	WT1	ENSG00000184937	GVFRGIQDV	2591	HLA-A*02:01
5862	WT1	ENSG00000184937	GVFRGIQDV	2591	HLA-A*02:03
5863	WT1	ENSG00000184937	GVFRGIQDV	2591	HLA-A*02:04
5864	WT1	ENSG00000184937	GVFRGIQDV	2591	HLA-B*13:02
5865	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-A*25:01
5866	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-A*26:01
5867	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-A*32:01
5868	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-A*33:01
5869	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-A*68:02
5870	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*35:01
5871	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*35:03
5872	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*46:01
5873	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*54:01
5874	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*57:01
5875	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-B*58:01
5876	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-C*02:02
5877	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-C*03:03
5878	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-C*03:04
5879	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-C*07:06
5880	WT1	ENSG00000184937	HAAQFPNHSF	2592	HLA-C*16:04
5881	WT1	ENSG00000184937	HEDPMGQQGSL	2593	HLA-A*30:01
5882	WT1	ENSG00000184937	HEDPMGQQGSL	2593	HLA-B*39:01
5883	WT1	ENSG00000184937	HEDPMGQQGSL	2593	HLA-B*40:01
5884	WT1	ENSG00000184937	HEDPMGQQGSL	2593	HLA-B*49:01
5885	WT1	ENSG00000184937	HEDPMGQQG	2594	HLA-B*49:01
5886	WT1	ENSG00000184937	HEEQCLSAF	2595	HLA-B*18:01
5887	WT1	ENSG00000184937	HHAAQFPNHSF	2596	HLA-B*38:01
5888	WT1	ENSG00000184937	HQRNMTKL	2597	HLA-B*15:03
5889	WT1	ENSG00000184937	HSFIKQEPSW	2598	HLA-B*57:01
5890	WT1	ENSG00000184937	HTPSHHAAQF	2599	HLA-A*25:01
5891	WT1	ENSG00000184937	HTPSHHAAQF	2599	HLA-A*26:01
5892	WT1	ENSG00000184937	HTTPILCGA	2600	HLA-A*68:02
5893	WT1	ENSG00000184937	IRNQGYSTVTF	2601	HLA-B*27:02
5894	WT1	ENSG00000184937	IRNQGYSTVTF	2601	HLA-C*16:04
5895	WT1	ENSG00000184937	LDFAPPGASAY	2602	HLA-A*30:02
5896	WT1	ENSG00000184937	LDFAPPGASAY	2602	HLA-B*18:01
5897	WT1	ENSG00000184937	LDFAPPGASAY	2602	HLA-C*16:04
5898	WT1	ENSG00000184937	LGATLKGVAA	2603	HLA-B*54:01
5899	WT1	ENSG00000184937	LGGGGGCAL	2604	HLA-C*03:04
5900	WT1	ENSG00000184937	LLPAVPSLGG	2605	HLA-A*02:07
5901	WT1	ENSG00000184937	LLPAVPSL	2606	HLA-A*02:07
5902	WT1	ENSG00000184937	LLPAVPSL	2606	HLA-A*24:02
5903	WT1	ENSG00000184937	LLPAVPSL	2606	HLA-B*51:01
5904	WT1	ENSG00000184937	LLPAVPSL	2606	HLA-C*01:02
5905	WT1	ENSG00000184937	LPAVPSLGG	2607	HLA-B*51:01
5906	WT1	ENSG00000184937	LPAVPSLGG	2607	HLA-B*54:01
5907	WT1	ENSG00000184937	LPAVPSLGG	2607	HLA-B*56:01
5908	WT1	ENSG00000184937	LPVSGAAQW	2608	HLA-A*25:01

5909	WT1	ENSG00000184937	LPVSGAAQW	2608	HLA-B*35:01
5910	WT1	ENSG00000184937	LPVSGAAQW	2608	HLA-B*35:03
5911	WT1	ENSG00000184937	LPVSGAAQW	2608	HLA-B*51:01
5912	WT1	ENSG00000184937	LPVSGAAQW	2608	HLA-B*56:01
5913	WT1	ENSG00000184937	LSHLQMHSR	2609	HLA-A*33:01
5914	WT1	ENSG00000184937	LVRSASETSEK	2610	HLA-A*03:01
5915	WT1	ENSG00000184937	LYQMTSQL	2611	HLA-C*14:02
5916	WT1	ENSG00000184937	MGSDVRDL	2612	HLA-C*16:01
5917	WT1	ENSG00000184937	MHQRNMTKL	2613	HLA-B*38:01
5918	WT1	ENSG00000184937	MTKLQLAL	2614	HLA-B*08:01
5919	WT1	ENSG00000184937	MTKLQLAL	2614	HLA-C*03:04
5920	WT1	ENSG00000184937	MTKLQLAL	2614	HLA-C*07:01
5921	WT1	ENSG00000184937	MTSQLECMTW	2615	HLA-A*25:01
5922	WT1	ENSG00000184937	MTSQLECMTW	2615	HLA-B*57:01
5923	WT1	ENSG00000184937	MTSQLECMTW	2615	HLA-B*58:01
5924	WT1	ENSG00000184937	NAPYLPSCL	2616	HLA-C*01:02
5925	WT1	ENSG00000184937	NAPYLPSC	2617	HLA-B*51:01
5926	WT1	ENSG00000184937	NLGATLKGV	2618	HLA-A*02:03
5927	WT1	ENSG00000184937	NLYQMTSQL	2619	HLA-A*02:01
5928	WT1	ENSG00000184937	NLYQMTSQL	2619	HLA-A*02:03
5929	WT1	ENSG00000184937	NLYQMTSQL	2619	HLA-C*01:02
5930	WT1	ENSG00000184937	NLYQMTSQL	2619	HLA-C*14:02
5931	WT1	ENSG00000184937	NMTKLQLAL	2620	HLA-B*08:01
5932	WT1	ENSG00000184937	NMTKLQLAL	2620	HLA-B*13:02
5933	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-B*15:01
5934	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-B*15:03
5935	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-B*18:01
5936	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-B*38:01
5937	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-B*39:01
5938	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-C*07:04
5939	WT1	ENSG00000184937	NQGYSTVTF	2621	HLA-C*14:02
5940	WT1	ENSG00000184937	NQMNLGATLK	2622	HLA-A*11:01
5941	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-A*23:01
5942	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*13:02
5943	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*15:01
5944	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*15:03
5945	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*27:05
5946	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*38:01
5947	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-B*39:01
5948	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-C*03:03
5949	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-C*07:02
5950	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-C*07:04
5951	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-C*14:02
5952	WT1	ENSG00000184937	NQMNLGATL	2623	HLA-C*16:04
5953	WT1	ENSG00000184937	PPPPPPPPP	2624	HLA-C*04:01
5954	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-A*01:01
5955	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-A*29:02
5956	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-A*30:02
5957	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-B*15:03
5958	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-B*35:01
5959	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-B*46:01
5960	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-B*57:01
5961	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-C*02:02
5962	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-C*07:01
5963	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-C*07:04
5964	WT1	ENSG00000184937	QALLLRTPY	2625	HLA-C*16:01
5965	WT1	ENSG00000184937	QASSGQARMF	2626	HLA-C*16:01
5966	WT1	ENSG00000184937	QASSGQARMF	2626	HLA-C*16:02
5967	WT1	ENSG00000184937	QASSGQARM	2627	HLA-C*16:01
5968	WT1	ENSG00000184937	QDVRRVPGV	2628	HLA-B*37:01
5969	WT1	ENSG00000184937	QFTGTAGACRY	2629	HLA-A*29:02
5970	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-B*08:01
5971	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-B*15:03
5972	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-B*18:01

5973	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-B*37:01
5974	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-B*46:01
5975	WT1	ENSG00000184937	QGYSTVTF	2630	HLA-C*12:03
5976	WT1	ENSG00000184937	QMNLGATLK	2631	HLA-A*03:01
5977	WT1	ENSG00000184937	QMNLGATLK	2631	HLA-A*03:02
5978	WT1	ENSG00000184937	QMNLGATLK	2631	HLA-A*11:01
5979	WT1	ENSG00000184937	QMNLGATL	2632	HLA-B*07:02
5980	WT1	ENSG00000184937	QMNLGATL	2632	HLA-B*08:01
5981	WT1	ENSG00000184937	QMNLGATL	2632	HLA-C*01:02
5982	WT1	ENSG00000184937	QMNLGATL	2632	HLA-C*14:02
5982	WT1	ENSG00000184937	QPAIRNQGY	2633	HLA-B*35:01
5984	WT1	ENSG00000184937	QPAIRNQGY	2633	HLA-B*55:01
5985	WT1	ENSG00000184937	QQGSLGEQQY	2634	HLA-A*30:02
5986	WT1	ENSG00000184937	QQGSLGEQQY	2634	HLA-B*15:01
5987	WT1	ENSG00000184937	QQGSLGEQQY	2634	HLA-C*07:04
5988	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-A*30:02
5989	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-A*32:01
5990	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-B*15:01
5991	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-B*15:03
5992	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-B*39:01
5993	WT1	ENSG00000184937	QQYSVPPPVY	2635	HLA-C*16:04
5994	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-A*02:01
5995	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-A*02:03
5996	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-A*02:07
5997	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-A*30:01
5998	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-A*32:01
5999	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-B*13:02
6000	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-B*37:01
6001	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-B*49:01
6002	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-B*55:01
6003	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-B*56:01
6004	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-C*02:02
6005	WT1	ENSG00000184937	QQYSVPPPV	2636	HLA-C*06:02
6006	WT1	ENSG00000184937	QRNMTKLQL	2637	HLA-C*06:02
6007	WT1	ENSG00000184937	QSNHSTGY	2638	HLA-A*30:02
6008	WT1	ENSG00000184937	QSNHSTGY	2638	HLA-A*32:01
6009	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-A*23:01
6010	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-A*24:02
6011	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-A*29:02
6012	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-A*30:02
6013	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-A*32:01
6014	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-B*15:03
6015	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-C*01:02
6016	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-C*14:02
6017	WT1	ENSG00000184937	QYSVPPPVY	2639	HLA-C*16:01
6018	WT1	ENSG00000184937	RIHTHGVFR	2640	HLA-A*03:01
6019	WT1	ENSG00000184937	RIHTHGVFR	2640	HLA-A*31:01
6020	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*02:01
6021	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*02:04
6022	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*02:07
6023	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*03:01
6024	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*23:01
6025	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*24:02
6026	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-A*32:01
6027	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-B*57:01
6028	WT1	ENSG00000184937	RMFPNAPYL	2641	HLA-C*02:02
6029	WT1	ENSG00000184937	RMFPNAPY	2642	HLA-A*30:02
6030	WT1	ENSG00000184937	RNMTKLQL	2643	HLA-B*08:01
6031	WT1	ENSG00000184937	RRVPGVAPTL	2644	HLA-B*27:05
6032	WT1	ENSG00000184937	RRVPGVAPTL	2644	HLA-C*16:04
6033	WT1	ENSG00000184937	RTPYSSDNLY	2645	HLA-A*01:01
6034	WT1	ENSG00000184937	RTPYSSDNL	2646	HLA-C*01:02
6035	WT1	ENSG00000184937	RVPGVAPTLVR	2647	HLA-A*03:01
6036	WT1	ENSG00000184937	RVPGVAPTLVR	2647	HLA-A*31:01

6037	WT1	ENSG00000184937	RVPGVAPTLV	2648	HLA-A*02:01
6038	WT1	ENSG00000184937	RVPGVAPTLV	2648	HLA-A*02:03
6039	WT1	ENSG00000184937	RVPGVAPTLV	2648	HLA-A*02:07
6040	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*02:04
6041	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*02:07
6042	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*23:01
6043	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*24:02
6044	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*25:01
6045	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-A*32:01
6046	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-B*07:02
6047	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-B*13:02
6048	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-B*58:01
6049	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-C*01:02
6050	WT1	ENSG00000184937	RVPGVAPTL	2649	HLA-C*03:04
6051	WT1	ENSG00000184937	RYFKLSHLQM	2650	HLA-A*24:02
6052	WT1	ENSG00000184937	SASETSEKRPF	2651	HLA-C*16:01
6053	WT1	ENSG00000184937	SASETSEKR	2652	HLA-A*68:01
6054	WT1	ENSG00000184937	SASETSEKR	2652	HLA-C*07:06
6055	WT1	ENSG00000184937	SDELVRHHNM	2653	HLA-B*37:01
6056	WT1	ENSG00000184937	SDNHTTPIL	2654	HLA-B*37:01
6057	WT1	ENSG00000184937	SDNHTTPI	2655	HLA-B*37:01
6058	WT1	ENSG00000184937	SDVRDLNAL	2656	HLA-A*30:01
6059	WT1	ENSG00000184937	SDVRDLNAL	2656	HLA-B*37:01
6060	WT1	ENSG00000184937	SDVRDLNAL	2656	HLA-B*40:01
6061	WT1	ENSG00000184937	SDVRDLNAL	2656	HLA-B*40:02
6062	WT1	ENSG00000184937	SEKPFSCRW	2657	HLA-B*44:02
6063	WT1	ENSG00000184937	SEKPFSCRW	2657	HLA-B*44:03
6064	WT1	ENSG00000184937	SETSEKRPF	2658	HLA-B*37:01
6065	WT1	ENSG00000184937	SETSEKRPF	2658	HLA-B*44:02
6066	WT1	ENSG00000184937	SETSEKRPF	2658	HLA-B*44:03
6067	WT1	ENSG00000184937	SETSEKRPF	2658	HLA-C*16:01
6068	WT1	ENSG00000184937	SFIKQEPSW	2659	HLA-A*23:01
6069	WT1	ENSG00000184937	SFIKQEPSW	2659	HLA-A*24:02
6070	WT1	ENSG00000184937	SGQFTGTAGAC	2660	HLA-C*06:02
6071	WT1	ENSG00000184937	SGQFTGTAGAC	2660	HLA-C*12:03
6072	WT1	ENSG00000184937	SLGEQQYSV	2661	HLA-A*02:01
6073	WT1	ENSG00000184937	SLGEQQYSV	2661	HLA-A*02:03
6074	WT1	ENSG00000184937	SLGEQQYSV	2661	HLA-A*02:04
6075	WT1	ENSG00000184937	SLGEQQYSV	2661	HLA-B*13:02
6076	WT1	ENSG00000184937	SLGEQQYSV	2661	HLA-B*55:01
6077	WT1	ENSG00000184937	SLGGPAPPP	2662	HLA-A*03:02
6078	WT1	ENSG00000184937	SLGGPAPPP	2662	HLA-C*06:02
6079	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-A*30:02
6080	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-A*32:01
6081	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-B*15:01
6082	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-B*15:03
6083	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-C*02:02
6084	WT1	ENSG00000184937	SQALLLRTPY	2663	HLA-C*07:04
6085	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-A*26:01
6086	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-A*30:02
6087	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-A*32:01
6088	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-B*15:01
6089	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-B*15:03
6090	WT1	ENSG00000184937	SQPAIRNQGY	2664	HLA-C*07:04
6091	WT1	ENSG00000184937	SSDNLYQM	2665	HLA-C*05:01
6092	WT1	ENSG00000184937	SSGQARMF	2666	HLA-C*16:01
6093	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-A*01:01
6094	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-A*25:01
6095	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-A*26:01
6096	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-A*29:02
6097	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-A*30:02
6098	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-B*46:01
6099	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-B*57:01
6100	WT1	ENSG00000184937	STVTFDGTPSY	2667	HLA-B*58:01

6101	WT1	ENSG00000184937	SVPPPVYGC	2668	HLA-A*02:01
6102	WT1	ENSG00000184937	SVPPPVYGC	2668	HLA-A*02:07
6103	WT1	ENSG00000184937	TEGQSNHSTGY	2669	HLA-B*27:02
6104	WT1	ENSG00000184937	TEGQSNHSTGY	2669	HLA-B*44:02
6105	WT1	ENSG00000184937	TEGQSNHSTGY	2669	HLA-B*44:03
6106	WT1	ENSG00000184937	TEGQSNHSTGY	2669	HLA-C*04:01
6107	WT1	ENSG00000184937	TEGQSNHSTGY	2669	HLA-C*16:04
6108	WT1	ENSG00000184937	TFDGTPSYG	2670	HLA-C*04:01
6109	WT1	ENSG00000184937	TFDGTPSY	2671	HLA-A*32:01
6110	WT1	ENSG00000184937	TFDGTPSY	2671	HLA-B*18:01
6111	WT1	ENSG00000184937	TFDGTPSY	2671	HLA-C*04:01
6112	WT1	ENSG00000184937	TFDGTPSY	2671	HLA-C*14:02
6113	WT1	ENSG00000184937	TGKTSEKPF	2672	HLA-C*16:01
6114	WT1	ENSG00000184937	TGSQALLLR	2673	HLA-A*68:01
6115	WT1	ENSG00000184937	TGSQALLLR	2673	HLA-C*07:06
6116	WT1	ENSG00000184937	TGTAGACRY	2674	HLA-B*39:01
6117	WT1	ENSG00000184937	TGTAGACRY	2674	HLA-C*16:01
6118	WT1	ENSG00000184937	TGTAGACRY	2674	HLA-C*16:02
6119	WT1	ENSG00000184937	TPILCGAQY	2675	HLA-B*35:01
6120	WT1	ENSG00000184937	TPILCGAQY	2675	HLA-B*55:01
6121	WT1	ENSG00000184937	TPSHHAAQF	2676	HLA-B*07:02
6122	WT1	ENSG00000184937	TPSHHAAQF	2676	HLA-B*35:01
6123	WT1	ENSG00000184937	TPSHHAAQF	2676	HLA-B*35:03
6124	WT1	ENSG00000184937	TPYSSDNLYQM	2677	HLA-B*35:01
6125	WT1	ENSG00000184937	TPYSSDNLYQM	2677	HLA-B*35:03
6126	WT1	ENSG00000184937	TPYSSDNLYQM	2677	HLA-B*55:01
6127	WT1	ENSG00000184937	TPYSSDNLYQM	2677	HLA-B*56:01
6128	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-A*26:01
6129	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-B*15:01
6130	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-B*15:03
6131	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-B*35:01
6132	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-B*35:03
6133	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-B*55:01
6134	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-C*03:03
6135	WT1	ENSG00000184937	TPYSSDNLY	2678	HLA-C*07:04
6136	WT1	ENSG00000184937	TPYSSDNL	2679	HLA-B*07:02
6137	WT1	ENSG00000184937	TPYSSDNL	2679	HLA-B*35:03
6138	WT1	ENSG00000184937	TPYSSDNL	2679	HLA-B*39:01
6139	WT1	ENSG00000184937	TPYSSDNL	2679	HLA-B*51:01
6140	WT1	ENSG00000184937	TPYSSDNL	2679	HLA-C*07:02
6141	WT1	ENSG00000184937	TSQLECMTW	2680	HLA-B*57:01
6142	WT1	ENSG00000184937	TSQLECMTW	2680	HLA-B*58:01
6143	WT1	ENSG00000184937	TTPILCGAQY	2681	HLA-A*26:01
6144	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-A*01:01
6145	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-A*25:01
6146	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-A*26:01
6147	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-A*30:02
6148	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-B*15:01
6149	WT1	ENSG00000184937	TVTFDGTPSY	2682	HLA-B*39:01
6150	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-A*25:01
6151	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-A*32:01
6152	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-A*33:01
6153	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-B*57:01
6154	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-B*58:01
6155	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-C*02:02
6156	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-C*16:02
6157	WT1	ENSG00000184937	VAAGSSSSVKW	2683	HLA-C*16:04
6158	WT1	ENSG00000184937	VAAGSSSSVK	2684	HLA-A*03:02
6159	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-A*02:03
6160	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*13:02
6161	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*15:03
6162	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*39:01
6163	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*46:01
6164	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*51:01

6165	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-B*56:01
6166	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*01:02
6167	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*02:02
6168	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*03:03
6169	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*03:04
6170	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*05:01
6171	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*12:03
6172	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*14:02
6173	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*16:02
6174	WT1	ENSG00000184937	VAAGSSSSV	2685	HLA-C*16:04
6175	WT1	ENSG00000184937	VAPTLVRSA	2686	HLA-B*46:01
6176	WT1	ENSG00000184937	VAPTLVRSA	2686	HLA-C*01:02
6177	WT1	ENSG00000184937	VAPTLVRSA	2686	HLA-C*16:01
6178	WT1	ENSG00000184937	VLDFAPPGA	2687	HLA-A*02:01
6179	WT1	ENSG00000184937	VLDFAPPGA	2687	HLA-A*02:07
6180	WT1	ENSG00000184937	VPGVAPTLV	2688	HLA-B*51:01
6181	WT1	ENSG00000184937	VPGVAPTLV	2688	HLA-B*56:01
6182	WT1	ENSG00000184937	VPGVAPTLV	2688	HLA-C*04:01
6183	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-A*23:01
6184	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*07:02
6185	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*08:01
6186	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*35:01
6187	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*35:03
6188	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*51:01
6189	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*55:01
6190	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-B*56:01
6191	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-C*05:01
6192	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-C*07:02
6193	WT1	ENSG00000184937	VPGVAPTL	2689	HLA-C*14:02
6194	WT1	ENSG00000184937	VPPPVYGC	2690	HLA-B*51:01
6195	WT1	ENSG00000184937	VTFDGTPSYG	2691	HLA-C*12:03
6196	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*01:01
6197	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*03:01
6198	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*03:02
6199	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*11:01
6200	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*23:01
6201	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*25:01
6202	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*26:01
6203	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*29:02
6204	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*30:02
6205	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-A*32:01
6206	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*13:02
6207	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*15:01
6208	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*15:03
6209	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*18:01
6210	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*27:02
6211	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*27:05
6212	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*35:01
6213	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*39:01
6214	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*44:03
6215	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*46:01
6216	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*57:01
6217	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-B*58:01
6218	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*01:02
6219	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*02:02
6220	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*03:03
6221	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*03:04
6222	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*05:01
6223	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*07:04
6224	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*07:06
6225	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*12:03
6226	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*14:02
6227	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*16:01
6228	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*16:02

6229	WT1	ENSG00000184937	VTFDGTPSY	2692	HLA-C*16:04
6230	WT1	ENSG00000184937	YESDNHTTPIL	2693	HLA-A*30:01
6231	WT1	ENSG00000184937	YESDNHTTPIL	2693	HLA-B*40:01
6232	WT1	ENSG00000184937	YESDNHTTPIL	2693	HLA-B*40:02
6233	WT1	ENSG00000184937	YESDNHTTPIL	2693	HLA-C*16:04
6234	WT1	ENSG00000184937	YESDNHTTPI	2694	HLA-B*40:01
6235	WT1	ENSG00000184937	YESDNHTTPI	2694	HLA-B*49:01
6236	WT1	ENSG00000184937	YESDNHTTP	2695	HLA-B*49:01
6237	WT1	ENSG00000184937	YESDNHTTP	2695	HLA-C*16:04
6238	WT1	ENSG00000184937	YGPFGPPPPS	2696	HLA-C*04:01
6239	WT1	ENSG00000184937	YGPFGPPPPS	2696	HLA-C*06:02
6240	WT1	ENSG00000184937	YGPFGPPPPS	2696	HLA-C*07:02
6241	WT1	ENSG00000184937	YGPFGPPPP	2697	HLA-B*54:01
6242	WT1	ENSG00000184937	YGPFGPPPP	2697	HLA-C*04:01
6243	WT1	ENSG00000184937	YQMTSQLECM	2698	HLA-C*07:04
6244	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-B*13:02
6245	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-B*15:01
6246	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-B*39:01
6247	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-C*03:03
6248	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-C*03:04
6249	WT1	ENSG00000184937	YQMTSQLEC	2699	HLA-C*16:02
6250	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-A*01:01
6251	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-A*02:01
6252	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-A*26:01
6253	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-A*68:02
6254	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-B*35:01
6255	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-B*35:03
6256	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-B*39:01
6257	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-B*46:01
6258	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-B*58:01
6259	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*02:02
6260	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*03:03
6261	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*03:04
6262	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*07:04
6263	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*12:03
6264	WT1	ENSG00000184937	YSSDNLYQM	2700	HLA-C*16:02
6265	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-A*01:01
6266	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*15:01
6267	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*15:03
6268	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*18:01
6269	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*39:01
6270	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*46:01
6271	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*57:01
6272	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-B*58:01
6273	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-C*02:02
6274	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-C*03:04
6275	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-C*12:03
6276	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-C*16:01
6277	WT1	ENSG00000184937	YSVPPPVY	2701	HLA-C*16:02
6278	KKLC-1	ENSG00000204019	ALALVRPSSS	2702	HLA-A*02:03
6279	KKLC-1	ENSG00000204019	ALALVRPSS	2703	HLA-A*32:01
6280	KKLC-1	ENSG00000204019	ALALVRPSS	2703	HLA-C*16:01
6281	KKLC-1	ENSG00000204019	ALIVFWKY	2704	HLA-A*29:02
6282	KKLC-1	ENSG00000204019	ALVRPSSSGL	2705	HLA-A*02:03
6283	KKLC-1	ENSG00000204019	AVYDLSRDIL	2706	HLA-A*25:01
6284	KKLC-1	ENSG00000204019	AVYDLSRDIL	2706	HLA-B*07:02
6285	KKLC-1	ENSG00000204019	AVYDLSRDIL	2706	HLA-C*12:03
6286	KKLC-1	ENSG00000204019	AVYDLSRDI	2707	HLA-B*13:02
6287	KKLC-1	ENSG00000204019	CALIVFWKY	2708	HLA-A*29:02
6288	KKLC-1	ENSG00000204019	CALIVFWKY	2708	HLA-B*57:01
6289	KKLC-1	ENSG00000204019	DLSRDILNNF	2709	HLA-A*25:01
6290	KKLC-1	ENSG00000204019	DNNLAVYDLSR	2710	HLA-A*33:01
6291	KKLC-1	ENSG00000204019	DNNLAVYDLSR	2710	HLA-B*27:02
6292	KKLC-1	ENSG00000204019	EHTLLSKGF	2711	HLA-B*38:01

6293	KKLC-1	ENSG00000204019	EHTLLSKGF	2711	HLA-B*44:02
6294	KKLC-1	ENSG00000204019	EHTLLSKGF	2711	HLA-C*07:01
6295	KKLC-1	ENSG00000204019	ELEHTLLSKGF	2712	HLA-C*07:01
6296	KKLC-1	ENSG00000204019	ELEHTLLSK	2713	HLA-A*01:01
6297	KKLC-1	ENSG00000204019	ELEHTLLSK	2713	HLA-A*33:01
6298	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-A*02:03
6299	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-A*25:01
6300	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-A*26:01
6301	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-A*32:01
6302	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-A*33:03
6303	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*07:02
6304	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*08:01
6305	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*27:05
6306	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*35:03
6307	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*38:01
6308	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*39:01
6309	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-B*55:01
6310	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-C*01:02
6311	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-C*07:02
6312	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-C*07:04
6313	KKLC-1	ENSG00000204019	EMSSNSTAL	2714	HLA-C*14:02
6314	KKLC-1	ENSG00000204019	FPHSIARQK	2715	HLA-B*54:01
6315	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-B*07:02
6316	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-B*15:01
6317	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-B*15:03
6318	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-B*40:02
6319	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-B*46:01
6320	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*03:03
6321	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*03:04
6322	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*05:01
6323	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*07:04
6324	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*12:03
6325	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*14:02
6326	KKLC-1	ENSG00000204019	FQRNTGEM	2716	HLA-C*16:01
6327	KKLC-1	ENSG00000204019	FYLLLASSIL	2717	HLA-A*24:02
6328	KKLC-1	ENSG00000204019	FYLLLASSI	2718	HLA-A*23:01
6329	KKLC-1	ENSG00000204019	FYLLLASSI	2718	HLA-A*24:02
6330	KKLC-1	ENSG00000204019	FYLLLASSI	2718	HLA-C*14:02
6331	KKLC-1	ENSG00000204019	GASPHRKST	2719	HLA-C*16:02
6332	KKLC-1	ENSG00000204019	GEMSSNSTALA	2720	HLA-A*30:01
6333	KKLC-1	ENSG00000204019	GEMSSNSTALA	2720	HLA-B*40:01
6334	KKLC-1	ENSG00000204019	GEMSSNSTALA	2720	HLA-B*49:01
6335	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-A*30:01
6336	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*15:01
6337	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*15:03
6338	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*27:02
6339	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*27:05
6340	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*38:01
6341	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*39:01
6342	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*40:01
6343	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*40:02
6344	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*44:02
6345	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*44:03
6346	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-B*49:01
6347	KKLC-1	ENSG00000204019	GEMSSNSTAL	2721	HLA-C*16:04
6348	KKLC-1	ENSG00000204019	GEMSSNSTA	2722	HLA-A*30:01
6349	KKLC-1	ENSG00000204019	GEMSSNSTA	2722	HLA-B*40:01
6350	KKLC-1	ENSG00000204019	GEMSSNSTA	2722	HLA-B*40:02
6351	KKLC-1	ENSG00000204019	GEMSSNSTA	2722	HLA-B*49:01
6352	KKLC-1	ENSG00000204019	GLINSNTDNNL	2723	HLA-A*02:01
6353	KKLC-1	ENSG00000204019	GLINSNTDNNL	2723	HLA-A*02:04
6354	KKLC-1	ENSG00000204019	GLINSNTDNNL	2723	HLA-B*27:05
6355	KKLC-1	ENSG00000204019	HTLLSKGFR	2724	HLA-A*31:01
6356	KKLC-1	ENSG00000204019	HTLLSKGFR	2724	HLA-A*33:01

6357	KKLC-1	ENSG00000204019	HTLLSKGFR	2724	HLA-A*33:03
6358	KKLC-1	ENSG00000204019	HTLLSKGF	2725	HLA-B*57:01
6359	KKLC-1	ENSG00000204019	ILNNFPHSIAR	2726	HLA-A*03:01
6360	KKLC-1	ENSG00000204019	ILNNFPHSIAR	2726	HLA-A*31:01
6361	KKLC-1	ENSG00000204019	ILNNFPHSIAR	2726	HLA-A*33:01
6362	KKLC-1	ENSG00000204019	ILNNFPHSIAR	2726	HLA-A*33:03
6363	KKLC-1	ENSG00000204019	ILNNFPHSIA	2727	HLA-A*02:03
6364	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*02:01
6365	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*02:03
6366	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*02:04
6367	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*02:07
6368	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*23:01
6369	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*24:02
6370	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*30:01
6371	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*31:01
6372	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*32:01
6373	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-A*68:02
6374	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-B*13:02
6375	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-B*38:01
6376	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-B*51:01
6377	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-B*55:01
6378	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*01:02
6379	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*02:02
6380	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*06:02
6381	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*14:02
6382	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*16:01
6383	KKLC-1	ENSG00000204019	ILNNFPHSI	2728	HLA-C*16:02
6384	KKLC-1	ENSG00000204019	INSNTDNNL	2729	HLA-B*35:03
6385	KKLC-1	ENSG00000204019	INSNTDNNL	2729	HLA-B*39:01
6386	KKLC-1	ENSG00000204019	KLVELEHTLL	2730	HLA-A*02:01
6387	KKLC-1	ENSG00000204019	KLVELEHTLL	2730	HLA-A*02:03
6388	KKLC-1	ENSG00000204019	KLVELEHTLL	2730	HLA-A*02:04
6389	KKLC-1	ENSG00000204019	KLVELEHTLL	2730	HLA-A*02:07
6390	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*02:01
6391	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*02:03
6392	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*02:04
6393	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*02:07
6394	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*23:01
6395	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*24:02
6396	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*30:01
6397	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-A*32:01
6398	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*13:02
6399	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*15:01
6400	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*15:03
6401	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*38:01
6402	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*40:01
6403	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*40:02
6404	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*55:01
6405	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-B*58:01
6406	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-C*02:02
6407	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-C*06:02
6408	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-C*07:04
6409	KKLC-1	ENSG00000204019	KLVELEHTL	2731	HLA-C*16:02
6410	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-A*68:02
6411	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-B*27:05
6412	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-B*35:03
6413	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-B*46:01
6414	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*02:02
6415	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*03:03
6416	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*03:04
6417	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*07:04
6418	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*12:03
6419	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*16:01
6420	KKLC-1	ENSG00000204019	LASSILCAL	2732	HLA-C*16:02

6421	KKLC-1	ENSG00000204019	LASSILCA	2733	HLA-B*54:01
6422	KKLC-1	ENSG00000204019	LEHTLLSKGF	2734	HLA-B*44:02
6423	KKLC-1	ENSG00000204019	LEHTLLSKGF	2734	HLA-B*44:03
6424	KKLC-1	ENSG00000204019	LINSNTDNNL	2735	HLA-B*27:05
6425	KKLC-1	ENSG00000204019	LLASSILCAL	2736	HLA-A*02:03
6426	KKLC-1	ENSG00000204019	LLASSILCAL	2736	HLA-A*02:04
6427	KKLC-1	ENSG00000204019	LLASSILCA	2737	HLA-A*02:01
6428	KKLC-1	ENSG00000204019	LLASSILCA	2737	HLA-A*02:03
6429	KKLC-1	ENSG00000204019	LLLASSILCAL	2738	HLA-A*02:01
6430	KKLC-1	ENSG00000204019	LLLASSILCAL	2738	HLA-A*02:04
6431	KKLC-1	ENSG00000204019	LLLASSILC	2739	HLA-A*02:01
6432	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-A*23:01
6433	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-A*24:02
6434	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-A*32:01
6435	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-A*33:01
6436	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-A*33:03
6437	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-B*46:01
6438	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-B*57:01
6439	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-B*58:01
6440	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-C*02:02
6441	KKLC-1	ENSG00000204019	LSRDILNNF	2740	HLA-C*16:01
6442	KKLC-1	ENSG00000204019	LVELEHTLL	2741	HLA-A*01:01
6443	KKLC-1	ENSG00000204019	LVELEHTLL	2741	HLA-A*02:07
6444	KKLC-1	ENSG00000204019	LVELEHTLL	2741	HLA-B*38:01
6445	KKLC-1	ENSG00000204019	LVELEHTLL	2741	HLA-C*05:01
6446	KKLC-1	ENSG00000204019	LVELEHTLL	2741	HLA-C*07:01
6447	KKLC-1	ENSG00000204019	LVELEHTL	2742	HLA-C*05:01
6448	KKLC-1	ENSG00000204019	LVELEHTL	2742	HLA-C*07:04
6449	KKLC-1	ENSG00000204019	LVNLSMVENK	2743	HLA-A*03:02
6450	KKLC-1	ENSG00000204019	LVNLSMVENK	2743	HLA-B*27:02
6451	KKLC-1	ENSG00000204019	LVRPSSSGLI	2744	HLA-C*07:02
6452	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-A*02:03
6453	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-A*32:01
6454	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-B*07:02
6455	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-B*08:01
6456	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-B*15:01
6457	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-B*40:02
6458	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-B*46:01
6459	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*01:02
6460	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*03:03
6461	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*03:04
6462	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*07:02
6463	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*07:04
6464	KKLC-1	ENSG00000204019	LVRPSSSGL	2745	HLA-C*14:02
6465	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*01:02
6466	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*03:03
6467	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*03:04
6468	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*05:01
6469	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*07:04
6470	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*14:02
6471	KKLC-1	ENSG00000204019	MSSNSTAL	2746	HLA-C*16:01
6472	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-A*02:07
6473	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-A*68:02
6474	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-B*08:01
6475	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-B*35:03
6476	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-B*38:01
6477	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-B*55:01
6478	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-C*01:02
6479	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-C*03:04
6480	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-C*05:01
6481	KKLC-1	ENSG00000204019	MVENKLVEL	2747	HLA-C*07:04
6482	KKLC-1	ENSG00000204019	NLSMVENKL	2748	HLA-A*02:04
6483	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-A*31:01
6484	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-A*33:01

6485	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-A*33:03
6486	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-A*68:01
6487	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-A*68:02
6488	KKLC-1	ENSG00000204019	NNFPHSIAR	284	HLA-C*07:06
6489	KKLC-1	ENSG00000204019	NSNTDNNLAVY	2749	HLA-A*01:01
6490	KKLC-1	ENSG00000204019	NSNTDNNLAVY	2749	HLA-A*30:02
6491	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-A*29:02
6492	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-A*33:01
6493	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-A*33:03
6494	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-A*68:01
6495	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-B*27:02
6496	KKLC-1	ENSG00000204019	NSTALALVR	2750	HLA-C*07:06
6497	KKLC-1	ENSG00000204019	NTDNNLAVYDL	2751	HLA-B*27:05
6498	KKLC-1	ENSG00000204019	NTDNNLAVYDL	2751	HLA-B*39:01
6499	KKLC-1	ENSG00000204019	NTDNNLAVYDL	2751	HLA-C*04:01
6500	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*01:01
6501	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*25:01
6502	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*26:01
6503	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*29:02
6504	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*30:02
6505	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-A*32:01
6506	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-B*18:01
6507	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-B*27:05
6508	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-B*35:01
6509	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-B*39:01
6510	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-B*55:01
6511	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*03:03
6512	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*04:01
6513	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*05:01
6514	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*07:01
6515	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*07:04
6516	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*07:06
6517	KKLC-1	ENSG00000204019	NTDNNLAVY	23	HLA-C*16:02
6518	KKLC-1	ENSG00000204019	NTDNNLAV	2752	HLA-A*01:01
6519	KKLC-1	ENSG00000204019	NTDNNLAV	2752	HLA-C*05:01
6520	KKLC-1	ENSG00000204019	RFQRNTGEM	2753	HLA-C*14:02
6521	KKLC-1	ENSG00000204019	RILVNLSMV	2754	HLA-A*02:01
6522	KKLC-1	ENSG00000204019	RILVNLSMV	2754	HLA-A*02:03
6523	KKLC-1	ENSG00000204019	RILVNLSMV	2754	HLA-A*02:04
6524	KKLC-1	ENSG00000204019	RILVNLSMV	2754	HLA-A*02:07
6525	KKLC-1	ENSG00000204019	RPSSSGLI	2755	HLA-C*07:02
6526	KKLC-1	ENSG00000204019	RQKRILVNL	2756	HLA-A*31:01
6527	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-A*02:01
6528	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-A*02:03
6529	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-A*02:04
6530	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-A*02:07
6531	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-B*46:01
6532	KKLC-1	ENSG00000204019	SMVENKLVEL	2757	HLA-B*55:01
6533	KKLC-1	ENSG00000204019	SNSTALALVR	2758	HLA-A*68:01
6534	KKLC-1	ENSG00000204019	SNSTALALVR	2758	HLA-B*27:02
6535	KKLC-1	ENSG00000204019	SNSTALALVR	2758	HLA-C*07:06
6536	KKLC-1	ENSG00000204019	SNTDNNLAVY	2759	HLA-A*25:01
6537	KKLC-1	ENSG00000204019	SNTDNNLAVY	2759	HLA-A*26:01
6538	KKLC-1	ENSG00000204019	SNTDNNLAVY	2759	HLA-A*29:02
6539	KKLC-1	ENSG00000204019	SNTDNNLAVY	2759	HLA-A*30:02
6540	KKLC-1	ENSG00000204019	SNTDNNLAV	2760	HLA-B*13:02
6541	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-A*03:02
6542	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-A*11:01
6543	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-A*31:01
6544	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-A*33:03
6545	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-A*68:01
6546	KKLC-1	ENSG00000204019	SSNSTALALVR	2761	HLA-C*07:06
6547	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-A*03:01
6548	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-B*07:02

6549	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-B*13:02
6550	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-B*35:03
6551	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-B*46:01
6552	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-B*58:01
6553	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*01:02
6554	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*03:03
6555	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*03:04
6556	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*07:02
6557	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*07:06
6558	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*14:02
6559	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*16:01
6560	KKLC-1	ENSG00000204019	SSNSTALAL	2762	HLA-C*16:02
6561	KKLC-1	ENSG00000204019	SSSGLINSN	2763	HLA-C*12:03
6562	KKLC-1	ENSG00000204019	STALALVRPSS	2764	HLA-C*06:02
6563	KKLC-1	ENSG00000204019	STALALVRPS	2765	HLA-C*06:02
6564	KKLC-1	ENSG00000204019	STALALVRPS	2765	HLA-C*07:01
6565	KKLC-1	ENSG00000204019	STALALVRPS	2765	HLA-C*07:02
6566	KKLC-1	ENSG00000204019	TALALVRPS	2766	HLA-A*31:01
6567	KKLC-1	ENSG00000204019	TALALVRPS	2766	HLA-A*33:01
6568	KKLC-1	ENSG00000204019	TALALVRPS	2766	HLA-C*06:02
6569	KKLC-1	ENSG00000204019	TALALVRPS	2766	HLA-C*07:01
6570	KKLC-1	ENSG00000204019	TALALVRPS	2766	HLA-C*12:03
6571	KKLC-1	ENSG00000204019	TDNNLAVY	2767	HLA-A*30:02
6572	KKLC-1	ENSG00000204019	TDNNLAVY	2767	HLA-B*18:01
6573	KKLC-1	ENSG00000204019	TDNNLAVY	2767	HLA-C*04:01
6574	KKLC-1	ENSG00000204019	TDNNLAVY	2767	HLA-C*07:01
6575	KKLC-1	ENSG00000204019	TDNNLAVY	2767	HLA-C*07:04
6576	KKLC-1	ENSG00000204019	TGEMSSNSTAL	2768	HLA-B*35:03
6577	KKLC-1	ENSG00000204019	TGEMSSNSTAL	2768	HLA-B*40:01
6578	KKLC-1	ENSG00000204019	TLLSKGFRGA	2769	HLA-A*02:03
6579	KKLC-1	ENSG00000204019	VELEHTLLS	2770	HLA-B*49:01
6580	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-A*23:01
6581	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-A*30:01
6582	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*08:01
6583	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*18:01
6584	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*37:01
6585	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*40:01
6586	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*40:02
6587	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-B*49:01
6588	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-C*04:01
6589	KKLC-1	ENSG00000204019	VELEHTLL	2771	HLA-C*07:01
6590	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-A*30:01
6591	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-B*18:01
6592	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-B*37:01
6593	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-B*40:01
6594	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-B*40:02
6595	KKLC-1	ENSG00000204019	VENKLVEL	2772	HLA-B*49:01
6596	KKLC-1	ENSG00000204019	VNLSMVENKL	2773	HLA-A*23:01
6597	KKLC-1	ENSG00000204019	VNLSMVENK	2774	HLA-B*27:02
6598	KKLC-1	ENSG00000204019	VRPSSSGLIN	2775	HLA-C*07:01
6599	KKLC-1	ENSG00000204019	VRPSSSGLI	2776	HLA-C*06:02
6600	KKLC-1	ENSG00000204019	VRPSSSGL	2777	HLA-C*01:02
6601	KKLC-1	ENSG00000204019	VRPSSSGL	2777	HLA-C*07:02
6602	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-A*23:01
6603	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-A*24:02
6604	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-B*35:01
6605	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-B*35:03
6606	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-B*55:01
6607	KKLC-1	ENSG00000204019	VYDLSRDIL	2778	HLA-C*04:01
6608	KKLC-1	ENSG00000204019	VYDLSRDI	2779	HLA-B*35:03
6609	KKLC-1	ENSG00000204019	VYDLSRDI	2779	HLA-B*51:01
6610	KKLC-1	ENSG00000204019	VYDLSRDI	2779	HLA-C*04:01
6611	KKLC-1	ENSG00000204019	YLLLASSI	2780	HLA-B*13:02
6612	KKLC-1	ENSG00000204019	YLLLASSI	2780	HLA-B*51:01

CLAIMS

1. An isolated antigen binding protein (ABP) that specifically binds to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA-restricted peptide is located in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein:

a. the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide consists of the sequence LLASSILCA,
b. the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide consists of the sequence EVDPIGHLY,
c. the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide consists of the sequence GEMSSNSTAL,
d. the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide consists of the sequence GVYDGEEHSV,
e. the HLA Class I molecule is HLA subtype *01:01 and the HLA-restricted peptide consists of the sequence EVDPIGHVY, or
f. the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide consists of the sequence NTDNNLAVY.

2. The isolated ABP of claim 1, wherein the HLA-restricted peptide is between about 5-15 amino acids in length.

3. The isolated ABP of claim 2, wherein the HLA-restricted peptide is between about 8-12 amino acids in length.

4. The isolated ABP of any of the preceding claims, wherein the ABP comprises an antibody or antigen-binding fragment thereof.

5. The isolated ABP of claim 4, wherein the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA.

6. The isolated ABP of claim 5, wherein the ABP comprises a CDR-H3 comprising a sequence set forth in any one of SEQ ID NOS: 3025-3032.

7. The isolated ABP of claim 5 or 6, wherein the ABP comprises a CDR-L3 comprising a sequence set forth in any one of SEQ ID NOS: 3043-3050.

8. The isolated ABP of any one of claims 5-7, wherein the ABP comprises the CDR-H3 and the CDR-L3 from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9).

9. The isolated ABP of any one of claims 5-8, wherein the ABP comprises all three heavy chain CDRs and all three light chain CDRs from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9).

10. The isolated ABP of any one of claims 5-9, wherein the ABP comprises a VH sequence selected from SEQ ID NO: 2994-3001.

11. The isolated ABP of any one of claims 5-10, wherein the ABP comprises a VL sequence selected from 3002-3009.

12. The isolated ABP of any one of claims 5-11, wherein the ABP comprises the VH sequence and VL sequence from the scFv designated G7R3-P1C6, G7R3-P1G10, 1-G7R3-P1B4, 2-G7R4-P2C2, 3-G7R4-P1A3, 4-G7R4-B5-P2E9, 5-G7R4-B10-P1F8, or B7 (G7R3-P3A9).

13. The isolated ABP of any one of claims 5-12, wherein the ABP binds to the HLA-PEPTIDE target via any one or more of residues 1-5 of the restricted peptide LLASSILCA.

14. The isolated ABP of claim 4, wherein the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY.

15. The isolated ABP of claim 14, wherein the ABP comprises a CDR-H3 comprising a sequence set forth in any one of SEQ ID NOS: 2902-2933.

16. The isolated ABP of claim 14 or 15, wherein the ABP comprises a CDR-L3 comprising a sequence set forth in any one of SEQ ID NOS: 2971-2993.

17. The isolated ABP of any one of claims 14-16, wherein the ABP comprises the CDR-H3 and the CDR-L3 from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 ,

G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06.

18. The isolated ABP of any one of claims 14-17, wherein the ABP comprises all three heavy chain CDRs and all three light chain CDRs from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 , G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06:

19. The isolated ABP of any one of claims 14-18, wherein the ABP comprises a VH sequence selected from 2781-2815.

20. The isolated ABP of any one of claims 14-19, wherein the ABP comprises a VL sequence selected from 2816-2850.

21. The isolated ABP of any one of claims 14-20, wherein the ABP comprises the VH sequence and VL sequence from the scFv designated G2-P2E07, G2-P2E03, G2-P2A11, G2-P2C06, G2-P1G01, G2-P1C02, G2-P1H01, G2-P1B12, G2-P1B06, G2-P2H10, G2-P1H10, G2-P2C11, G2-P1C09, G2-P1A10, G2-P1B10 , G2-P1D07 , G2-P1E05, G2-P1D03 , G2-P1G12 , G2-P2H11, G2-P1C03 , G2-P1G07 , G2-P1F12 , G2-P1G03 , G2-P2B08, G2-P2A10 , G2-P2D04, G2-P1C06, G2-P2A09 , G2-P1B08, G2-P1E03, G2-P2A03, G2-P2F01, G2-P1H11 , or G2-P1D06.

22. The isolated ABP of any one of claims 14-21, wherein the ABP binds to the HLA-PEPTIDE target via residues 6-9 of the restricted peptide NTDNNLAVY and via residues 157-160 of the HLA subtype allele A*0101.

23. The isolated ABP of any one of claims 14-22, wherein the ABP binds to the HLA-PEPTIDE target via residues 3-8 of the restricted peptide NTDNNLAVY.

24. The isolated ABP of any one of claims 1-4, wherein the ABP comprises a T cell receptor (TCR) or an antigen-binding portion thereof.

25. The antigen binding protein of claim 24, wherein the TCR or antigen-binding portion thereof comprises a TCR variable region.

26. The antigen binding protein of claim 24 or 25, wherein the TCR or antigen-binding portion thereof comprises one or more TCR complementarity determining regions (CDRs).

27. The antigen binding protein of any one of claims 24-26, wherein the TCR comprises an alpha chain and a beta chain.

28. The antigen binding protein of any one of claims 24-27, wherein the TCR comprises a gamma chain and a delta chain.

29. The antigen binding protein of any of the above claims, wherein the antigen binding protein is a portion of a chimeric antigen receptor (CAR) comprising: an extracellular portion comprising the antigen binding protein; and an intracellular signaling domain.

30. The antigen binding protein of claim 29, wherein the antigen binding protein comprises an scFv and the intracellular signaling domain comprises an ITAM.

31. The antigen binding protein of claim 29 or 30, wherein the intracellular signaling domain comprises a signaling domain of a zeta chain of a CD3-zeta (CD3) chain.

32. The antigen binding protein of any of claims 29-31, further comprising a transmembrane domain linking the extracellular domain and the intracellular signaling domain.

33. The antigen binding protein of claim 32, wherein the transmembrane domain comprises a transmembrane portion of CD28.

34. The antigen binding protein of any of claims 29-33, further comprising an intracellular signaling domain of a T cell costimulatory molecule.

35. The antigen binding protein of claim 34, wherein the T cell costimulatory molecule is CD28, 4-1BB, OX-40, ICOS, or any combination thereof.

36. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA.

37. The isolated ABP of claim 36, wherein the ABP comprises a TCR alpha CDR3 sequence that is SEQ ID NO: 4277, 4278, 4279, 4280, or 4281.

38. The isolated ABP of claim 36 or 37, wherein the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS 4291-4295.

39. The isolated ABP of any one of claims 36-38, wherein the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, or TCR23.

40. The isolated ABP of any one of claims 36-39, wherein the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, and TCR23.

41. The isolated ABP of any one of claims 36-40, wherein the ABP comprises a TCR alpha constant (TRAC) amino acid sequence.

42. The isolated ABP of any one of claims 36-41, wherein the ABP comprises a TCR beta constant (TRBC) amino acid sequence.

43. The isolated ABP of any one of claims 36-42, wherein the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS 4306-4310.

44. The isolated ABP of any one of claims 36-43, wherein the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS 4321-4325.

45. The isolated ABP of any one of claims 36-44, wherein the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for any one of the TCR clonotypes selected from TCR clonotype ID #s: TCR19, TCR21, TCR22, TCR18, and TCR23.

46. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHLY.

47. The isolated ABP of claim 46, wherein the ABP comprises a TCR alpha CDR3 sequence that is any one of SEQ ID NOS: 4273-4276 or 3052-3350.

48. The isolated ABP of claim 46 or 47, wherein the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS: 4287-4290 or 3351-3655.

49. The isolated ABP of any one of claims 46-48, wherein the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, TCR54, or TCR101-TCR469.

50. The isolated ABP of any one of claims 46-49, wherein the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, TCR54, or TCR101-TCR469.

51. The isolated ABP of any one of claims 46-50, wherein the ABP comprises a TCR alpha constant (TRAC) amino acid sequence.

52. The isolated ABP of any one of claims 46-50, wherein the ABP comprises a TCR beta constant (TRBC) amino acid sequence.

53. The isolated ABP of any one of claims 46-52, wherein the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 3656-3961 or 4302-4305.

54. The isolated ABP of any one of claims 46-53, wherein the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 3962-4269 or 4317-4320.

55. The isolated ABP of any one of claims 46-54, wherein the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J

amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR101-TCR469, TCR2, TCR4, TCR53, and TCR54.

56. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide comprises the sequence GEMSSNSTAL.

57. The isolated ABP of claim 56, wherein the ABP comprises a TCR alpha CDR3 sequence that is be any one of SEQ ID NOS 4284-4286 or 3138.

58. The isolated ABP of claim 56 or 57, wherein the ABP comprises a TCR beta CDR3 sequence that is any one of SEQ ID NOS 4298-4301 .

59. The isolated ABP of any one of claims 56-58, wherein the ABP comprises an alpha CDR3 and a beta CDR3 sequence from any one of TCR ID #s: TCR29, TCR30, TCR32, or TCR33.

60. The isolated ABP of any one of claims 56-59, wherein the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR29, TCR30, TCR32, or TCR33.

61. The isolated ABP of any one of claims 56-60, wherein the ABP comprises a TCR alpha constant (TRAC) amino acid sequence.

62. The isolated ABP of any one of claims 56-61, wherein the ABP comprises a TCR beta constant (TRBC) amino acid sequence.

63. The isolated ABP of any one of claims 56-62, wherein the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 4313-4316.

64. The isolated ABP of any one of claims 56-63, wherein the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of SEQ ID NOS: 4328-4331.

65. The isolated ABP of any one of claims 56-64, wherein the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for any one of the TCR clonotypes selected from TCR ID #s: TCR29, TCR30, TCR32, or TCR33.

66. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence GVYDGEEHSV.

67. The isolated ABP of claim 66, wherein the ABP comprises a TCR alpha CDR3 sequence that is SEQ ID NO: 4282 or 4283.

68. The isolated ABP of claim 66 or 67, wherein the ABP comprises a TCR beta CDR3 sequence that is SEQ ID NO: 4296 or 4297.

69. The isolated ABP of any one of claims 66-68, wherein the ABP comprises an alpha CDR3 and a beta CDR3 sequence from TCR clonotype ID #: TCR26 or TCR28.

70. The isolated ABP of any one of claims 66-68, wherein the ABP comprises a TCR alpha variable (TRAV) amino acid sequence, a TCR alpha joining (TRAJ) amino acid sequence, a TCR beta variable (TRBV) amino acid sequence, a TCR beta diversity (TRBD) amino acid sequence, and a TCR beta joining (TRBJ) amino acid sequence, wherein each of the TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TRAV, TRAJ, TRBV, TRBD, and TRBJ amino acid sequences for TCR ID #: TCR26 or TCR28.

71. The isolated ABP of any one of claims 66-70, wherein the ABP comprises a TCR alpha constant (TRAC) amino acid sequence.

72. The isolated ABP of any one of claims 66-71, wherein the ABP comprises a TCR beta constant (TRBC) amino acid sequence.

73. The isolated ABP of any one of claims 66-72, wherein the ABP comprises a TCR alpha VJ sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4311 or 4312.

74. The isolated ABP of any one of claims 66-73, wherein the ABP comprises a TCR beta V(D)J sequence having at least 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4326 or 4327.

75. The isolated ABP of any one of claims 66-74, wherein the ABP comprises a TCR alpha VJ amino acid sequence and a TCR beta V(D)J amino acid sequence, wherein each of the TCR alpha VJ and the TCR beta V(D)J amino acid sequences are at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding TCR alpha VJ and TCR beta V(D)J amino acid sequences for TCR ID #: TCR26 or TCR28.

76. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY.

77. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype HLA-A*03:01 and the HLA-restricted peptide comprises the sequence GVHGGILNK.

78. The isolated ABP of any one of claims 24-35, wherein the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHVY.

79. An isolated antigen binding protein (ABP) that specifically binds to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA-restricted peptide is located in in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein the HLA-PEPTIDE target is selected from Table A.

80. The isolated ABP of claim 79, wherein the HLA-restricted peptide is not from a gene selected from WT1 or MART1.

81. The isolated ABP of claim 79 or 80, wherein the HLA-restricted peptide is between about 5-15 amino acids in length.

82. The isolated ABP of claim 81, wherein the HLA-restricted peptide is between about 8-12 amino acids in length.

83. The isolated ABP of any of claims 79-82, wherein the ABP comprises an antibody or antigen-binding fragment thereof.

84. The antigen binding protein of any of the above claims, wherein the antigen binding protein is linked to a scaffold, optionally wherein the scaffold comprises serum albumin or Fc, optionally wherein Fc is human Fc and is an IgG (IgG1, IgG2, IgG3, IgG4), an IgA (IgA1, IgA2), an IgD, an IgE, or an IgM.

85. The antigen binding protein of any of the above claims, wherein the antigen binding protein is linked to a scaffold via a linker, optionally wherein the linker is a peptide linker, optionally wherein the peptide linker is a hinge region of a human antibody.

86. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises an Fv fragment, a Fab fragment, a $F(ab')_2$ fragment, a Fab' fragment, an scFv fragment, an scFv-Fc fragment, and/or a single-domain antibody or antigen binding fragment thereof.

87. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises an scFv fragment.

88. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises one or more antibody complementarity determining regions (CDRs), optionally six antibody CDRs.

89. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises an antibody.

90. The antigen binding protein of any of the above claims, wherein the antigen binding protein is a monoclonal antibody.

91. The antigen binding protein of any of the above claims, wherein the antigen binding protein is a humanized, human, or chimeric antibody.

92. The antigen binding protein of any of the above claims, wherein the antigen binding protein is multispecific, optionally bispecific.

93. The antigen binding protein of any of the above claims, wherein the antigen binding protein binds greater than one antigen or greater than one epitope on a single antigen.

94. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises a heavy chain constant region of a class selected from IgG, IgA, IgD, IgE, and IgM.

95. The antigen binding protein of any of the above claims, wherein the antigen binding protein comprises a heavy chain constant region of the class human IgG and a subclass selected from IgG1, IgG4, IgG2, and IgG3.

96. The antigen binding protein of claims, wherein the antigen binding protein comprises a modified Fc, optionally wherein the modified Fc comprises one or more mutations that extend half-life, optionally wherein the one or more mutations that extend half-life is YTE.

97. An isolated HLA-PEPTIDE target, wherein the HLA-PEPTIDE target comprises an HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA-restricted peptide is located in in the peptide binding groove of an α1/α2 heterodimer portion of the HLA Class I molecule, and wherein the HLA-PEPTIDE target is selected from Table A, with the proviso that the isolated HLA-PEPTIDE target is not any one of Target nos. 6364-6369, 6386-6389, 6500, 6521-6524, or 6578 and is not an HLA-PEPTIDE target found in Table B or Table C.

98. The isolated HLA-PEPTIDE target of claim 97, wherein

a. the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence LLASSILCA,
b. the HLA Class I molecule is HLA subtype A*01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHLY,
c. the HLA Class I molecule is HLA subtype B*44:02 and the HLA-restricted peptide comprises the sequence GEMSSNSTAL,
d. the HLA Class I molecule is HLA subtype A*02:01 and the HLA-restricted peptide comprises the sequence GVYDGEEHSV,
e. the HLA Class I molecule is HLA subtype *01:01 and the HLA-restricted peptide comprises the sequence EVDPIGHVY, or
f. the HLA Class I molecule is HLA subtype HLA-A*01:01 and the HLA-restricted peptide comprises the sequence NTDNNLAVY.

99. The isolated HLA-PEPTIDE target of claim 98, comprising HLA subtype A*02:01 complexed with a restricted peptide consisting of or consisting essentially of the sequence LLASSILCA.

100. The isolated HLA-PEPTIDE target of any of claims 97-99, wherein the HLA-restricted peptide is between about 5-15 amino acids in length.

101. The isolated HLA-PEPTIDE target of any of claims 97-100, wherein the HLA-restricted peptide is between about 8-12 amino acids in length.

102. The isolated HLA-PEPTIDE target of any of claims 97-101, wherein the ABP comprises an antibody or antigen-binding fragment thereof.

103. The isolated HLA-PEPTIDE target of any of claims 97-102, wherein the association of the HLA subtype with the restricted peptide stabilizes non-covalent association of the β_2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype.

104. The isolated HLA-PEPTIDE target of claim 103, wherein the stabilized association of the β_2-microglobin subunit of the HLA subtype with the α-subunit of the HLA subtype is demonstrated by conditional peptide exchange.

105. The isolated HLA-PEPTIDE target of any of the preceding claims, further comprising an affinity tag.

106. The isolated HLA-PEPTIDE target of claim 105, wherein the affinity tag is a biotin tag.

107. The isolated HLA-PEPTIDE target of any of the above claims, wherein the isolated HLA-PEPTIDE target is complexed with a detectable label.

108. The isolated HLA-PEPTIDE target of claim 107, wherein the detectable label comprises a β_2-microglobin binding molecule.

109. The isolated HLA-PEPTIDE target of claim 108, wherein the β_2-microglobin binding molecule is a labeled antibody.

110. The isolated HLA-PEPTIDE target of claim 109, wherein the labeled antibody is a fluorochrome-labeled antibody.

111. A composition comprising an HLA-PEPTIDE target of any of the preceding claims attached to a solid support.

112. The composition of claim 111, wherein the solid support comprises a bead, well, membrane, tube, column, plate, sepharose, magnetic bead, or chip.

113. The composition of claim 111 or 112, wherein the HLA-PEPTIDE target comprises a first member of an affinity binding pair and the solid support comprises a second member of the affinity binding pair.

114. The composition of claim 113, wherein the first member is streptavidin and the second member is biotin.

115. A reaction mixture comprising

a. an isolated and purified α-subunit of an HLA subtype as described in Table A;
a. an isolated and purified β2-microglobin subunit of the HLA subtype;
b. an isolated and purified restricted peptide as described in Table A; and
c. a reaction buffer.

116. A reaction mixture comprising

a. an isolated HLA-PEPTIDE target of any of the preceding claims; and
b. a plurality of T-cells isolated from a human subject.

117. The reaction mixture of claim 116, wherein the T-cells are CD8+ T-cells.

118. An isolated polynucleotide comprising a first nucleic acid sequence encoding an HLA-restricted peptide as defined in claim 97 or 98, operably linked to a promoter, and a second nucleic acid sequence encoding an HLA subtype as defined in claim 97 or 98, wherein the second nucleic acid is operably linked to the same or different promoter as the first nucleic acid sequence, and wherein the encoded peptide and encoded HLA subtype form an HLA/peptide complex as defined in claim 97 or 98.

119. A kit for expressing a stable HLA-PEPTIDE target of claim, comprising a first construct comprising a first nucleic acid sequence encoding an HLA-restricted peptide as defined in claim 97 or 98 operably linked to a promoter; and instructions for use in expressing the stable HLA-PEPTIDE complex.

120. The kit of claim 119, wherein the first construct further comprises a second nucleic acid sequence encoding an HLA subtype as defined in claim 97 or 98.

121. The kit of claim 120, wherein the second nucleic acid sequence is operably linked to the same or a different promoter.

122. The kit of claim 119, further comprising a second construct comprising a second nucleic acid sequence encoding an HLA subtype as defined in claim 97 or 98.

123. The kit of any of claims 119-122, wherein one or both of the first and second constructs are lentiviral vector constructs.

124. A host cell comprising a heterologous HLA-PEPTIDE target of claim 97 or 98.

125. A host cell comprising a polynucleotide encoding an HLA-restricted peptide as described in Table A, e.g., a polynucleotide encoding an HLA-restricted peptide described in claim 97 or 98.

126. The host cell of claim 125, which does not comprise endogenous MHC.

127. The host cell of claim 126, comprising an exogenous HLA.

128. The host cell of claim 127, which is a K562 cell.

129. A cell culture system comprising

a. a host cell of claim 128, and
b. a cell culture medium comprising a restricted peptide as described in Table A.

130. The host cell of claim 124, which is a cultured cell from a tumor cell line.

131. The host cell of claim 130, wherein the tumor cell line is selected from the group consisting of HCC-1599, NCI-H510A, A375, LN229, NCI-H358, ZR-75-1, MS751, OE19, MOR, BV173, MCF-7, NCI-H82, and NCI-H146.

132. The ABP of any of the above claims, wherein the antigen binding protein binds to the HLA-PEPTIDE target through a contact point with the HLA Class I molecule and through a contact point with the HLA-restricted peptide of the HLA-PEPTIDE target.

133. The antigen binding protein of any of the above claims for use as a medicament.

134. The antigen binding protein of any of the above claims for use in treatment of cancer, optionally wherein the cancer expresses or is predicted to express the HLA-PEPTIDE target.

135. The antigen binding protein of any of the above claims for use in treatment of cancer, wherein the cancer is selected from a solid tumor and a hematological tumor.

136. An ABP which is a conservatively modified variant of the ABP of any one of the preceding claims.

137. An antigen binding protein (ABP) that competes for binding with the antigen binding protein of any of the above claims.

138. An antigen binding protein (ABP) that binds the same HLA-PEPTIDE epitope bound by the antigen binding protein of any of the above claims.

139. An engineered cell expressing a receptor comprising the antigen binding protein of any one of the preceding claims.

140. The engineered cell of claim 139, which is a T cell, optionally a cytotoxic T cell (CTL).

141. The engineered cell of claim 139 or 140, wherein the antigen binding protein is expressed from a heterologous promoter.

142. An isolated polynucleotide or set of polynucleotides encoding the antigen binding protein of any of the above claims or an antigen-binding portion thereof.

143. An isolated polynucleotide or set of polynucleotides encoding the HLA/peptide targets of any of the above claims.

144. A vector or set of vectors comprising the polynucleotide or set of polynucleotides of claim 142 or 143.

145. A host cell comprising the polynucleotide or set of polynucleotides of any of the preceding claims or the vector or set of vectors of claim 144, optionally wherein the host cell is CHO or HEK293, or optionally wherein the host cell is a T cell.

146. A method of producing an antigen binding protein comprising expressing the antigen binding protein with the host cell of claim 145 and isolating the expressed antigen binding protein.

147. A pharmaceutical composition comprising the antigen binding protein of any of the preceding claims and a pharmaceutically acceptable excipient.

148. A method of treating cancer in a subject, comprising administering to the subject an effective amount of the antigen binding protein of any of the preceding claims or a

pharmaceutical composition of claim 147, optionally wherein the cancer is selected from a solid tumor and a hematological tumor.

149. The method of claim 148, wherein the cancer expresses or is predicted to express the HLA-PEPTIDE target.

150. A kit comprising the antigen binding protein of any of the preceding claims or a pharmaceutical composition of claim 147 and instructions for use.

151. A composition comprising at least one HLA-PEPTIDE target of claim 97 and an adjuvant.

152. A composition comprising at least one HLA-PEPTIDE target of claim 97 and a pharmaceutically acceptable excipient.

153. A composition comprising an amino acid sequence comprising a polypeptide of at least one HLA-PEPTIDE target disclosed in Table A, optionally the amino acid sequence consisting essentially of or consisting of the polypeptide.

154. A virus comprising the isolated polynucleotide or set of polynucleotides of any of the preceding claims.

155. The virus of claim 154, wherein the virus is a filamentous phage.

156. A yeast cell comprising the isolated polynucleotide or set of polynucleotides of any of the preceding claims.

157. A method of identifying an antigen binding protein of any of the preceding claims, comprising providing at least one HLA-PEPTIDE target listed in Table A; and binding the at least one target with the antigen binding protein, thereby identifying the antigen binding protein.

158. The method of claim 157, wherein the antigen binding protein is present in a phage display library comprising a plurality of distinct antigen binding proteins.

159. The method of claim 158, wherein the phage display library is substantially free of antigen binding proteins that non-specifically bind the HLA of the HLA-PEPTIDE target.

160. The method of claim 157, wherein the antigen binding protein is present in a TCR library comprising a plurality of distinct TCRs or antigen binding fragments thereof.

161. The method of any one of claims 157-160, wherein the binding step is performed more than once, optionally at least three times.

162. The method of any one of claims 157-161, further comprising contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target to determine if the antigen binding protein selectively binds the HLA-PEPTIDE target, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to soluble target HLA-PEPTIDE complexes versus soluble HLA-PEPTIDE complexes that are distinct from target complexes, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to target HLA-PEPTIDE complexes expressed on the surface of one or more cells versus HLA-PEPTIDE complexes that are distinct from target complexes expressed on the surface of one or more cells.

163. A method of identifying an antigen binding protein of any of the preceding claims, comprising obtaining at least one HLA-PEPTIDE target listed in Table A; administering the HLA-PEPTIDE target to a subject, optionally in combination with an adjuvant; and isolating the antigen binding protein from the subject.

164. The method of claim 163, wherein isolating the antigen binding protein comprises screening the serum of the subject to identify the antigen binding protein.

165. The method of claim 163, further comprising contacting the antigen binding protein with one or more peptide-HLA complexes that are distinct from the HLA-PEPTIDE target to determine if the antigen binding protein selectively binds to the HLA-PEPTIDE target, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to soluble target HLA-PEPTIDE complexes versus soluble HLA-PEPTIDE complexes that are distinct from target complexes, optionally wherein selectivity is determined by measuring binding affinity of the antigen binding protein to target HLA-PEPTIDE complexes expressed on the surface of one or more cells versus HLA-PEPTIDE complexes that are distinct from target complexes expressed on the surface of one or more cells.

166. The method of claim 163, wherein the subject is a mouse, a rabbit, or a llama.

167. The method of claim 163, wherein isolating the antigen binding protein comprises isolating a B cell from the subject that expresses the antigen binding protein and optionally directly cloning sequences encoding the antigen binding protein from the isolated B cell.

168. The method of claim 167, further comprising creating a hybridoma using the B cell.

169. The method of claim 167, further comprising cloning CDRs from the B cell.

170. The method of claim 167, further comprising immortalizing the B cell, optionally via EBV transformation.

171. The method of claim 167, further comprising creating a library that comprises the antigen binding protein of the B cell, optionally wherein the library is phage display or yeast display.

172. The method of claim 163, further comprising humanizing the antigen binding protein.

173. A method of identifying an antigen binding protein of any of the preceding claims, comprising obtaining a cell comprising the antigen binding protein; contacting the cell with an HLA-multimer comprising at least one HLA-PEPTIDE target listed in Table A; and identifying the antigen binding protein via binding between the HLA-multimer and the antigen binding protein.

174. A method of identifying an antigen binding protein of any of the preceding claims, comprising obtaining one or more cells comprising the antigen binding protein; activating the one or more cells with at least one HLA-PEPTIDE target listed in Table A presented on a natural or an artificial antigen presenting cell (APC); and identifying the antigen binding protein via selection of one or more cells activated by interaction with at least one HLA-PEPTIDE target listed in Table A.

175. The method of claim 173 or 174, wherein the cell is a T cell, optionally a CTL.

176. The method of claim 173 or 174, further comprising isolating the cell, optionally using flow cytometry, magnetic separation, or single cell separation.

177. The method of claim 176, further comprising sequencing the antigen binding protein.

178. A method of identifying an antigen binding protein of any of the preceding claims, comprising providing at least one HLA-PEPTIDE target listed in Table A; and identifying the antigen binding protein using the target.

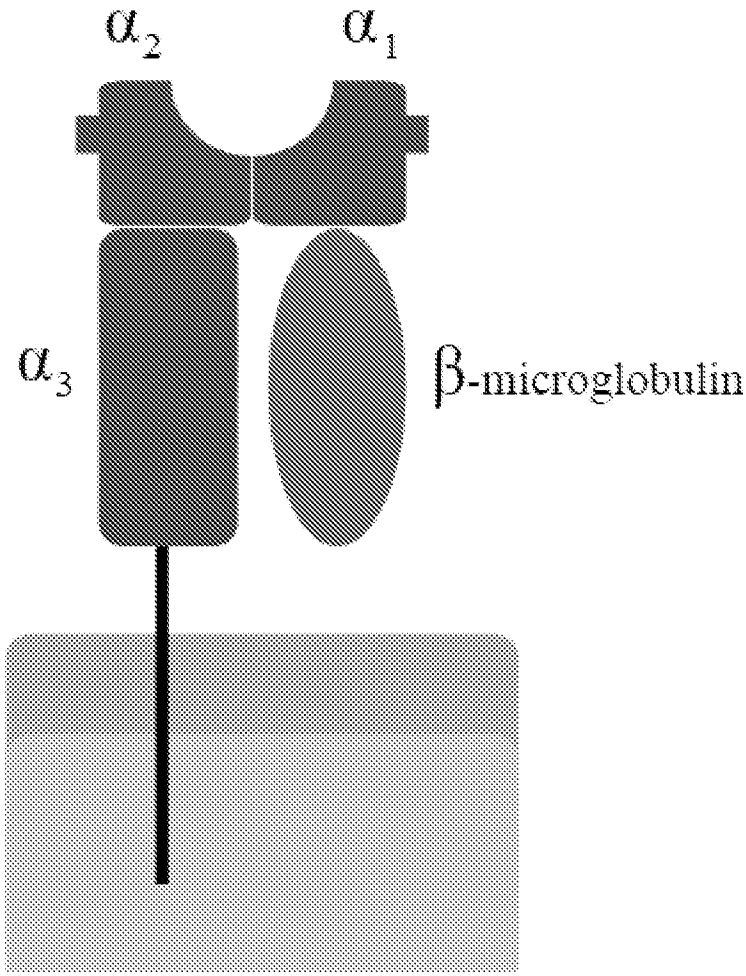


FIG. 1

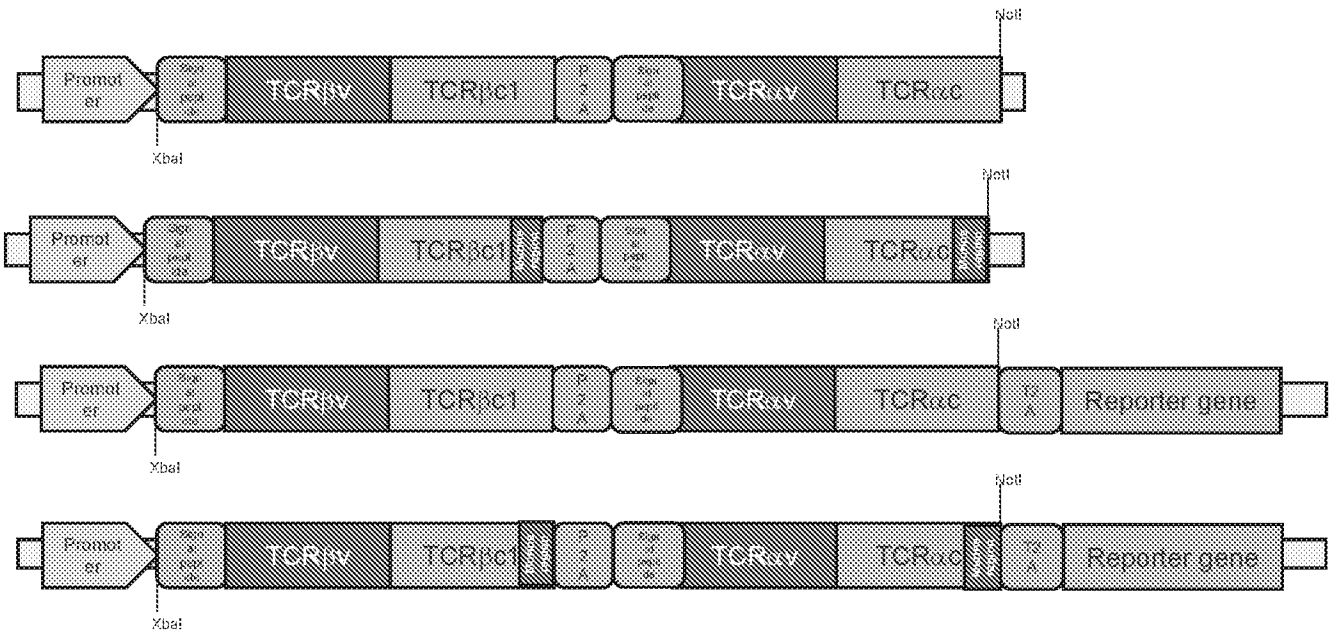
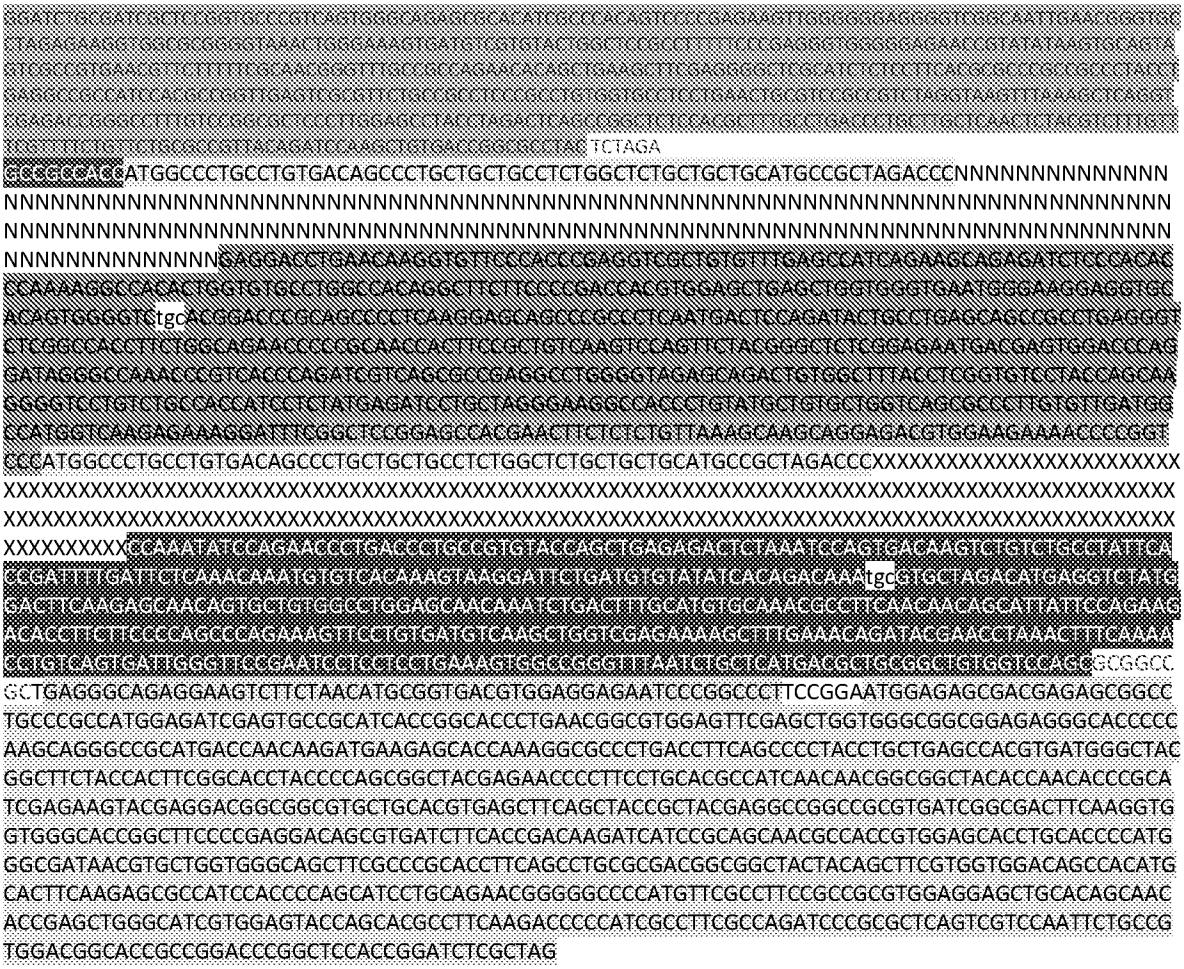


FIG. 2



EF1a Promoter
XbaI Restriction Site
KozAK
CD8 Signal Peptide
Beta Variable-NNNNNNNNNN
Beta Constant
Introduced Cysteine for preferential pairing
P2A Peptide
CD8 Signal Peptide
Alpha Variable-XXXXXXXXXXX
Alpha Constant
Cysteine
NotI Restriction Site
T2A Peptide
Copepod GFP

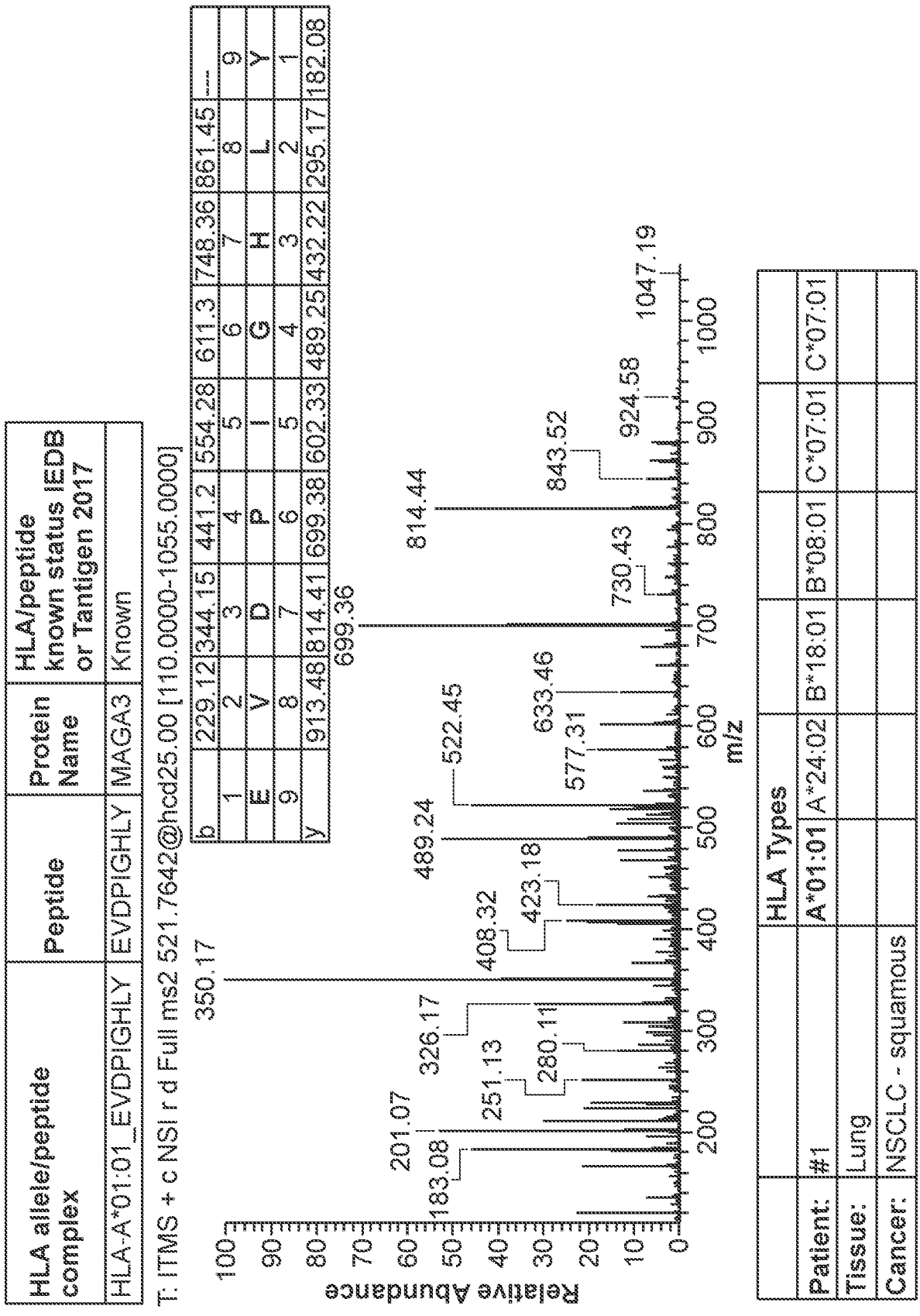
FIG. 3

LLASSILCA-specific TCR complex element (TCR# 21)

FIG. 4

EVDPIGHLY-specific TCR complex element (TCR# 53)

FIG. 5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Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
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EVDPIGHLY
MAGA3
Known
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b 229.12 344.15 441.2 554.28 611.3 748.36 861.45 ---
1 2 3 4 5 6 7 8 9
E V D P I G H L Y
9 8 7 6 5 4 3 2 1
y 913.48 814.41 699.38 602.33 489.25 432.22 295.17 182.08
Relative Abundance
m/z
HLA Types
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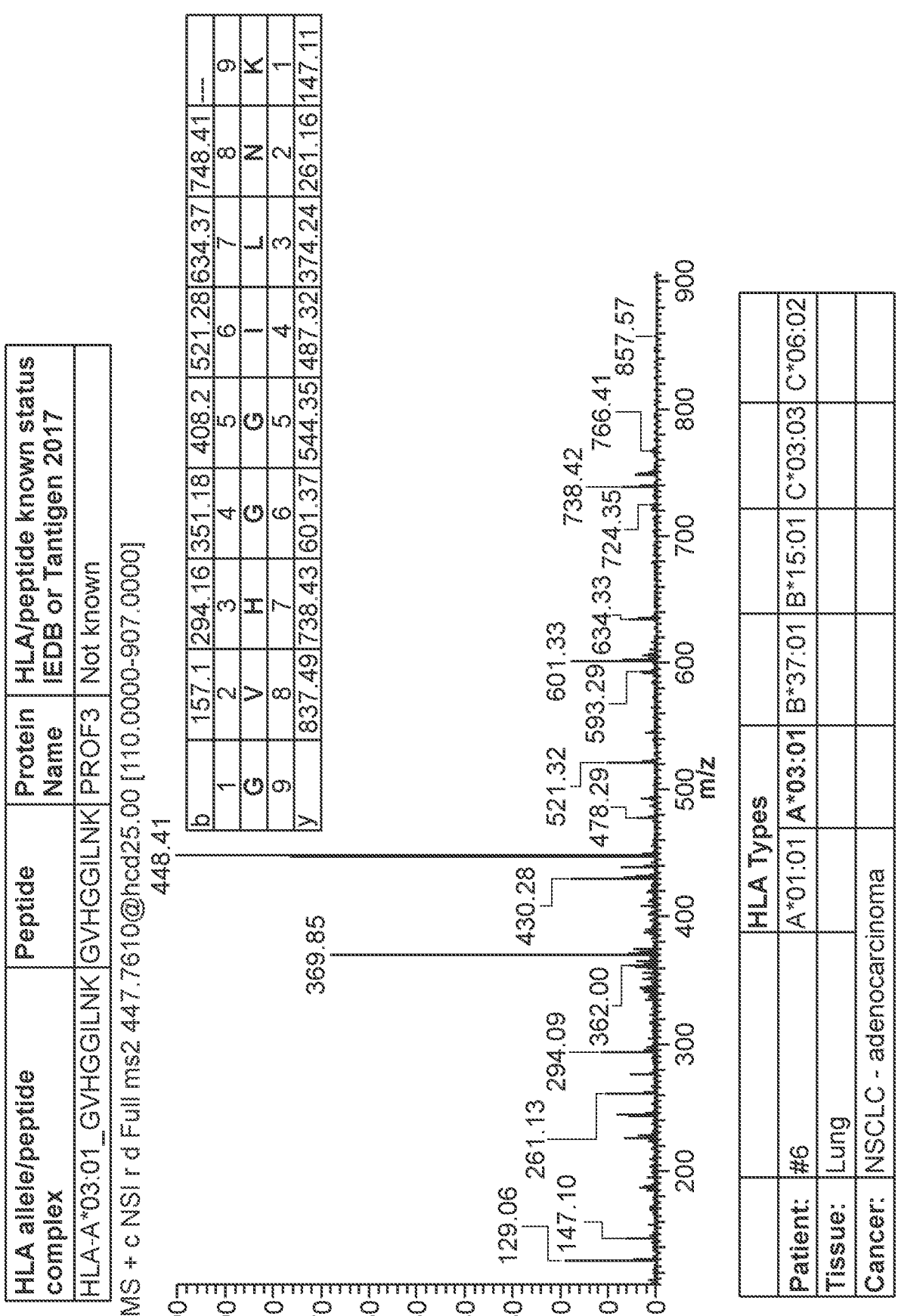
Tissue: Lung
Cancer: NSCLC - squamous

FIG. 6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Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
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GVHGGILNK
PROF3
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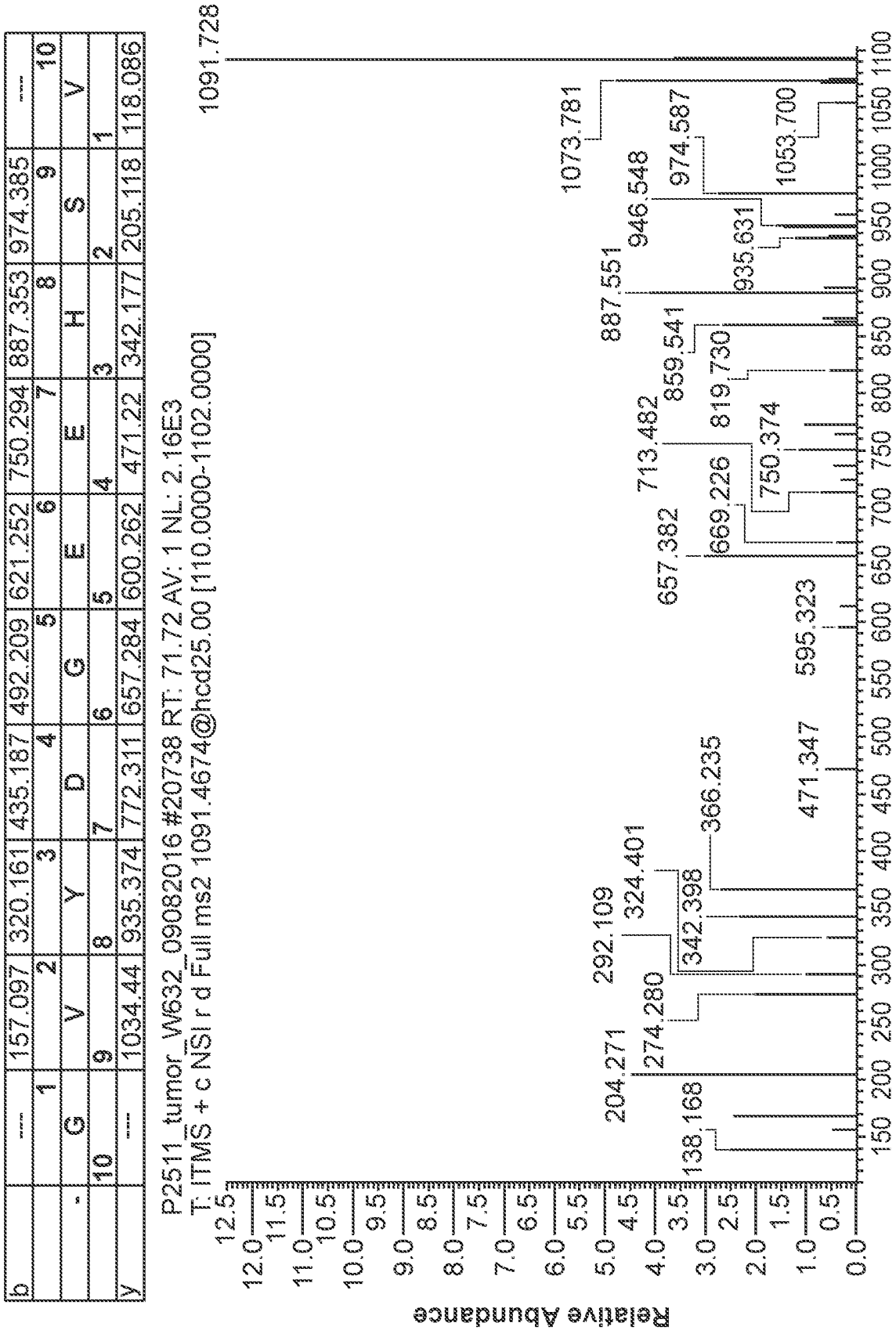
G V H G G I L N K
9 8 7 6 5 4 3 2 1
y 837.49 738.43 601.37 544.35 487.32 374.24 261.16 147.11
Relative Abundance
m/z
HLA Types
Patient: #6 A*01:01 A*03:01 B*37:01 B*15:01 C*03:03 C*06:02
Tissue: Lung
Cancer: NSCLC - adenocarcinoma

FIG. 7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1091.728
1073.781
946.548
974.587
887.551
935.631
1053.700
859.541
713.482
819.730
657.382
669.226
750.374
595.323
471.347
366.235
342.398
324.401
292.109
274.280
204.271
138.168

FIG. 7A

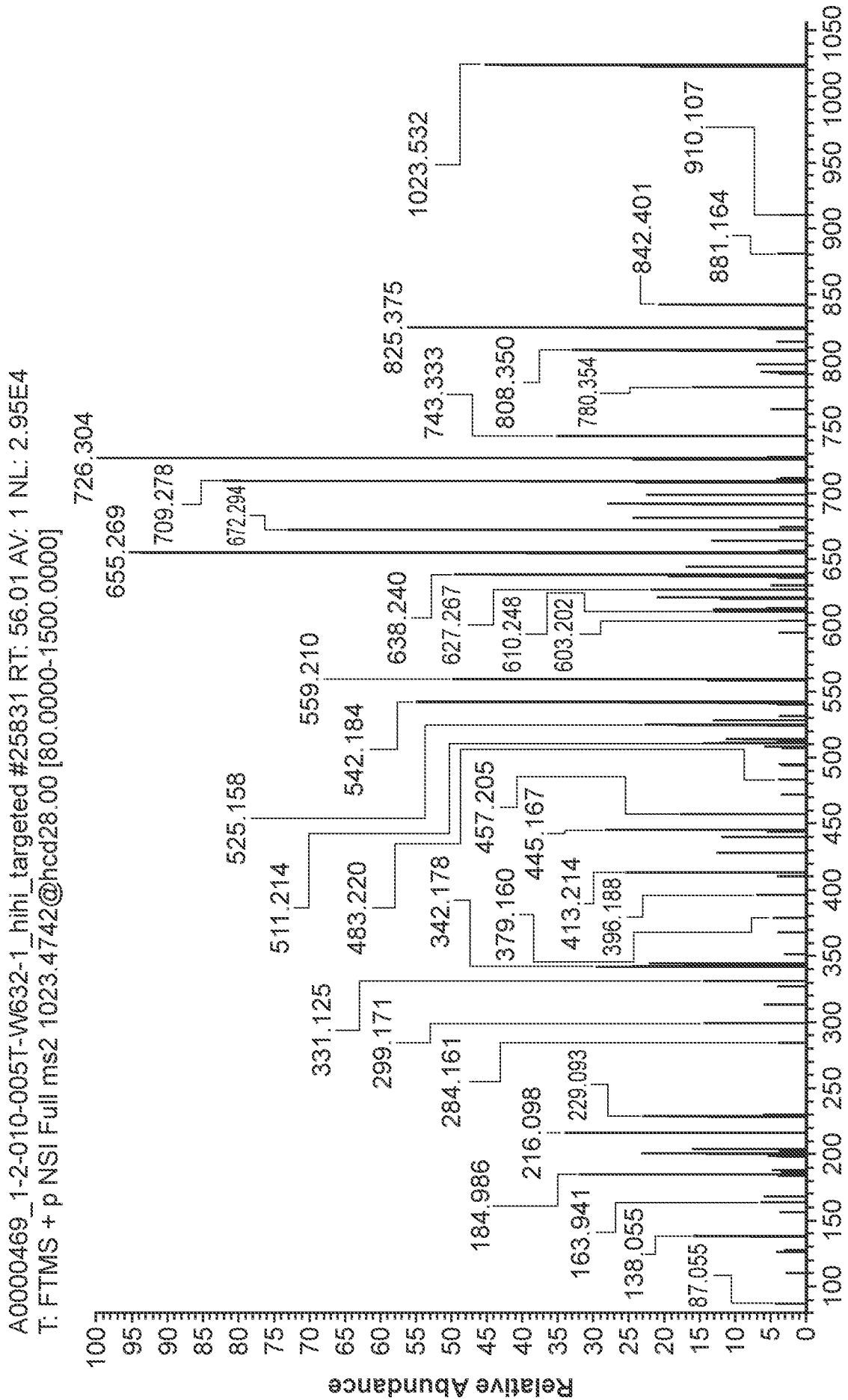

A0000469_1-2-010-005T-W632-1_hihi_targeted #25831 RT: 56.01 AV: 1 NL: 2.95E4
T: FTMS + p NSI Full ms2 1023.4742@hcd28.00 [80.0000-1500.0000]
Relative Abundance
m/z
726.304
655.269
709.278
672.294
825.375
1023.532
743.333
808.350
780.354
842.401
910.107
881.164
559.210
638.240
627.267
610.248
603.202
525.158
542.184
511.214
483.220
457.205
445.167
342.178
379.160
413.214
396.188
331.125
299.171
284.161
229.093
216.098
184.986
163.941
138.055
87.055

FIG. 7B

b-NH3	---	199.0713	314.0983	428.1412	542.1841	655.2682	726.3053	825.3737	---
b-H2O	---	198.0873	313.1143	427.1572	541.2001	654.2842	725.3213	824.3897	---
b	---	216.0979	331.1248	445.1678	559.2107	672.2947	743.3319	842.4003	---
	1	2	3	4	5	6	7	8	9
-	N	T	D	N	N	L	A	V	Y
	9	8	7	6	5	4	3	2	1
C-terminal									
y	---	909.4312	808.3836	693.3566	579.3137	465.2708	352.1867	281.1496	182.0812
y-NH3	---	892.4047	791.357	676.3301	562.2871	---	---	---	---
y-H2O	---	891.4207	790.373	---	---	---	---	---	---

FIG. 7B (Cont.)

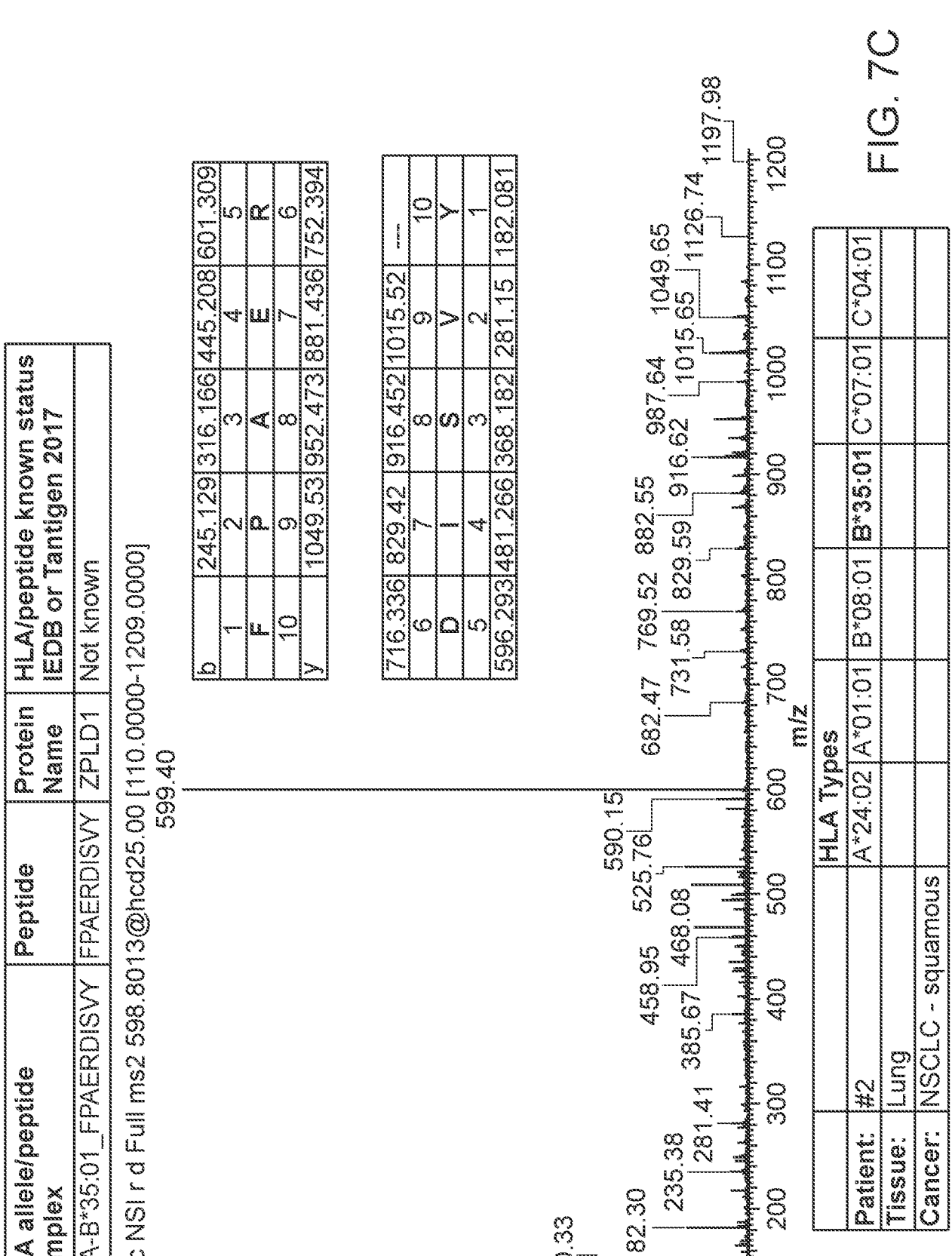

HLA allele/peptide complex
HLA-B*35:01_FPAERDISVY
Peptide
FPAERDISVY
Protein Name
ZPLD1
HLA/peptide known status IEDB or Tantigen 2017
Not known
T: ITMS + c NSI r d Full ms2 598.8013@hcd25.00 [110.0000-1209.0000]
Relative Abundance
m/z
b 245.129 316.166 445.208 601.309
1 2 3 4 5
F P A E R
10 9 8 7 6
y 1049.53 952.473 881.436 752.394
716.336 829.42 916.452 1015.52 ---
6 7 8 9 10
D I S V Y
5 4 3 2 1
596.293 481.266 368.182 281.15 182.081
HLA Types
Patient: #2
A*24:02 A*01:01 B*08:01 B*35:01 C*07:01 C*04:01
Tissue: Lung
Cancer: NSCLC - squamous

FIG. 7C

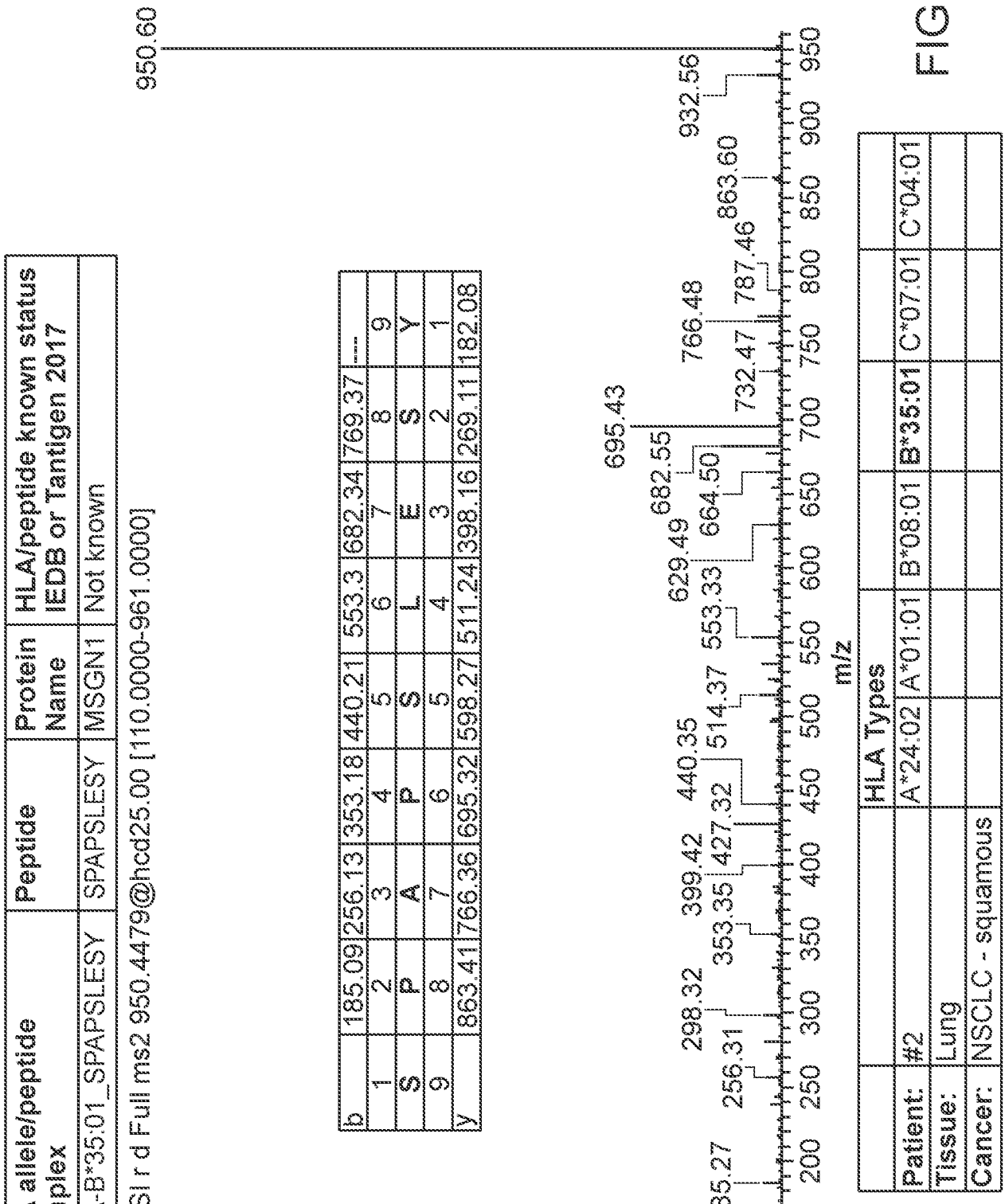

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-B*35:01_SPAPSLESY
SPAPSLESY
MSGN1
Not known
T: ITMS + c NSI r d Full ms2 950.4479@hcd25.00 [110.0000-961.0000]
Relative Abundance
m/z
b 185.09 256.13 353.18 440.21 553.3 682.34 769.37 ---
1 2 3 4 5 6 7 8 9
S P A P S L E S Y
9 8 7 6 5 4 3 2 1
y 863.41 766.36 695.32 598.27 511.24 398.16 269.11 182.08
HLA Types
Patient: #2 A*24:02 A*01:01 B*08:01 B*35:01 C*07:01 C*04:01
Tissue: Lung
Cancer: NSCLC - squamous

FIG. 7D

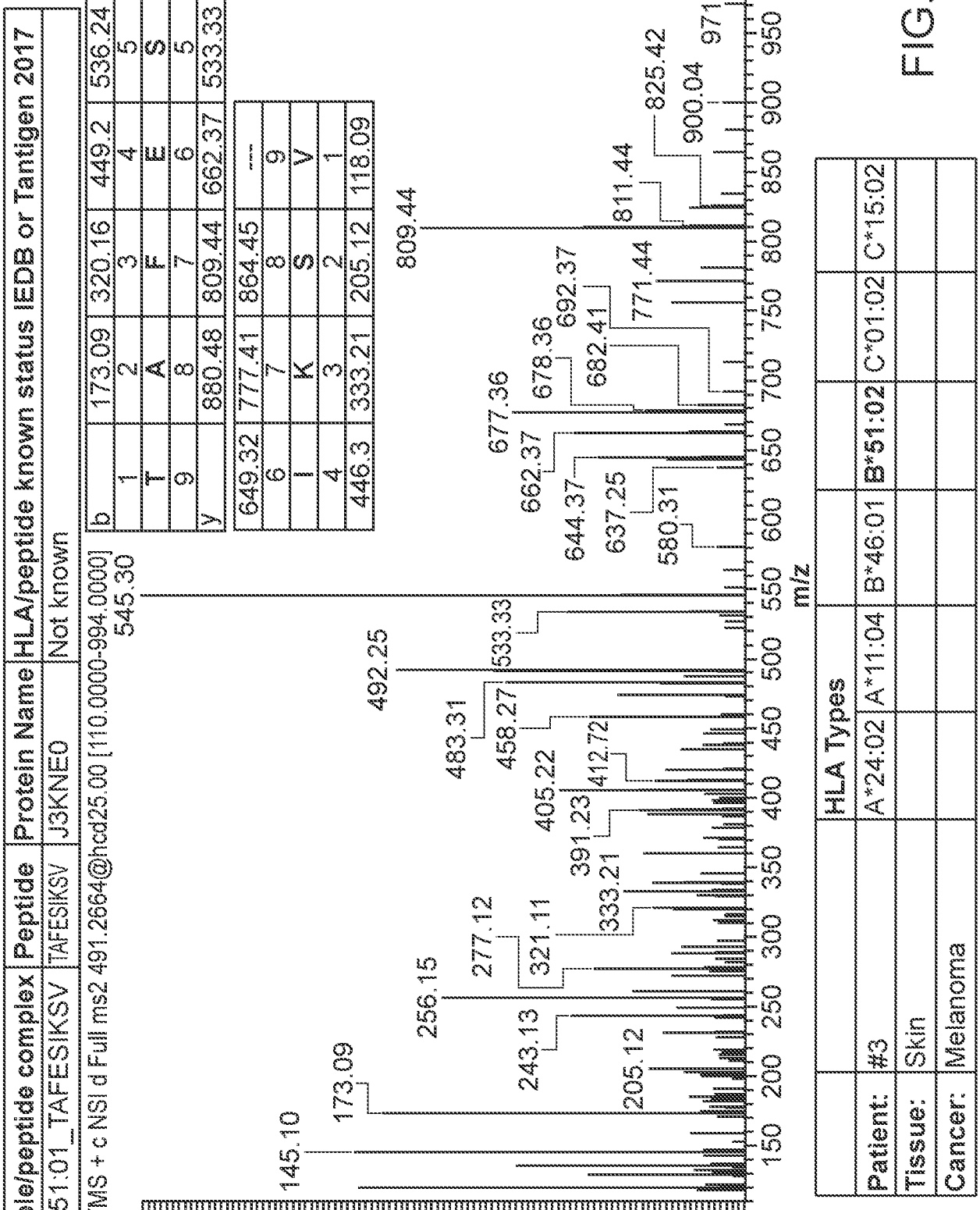

HLA allele/peptide complex
HLA-B*51:01_TAFESIKSV
Peptide
TAFESIKSV
Protein Name
J3KNE0
HLA/peptide known status IEDB or Tantigen 2017
Not known
T: FTMS + c NSI d Full ms2 491.2664@hcd25.00 [110.0000-994.0000]
b 173.09 320.16 449.2 536.24
1 2 3 4 5
T A F E S
9 8 7 6 5
y 880.48 809.44 662.37 533.33
649.32 777.41 864.45 ---
6 7 8 9
I K S V
4 3 2 1
446.3 333.21 205.12 118.09
Relative Abundance
m/z
HLA Types
Patient: #3 A*24:02 A*11:04 B*46:01 B*51:02 C*01:02 C*15:02
Tissue: Skin
Cancer: Melanoma

FIG. 7E

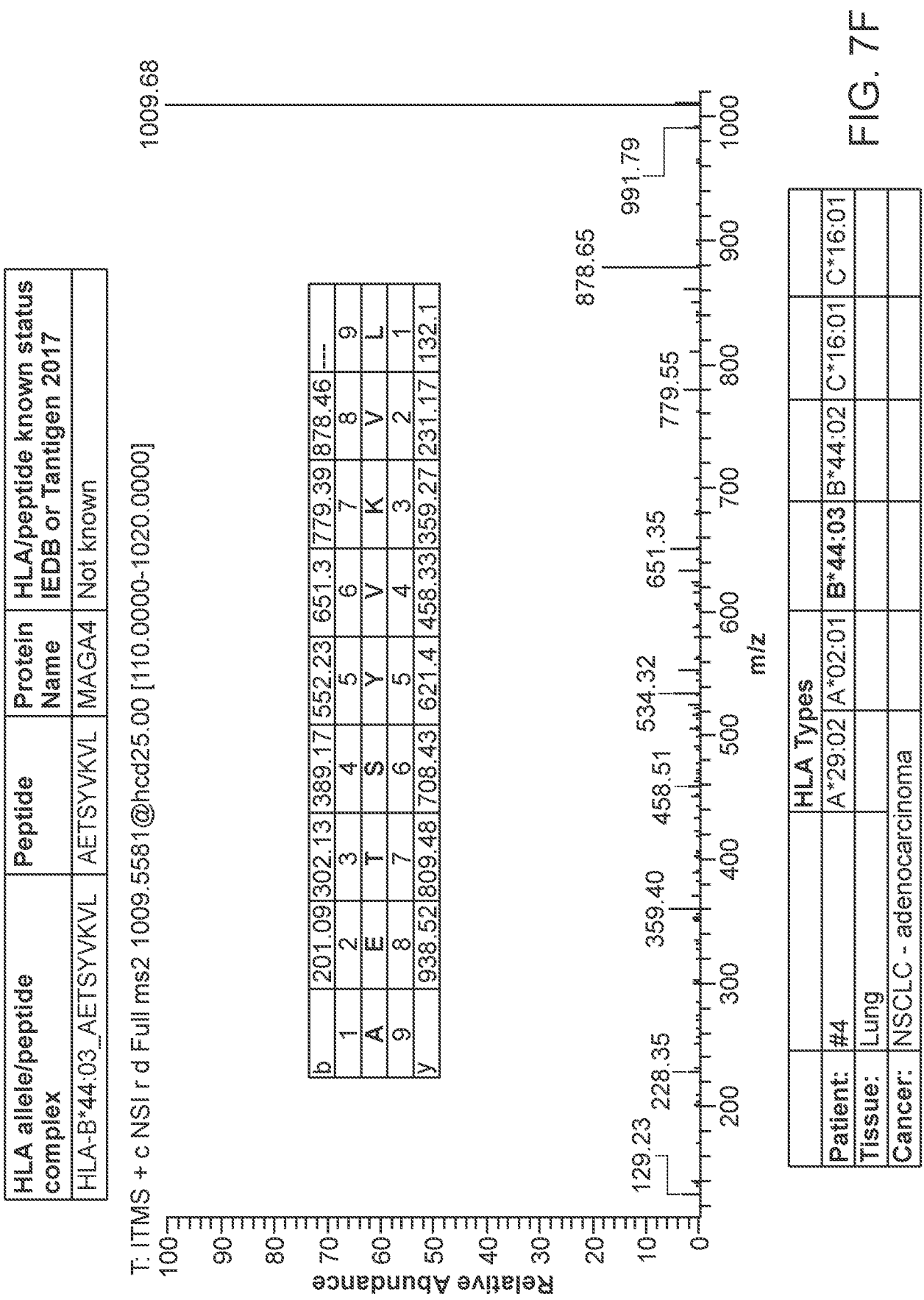

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-B*44:03_AETSYVKVL
AETSYVKVL
MAGA4
Not known
T: ITMS + c NSI r d Full ms2 1009.5581@hcd25.00 [110.0000-1020.0000]
b 201.09 302.13 389.17 552.23 651.3 779.39 878.46 ---
1 2 3 4 5 6 7 8 9
A E T S Y V K V L
9 8 7 6 5 4 3 2 1
y 938.52 809.48 708.43 621.4 458.33 359.27 231.17 132.1
Relative Abundance
m/z
129.23
228.35
359.40
458.51
534.32
651.35
779.55
878.65
991.79
1009.68
HLA Types
Patient: #4 A*29:02 A*02:01 B*44:03 B*44:02 C*16:01 C*16:01
Tissue: Lung
Cancer: NSCLC - adenocarcinoma

FIG. 7F

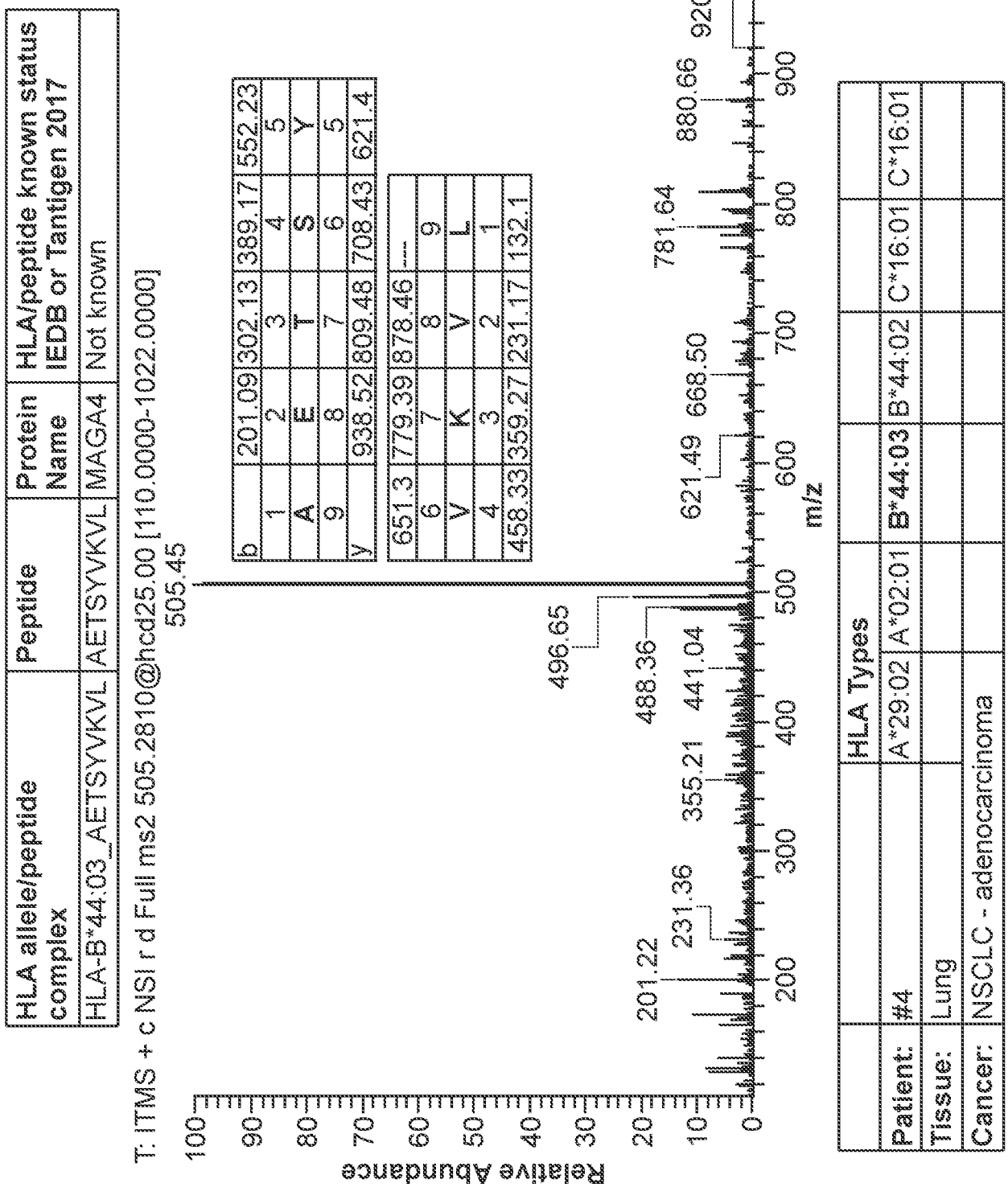

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-B*44:03_AETSYVKVL
AETSYVKVL
MAGA4
Not known
T: ITMS + c NSI r d Full ms2 505.2810@hcd25.00 [110.0000-1022.0000]
505.45
496.65
488.36
441.04
355.21
231.36
201.22
621.49
668.50
781.64
880.66
920.75
Relative Abundance
m/z
b 201.09 302.13 389.17 552.23
1 2 3 4 5
A E T S Y
9 8 7 6 5
y 938.52 809.48 708.43 621.4
651.3 779.39 878.46 ---
6 7 8 9
V K V L
4 3 2 1
458.33 359.27 231.17 132.1
HLA Types
Patient: #4 A*29:02 A*02:01 B*44:03 B*44:02 C*16:01 C*16:01
Tissue: Lung
Cancer: NSCLC - adenocarcinoma

FIG. 7G

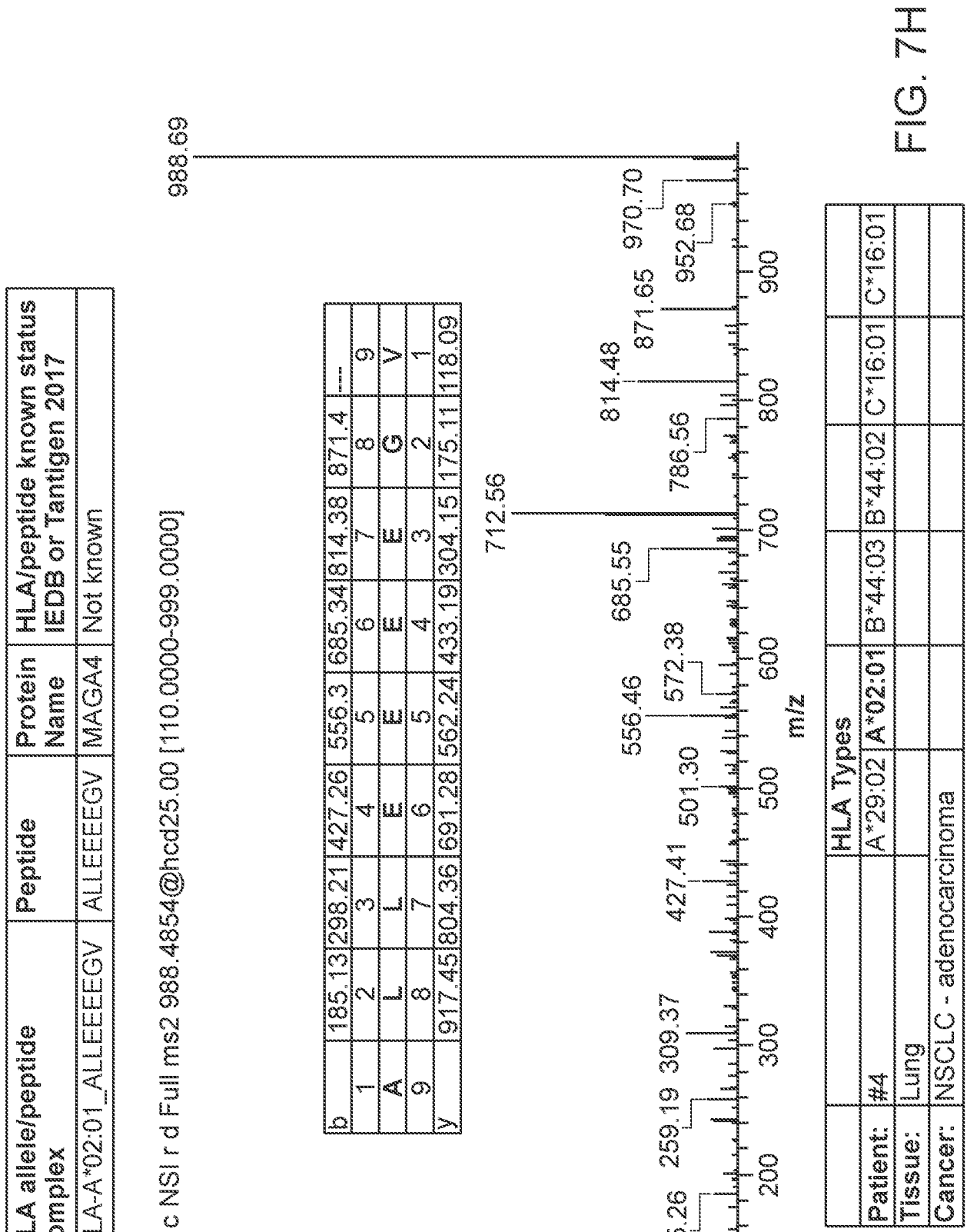

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-A*02:01_ALLEEEEEGV
ALLEEEEEGV
MAGA4
Not known
T: ITMS + c NSI r d Full ms2 988.4854@hcd25.00 [110.0000-999.0000]
Relative Abundance
m/z
b 185.13 298.21 427.26 556.3 685.34 814.38 871.4 ---
1 2 3 4 5 6 7 8 9
A L L E E E E G V
9 8 7 6 5 4 3 2 1
y 917.45 804.36 691.28 562.24 433.19 304.15 175.11 118.09
HLA Types
Patient: #4 A*29:02 A*02:01 B*44:03 B*44:02 C*16:01 C*16:01
Tissue: Lung
Cancer: NSCLC - adenocarcinoma

FIG. 7H

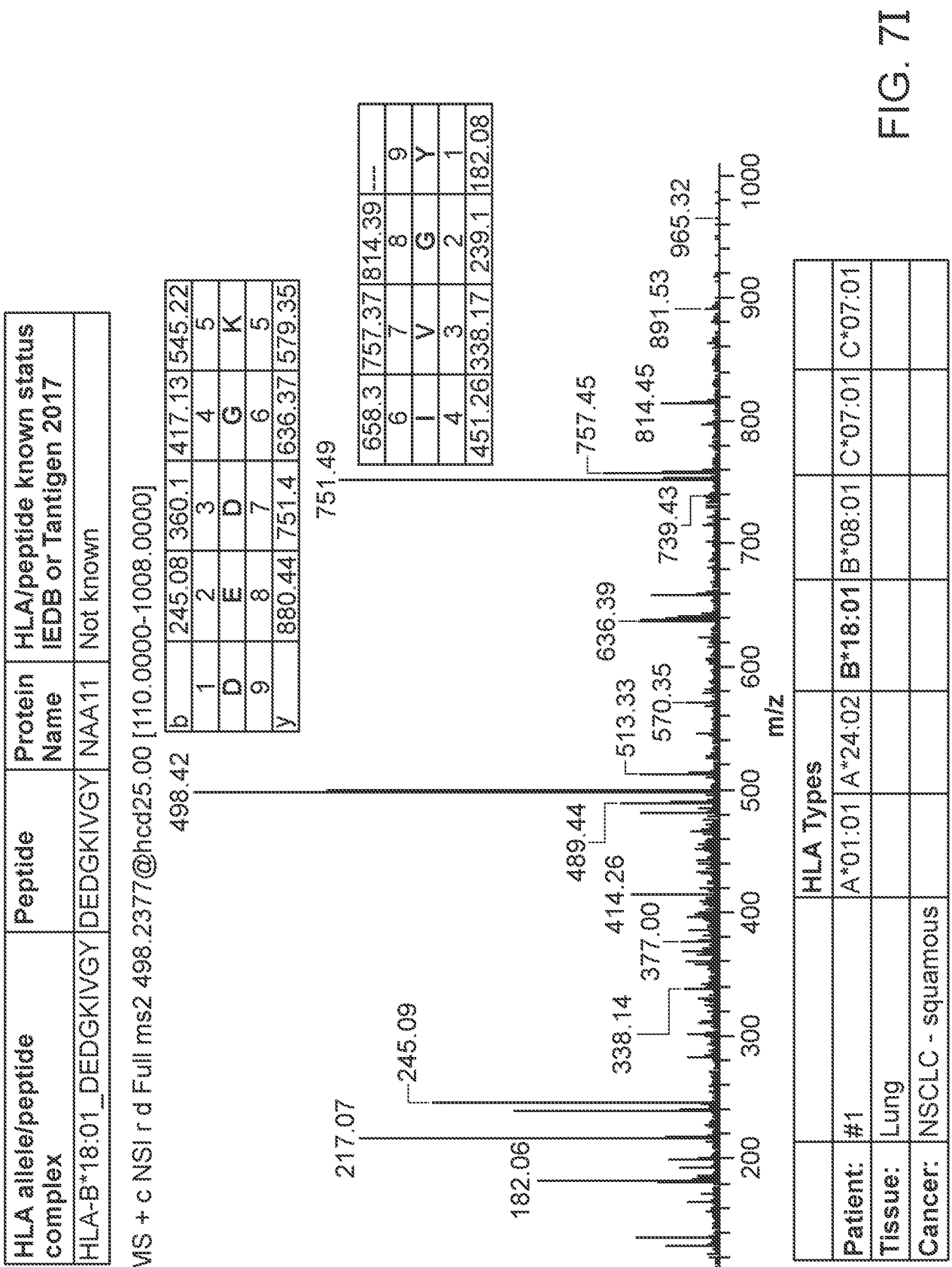

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-B*18:01_DEDGKIVGY
DEDGKIVGY
NAA11
Not known
T: ITMS + c NSI r d Full ms2 498.2377@hcd25.00 [110.0000-1008.0000]
b 245.08 360.1 417.13 545.22
1 2 3 4 5
D E D G K
9 8 7 6 5
y 880.44 751.4 636.37 579.35
658.3 757.37 814.39 ---
6 7 8 9
I V G Y
4 3 2 1
451.26 338.17 239.1 182.08
Relative Abundance
m/z
498.42
751.49
757.45
814.45
891.53
965.32
739.43
636.39
513.33
570.35
489.44
414.26
377.00
338.14
245.09
217.07
182.06
HLA Types
Patient: #1 A*01:01 A*24:02 B*18:01 B*08:01 C*07:01 C*07:01
Tissue: Lung
Cancer: NSCLC - squamous

FIG. 7I

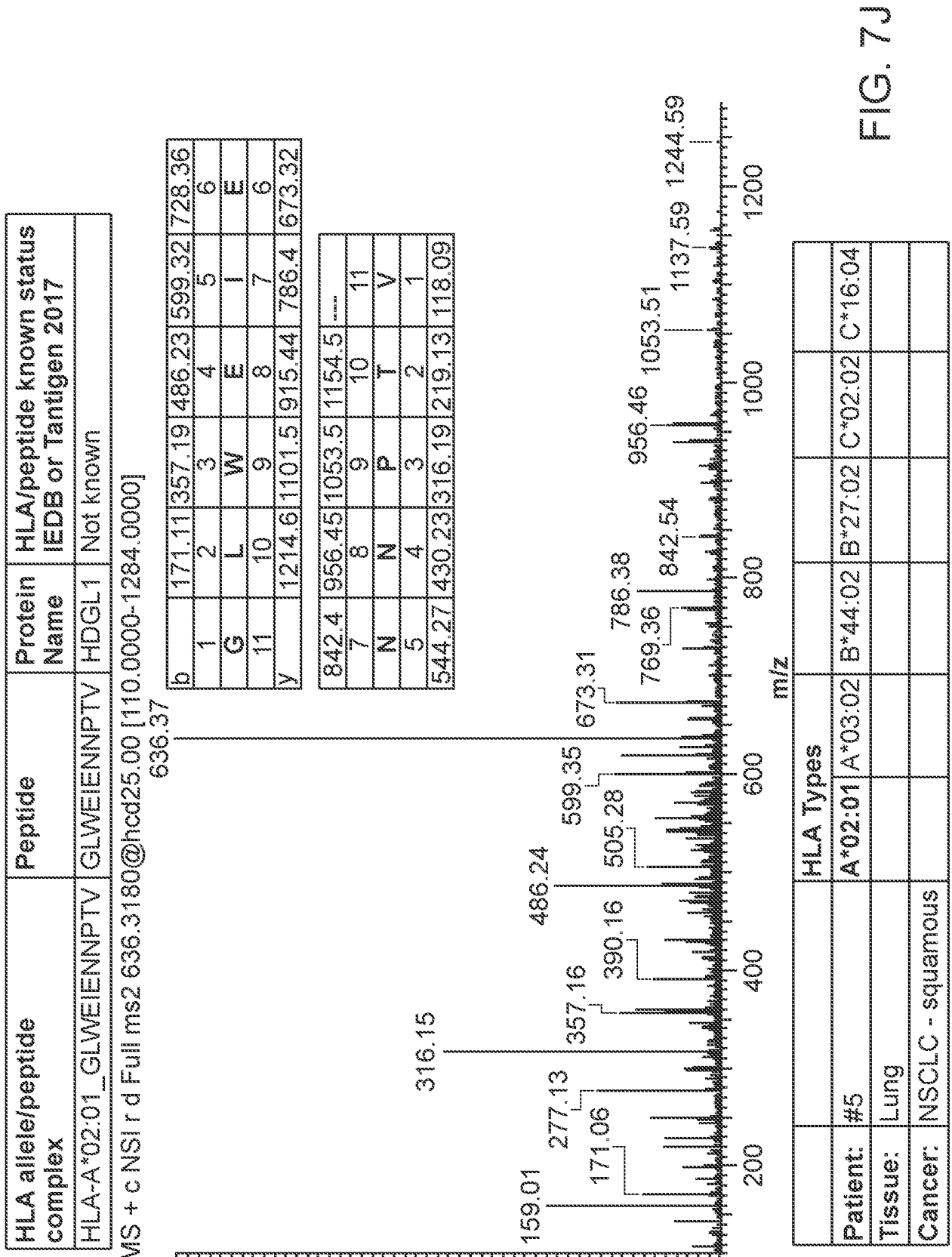

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-A*02:01_GLWEIENNPTV
GLWEIENNPTV
HDGL1
Not known
T: ITMS + c NSI r d Full ms2 636.3180@hcd25.00 [110.0000-1284.0000]
b 171.11 357.19 486.23 599.32 728.36
1 2 3 4 5 6
G L W E I E
11 10 9 8 7 6
y 1214.6 1101.5 915.44 786.4 673.32
842.4 956.45 1053.5 1154.5 ---
7 8 9 10 11
N N P T V
5 4 3 2 1
544.27 430.23 316.19 219.13 118.09
HLA Types
Patient: #5 A*02:01 A*03:02 B*44:02 B*27:02 C*02:02 C*16:04
Tissue: Lung
Cancer: NSCLC - squamous
Relative Abundance
m/z
636.37
316.15
159.01
277.13
171.06
357.16
390.16
486.24
505.28
599.35
673.31
769.36
786.38
842.54
956.46
1053.51
1137.59
1244.59

FIG. 7J

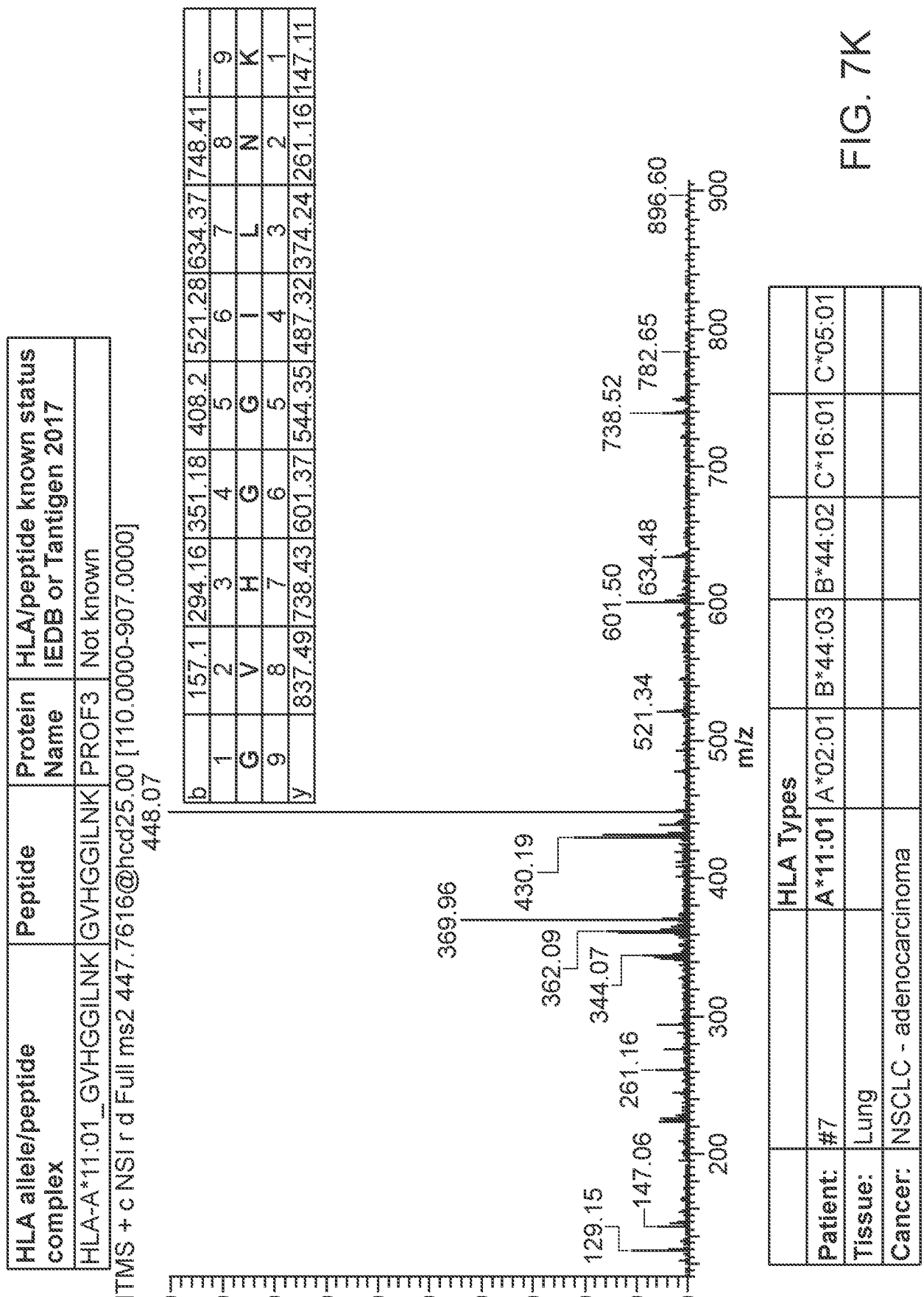

HLA allele/peptide complex
Peptide
Protein Name
HLA/peptide known status IEDB or Tantigen 2017
HLA-A*11:01_GVHGGILNK
GVHGGILNK
PROF3
Not known
T: ITMS + c NSI r d Full ms2 447.7616@hcd25.00 [110.0000-907.0000]
448.07
b 157.1 294.16 351.18 408.2 521.28 634.37 748.41 ---
1 2 3 4 5 6 7 8 9
G V H G G I L N K
9 8 7 6 5 4 3 2 1
y 837.49 738.43 601.37 544.35 487.32 374.24 261.16 147.11
Relative Abundance
m/z
HLA Types
Patient: #7 A*11:01 A*02:01 B*44:03 B*44:02 C*16:01 C*05:01
Tissue: Lung
Cancer: NSCLC - adenocarcinoma

FIG. 7K

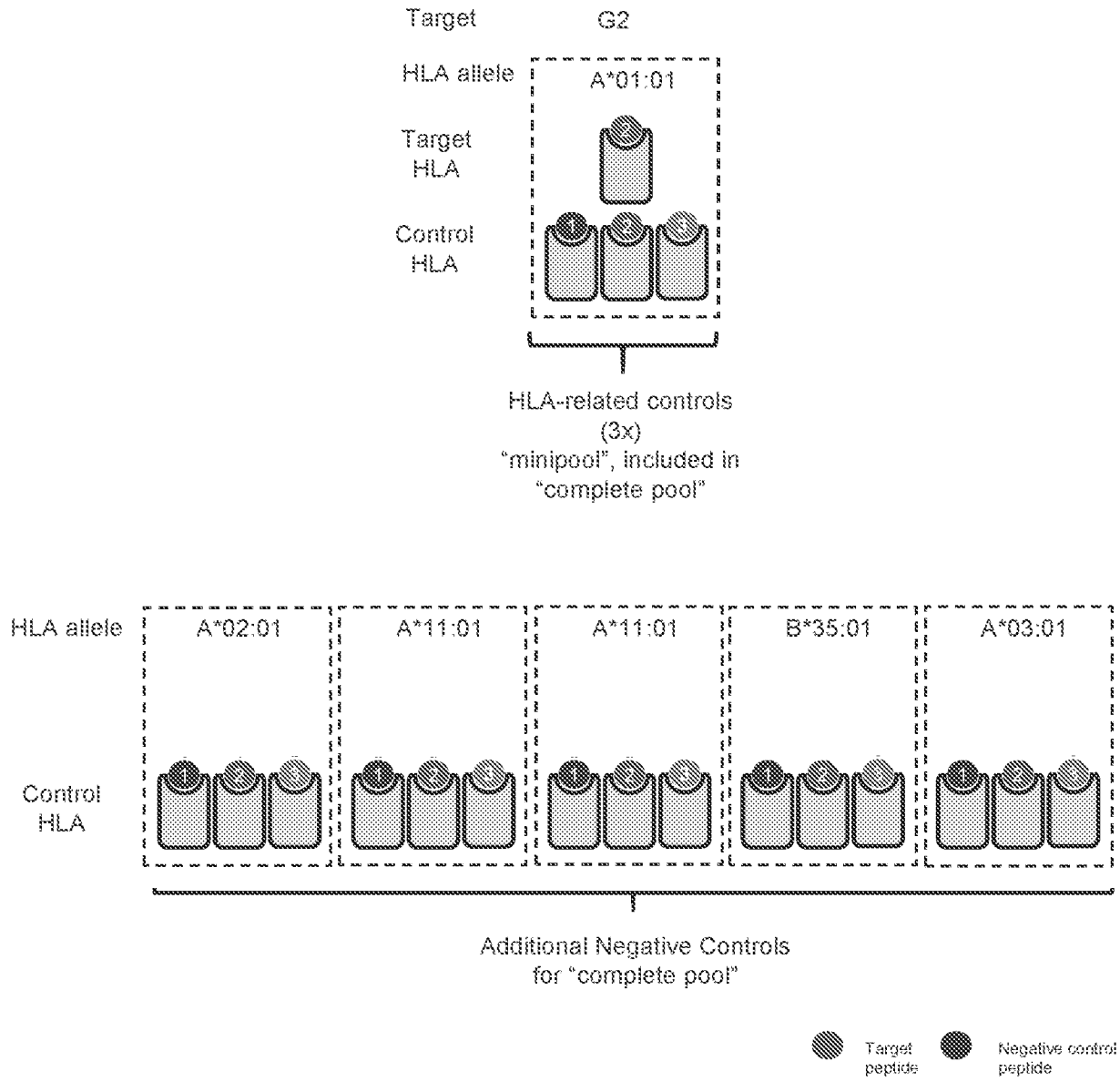

Target
G2
HLA allele
A*01:01
Target HLA
Control HLA
1
2
3
HLA-related controls (3x) "minipool", included in "complete pool"
HLA allele
A*02:01
A*11:01
A*11:01
B*35:01
A*03:01
Control HLA
Additional Negative Controls for "complete pool"
Target peptide
Negative control peptide

FIG. 8

A

G2	HLA	Peptide	Stability
Target	HLA-A*01:01	NTDNNLAVY	73%
Neg Ctrl 1	HLA-A*01:01	YSEHPTFTSQY	96%
Neg Ctrl 2	HLA-A*01:01	VSDGGPNLY	89%
Neg Ctrl 3	HLA-A*01:01	ATDALMTGY	76%

B

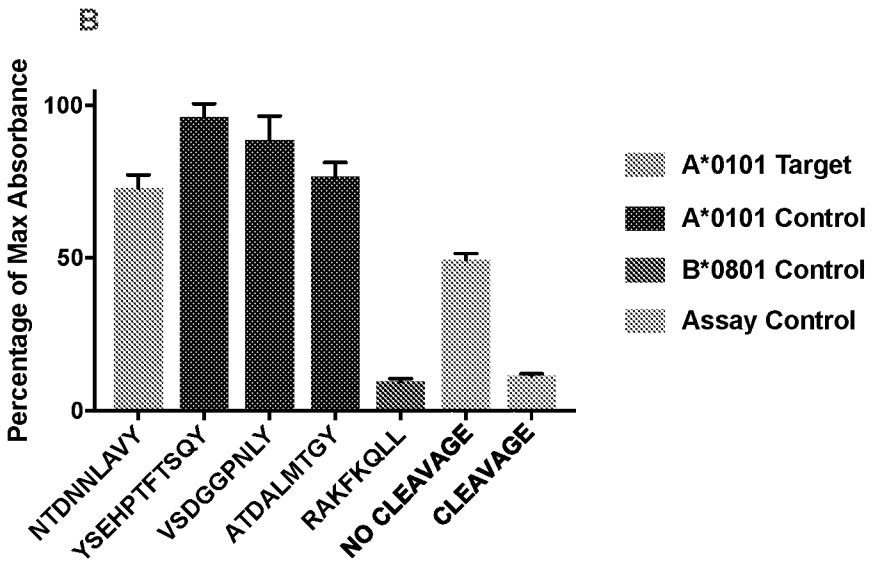


FIG. 9

G1	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*02:01	LL[F]GYPV[Y]V	95%
Neg Ctrl 2	HLA-A*02:01	GILG[F]VFTL	83%
Neg Ctrl 3	HLA-A*02:01	[F]LLTRILTI	83%

G3	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*11:01	IVTD[F]SVIK	64%
Neg Ctrl 2	HLA-A*11:01	KSMREE[Y]RK	46%
Neg Ctrl 3	HLA-A*11:01	SSCSSCPLSK	69%

G4	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*11:01	AFIGTAM[Y]K	90%
Neg Ctrl 2	HLA-A*11:01	AV[F]DRKSDAK	49%
Neg Ctrl 3	HLA-A*11:01	SIIPSGPLK	80%

G5	HLA	Peptide	Stability
Neg Ctrl 1	HLA-B*35:01	IPSINVHH[Y]	93%
Neg Ctrl 2	HLA-B*35:01	EPLPQGQLTA[Y]	81%
Neg Ctrl 3	HLA-B*35:00	VPLDED[F]RK[Y]	70%

G6	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*03:01	RLRAEAQVK	54%
Neg Ctrl 2	HLA-A*03:01	RLRPGGKKK	57%
Neg Ctrl 3	HLA-A*03:01	QVPLRPM[F]FK	63%

FIG. 10

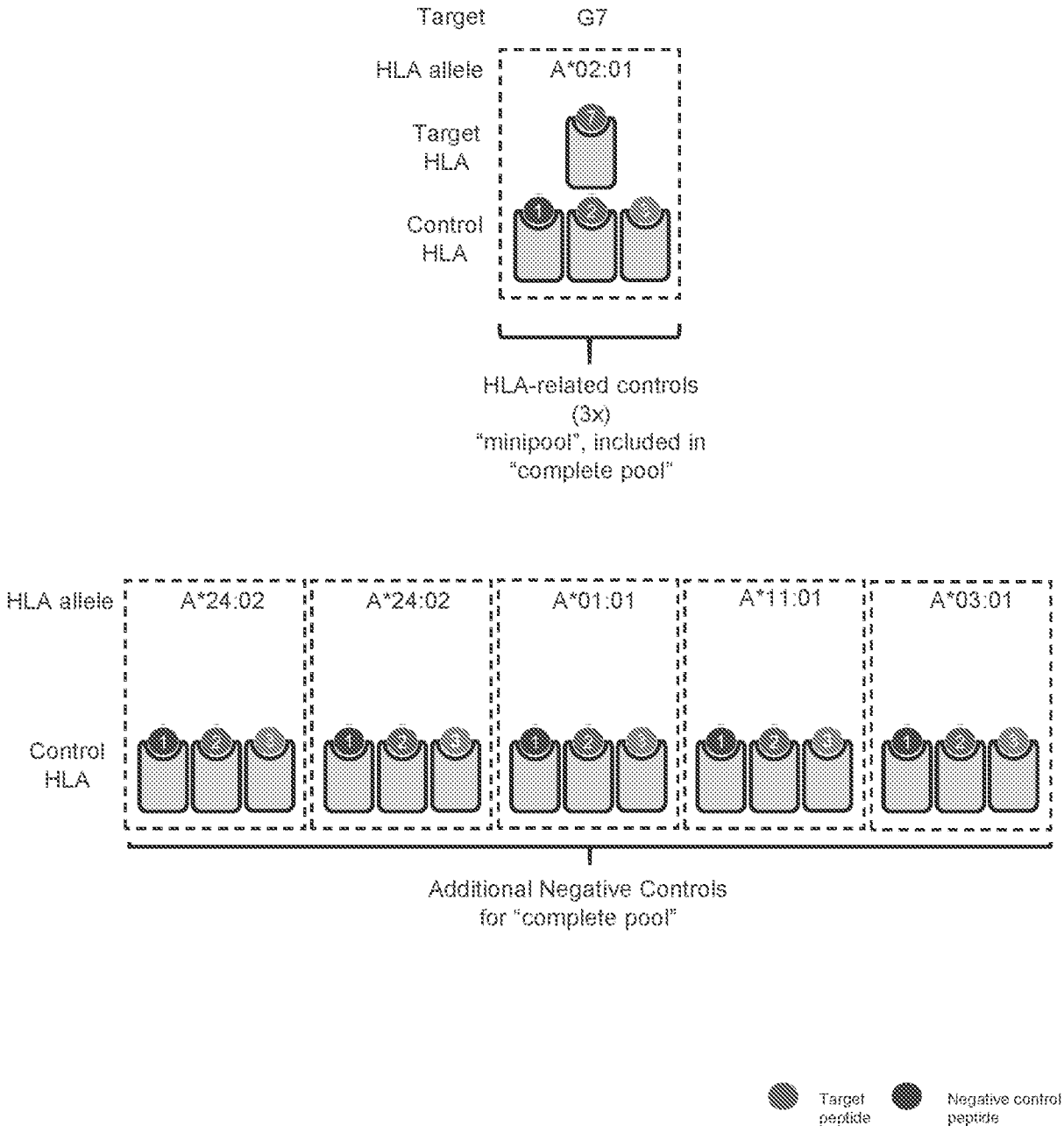

Target
G7
HLA allele
A*02:01
Target HLA
Control HLA
HLA-related controls (3x) "minipool", included in "complete pool"
HLA allele
A*24:02
A*24:02
A*01:01
A*11:01
A*03:01
Control HLA
Additional Negative Controls for "complete pool"
Target peptide
Negative control peptide

FIG. 11

G3	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*11:01	IVTD[F]SVIK	64%
Neg Ctrl 2	HLA-A*11:01	K[S]MREE[F]RK	46%
Neg Ctrl 3	HLA-A*11:01	SSCS[S]CPL[S]K	69%

G6	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*03:01	RLRAEAQVK	54%
Neg Ctrl 2	HLA-A*03:01	RLRPG[G]KKK	57%
Neg Ctrl 3	HLA-A*03:01	QVPLRPMT[Y]K	63%

G8	HLA	Peptide	Stability
Neg Ctrl 1	A*24:02**	Q[Y]DPVAAL[F]	78%
Neg Ctrl 2	A*24:02**	T[Y]GPV[W]MSL	86%
Neg Ctrl 3	A*24:02**	K[Y]TS[F]P[W]LL	94%

G9	HLA	Peptide	Stability
Neg Ctrl 1	A*24:02	T[Y]GPV[W]MCL	91%
Neg Ctrl 2	A*24:02	R[Y]LKDQQLL	53%
Neg Ctrl 3	A*24:02	P[Y]L[W]LAAI	55%

G10	HLA	Peptide	Stability
Neg Ctrl 1	HLA-A*01:01	[Y]SEHPT[F]TSQ[Y]	96%
Neg Ctrl 2	HLA-A*01:01	VSDGGPNL[Y]	89%
Neg Ctrl 3	HLA-A*01:01	AEDAIMTG[Y]	76%

FIG. 12

A

G7	HLA	Peptide	Stability
Target	A*02:01	LLASSILCA	71%
Neg Ctrl 1	A*02:01	LLFGYPVYV	94%
Neg Ctrl 2	A*02:01	GILGFVFTL	65%
Neg Ctrl 3	A*02:01	FLLTRILTI	74%

B

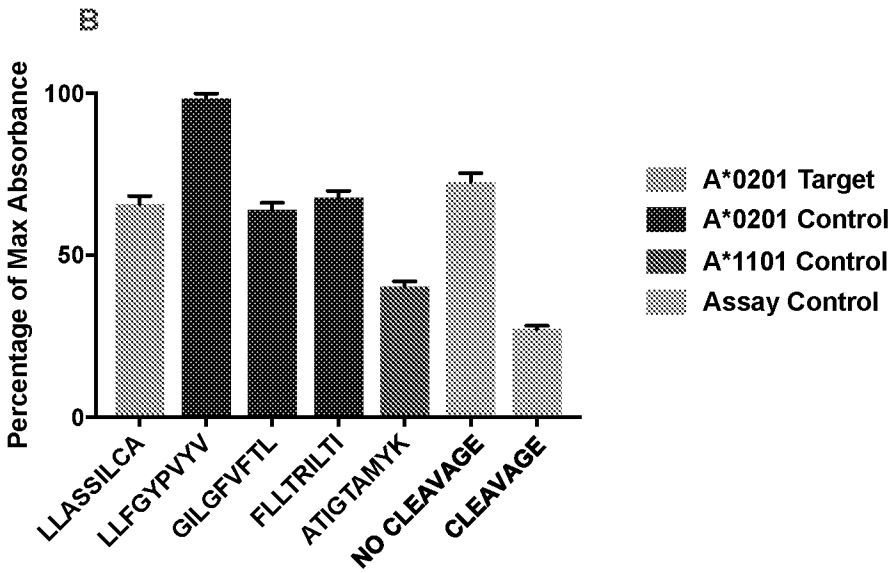
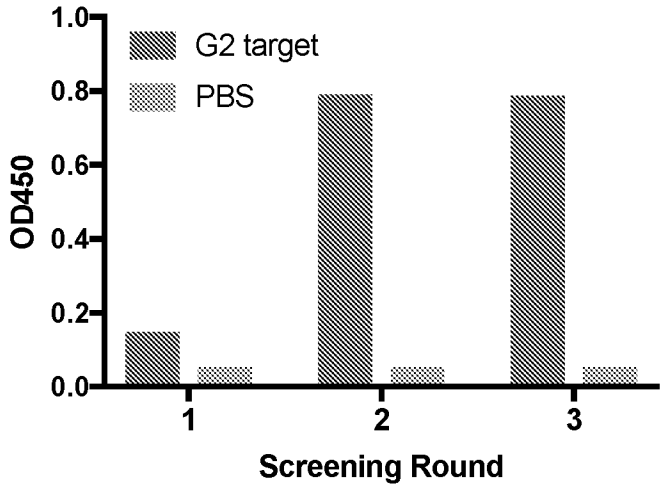


FIG. 13

A


1.0
0.8
0.6
0.4
0.2
0.0
OD450
G2 target
PBS
1
2
3
Screening Round

B

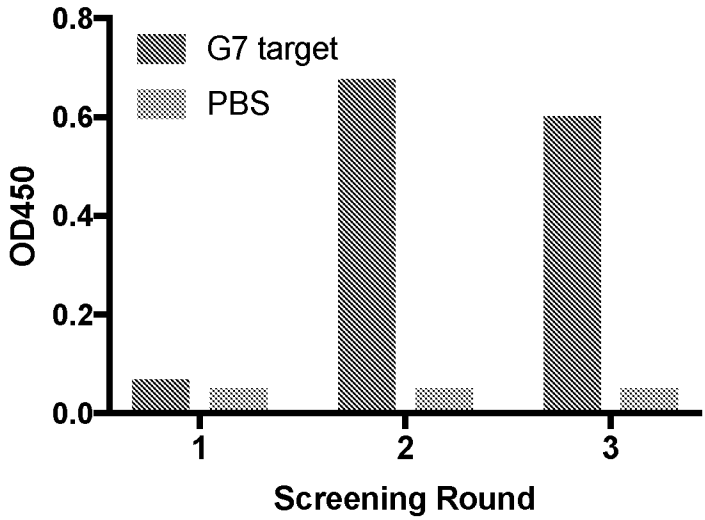
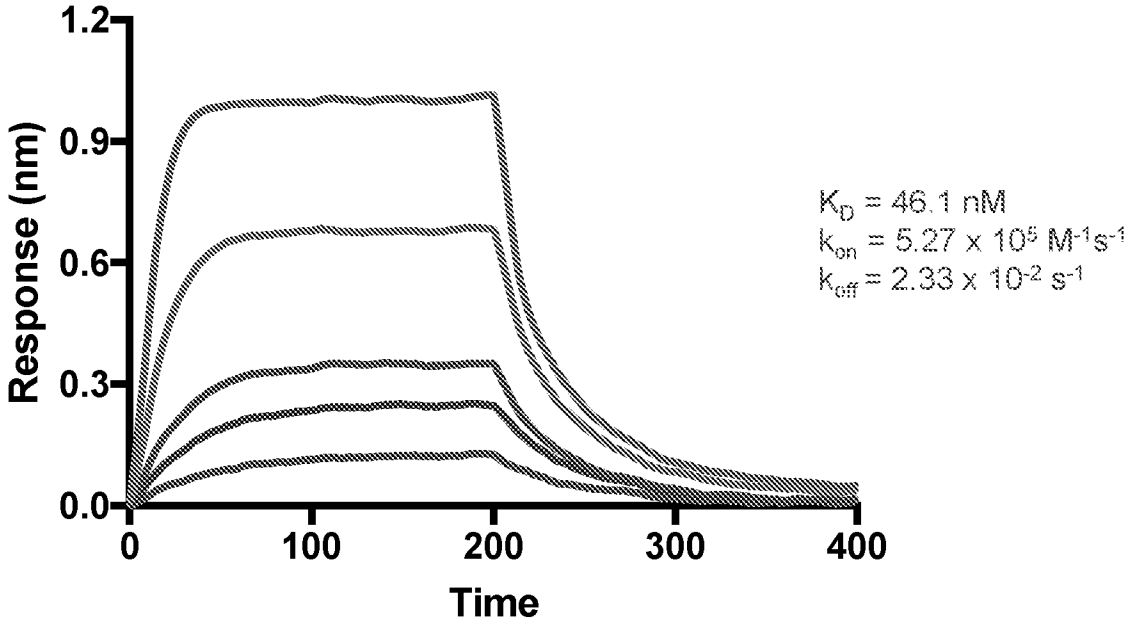

0.8
0.6
0.4
0.2
0.0
OD450
G7 target
PBS
1
2
3
Screening Round

FIG. 14

A


1.2
0.9
0.6
0.3
0.0
Response (nm)
0
100
200
300
400
Time
K_D = 46.1 nM
k_{on} = 5.27 x 10^5 $M^{-1}s^{-1}$
k_{off} = 2.33 x 10^{-2} s^{-1}

B

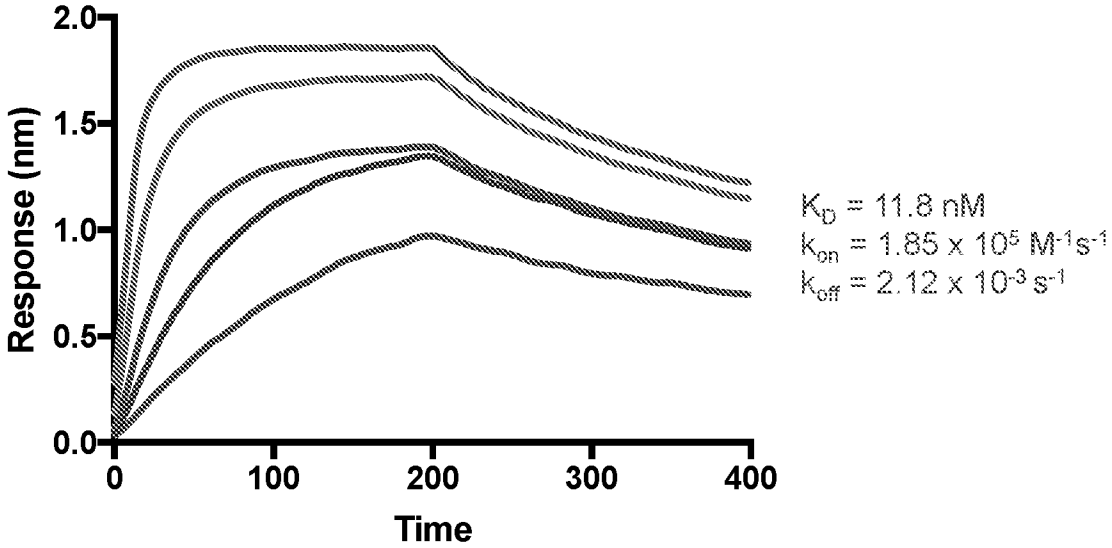
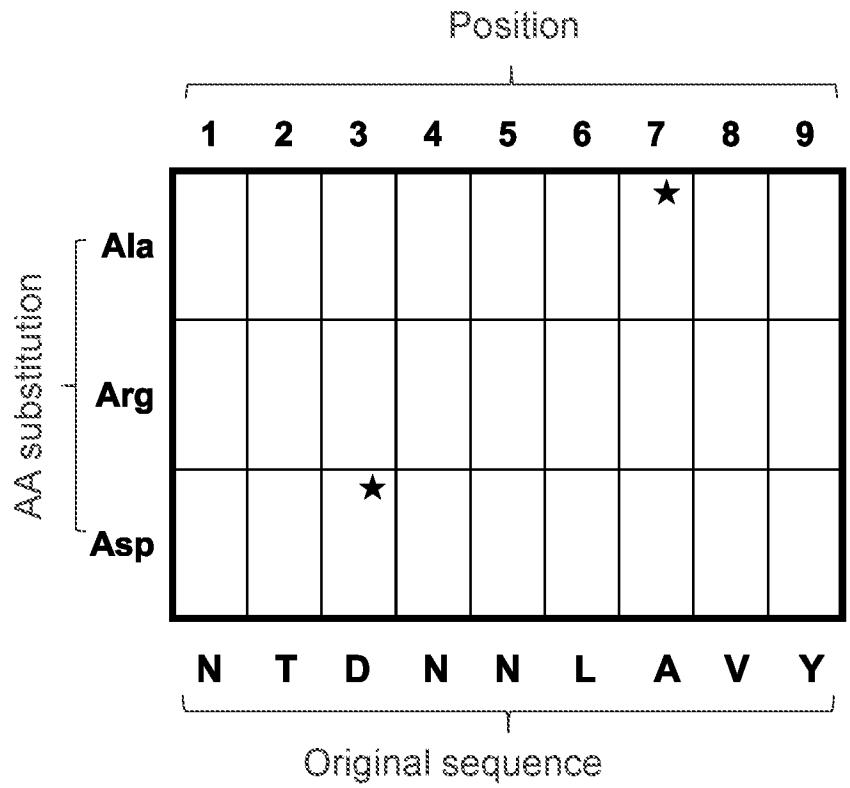

2.0
1.5
1.0
0.5
0.0
Response (nm)
0
100
200
300
400
Time
K_D = 11.8 nM
k_{on} = 1.85 x 10^5 $M^{-1}s^{-1}$
k_{off} = 2.12 x 10^{-3} s^{-1}

FIG. 15

A


Position
1 2 3 4 5 6 7 8 9
AA substitution
Ala
Arg
Asp
N T D N N L A V Y
Original sequence

B

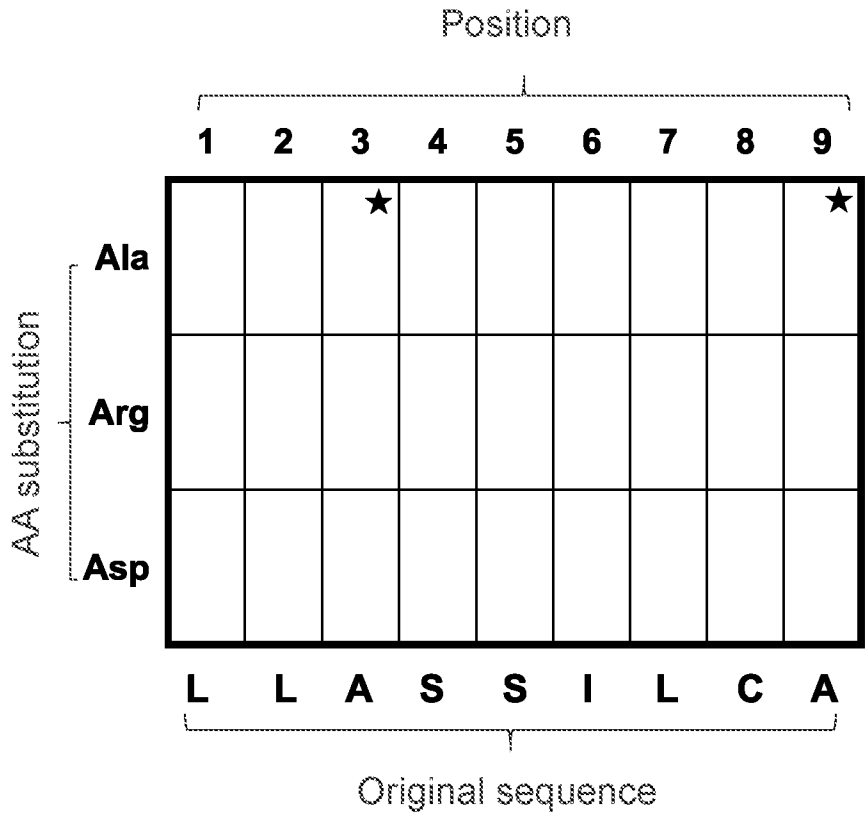

Position
1 2 3 4 5 6 7 8 9
AA substitution
Ala
Arg
Asp
L L A S S I L C A
Original sequence

FIG. 16

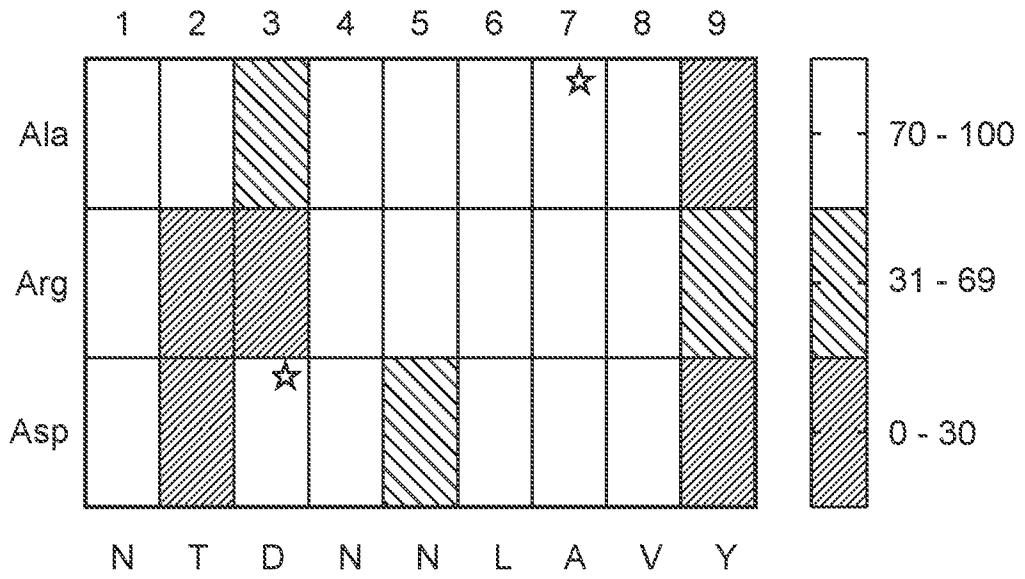


FIG. 17A

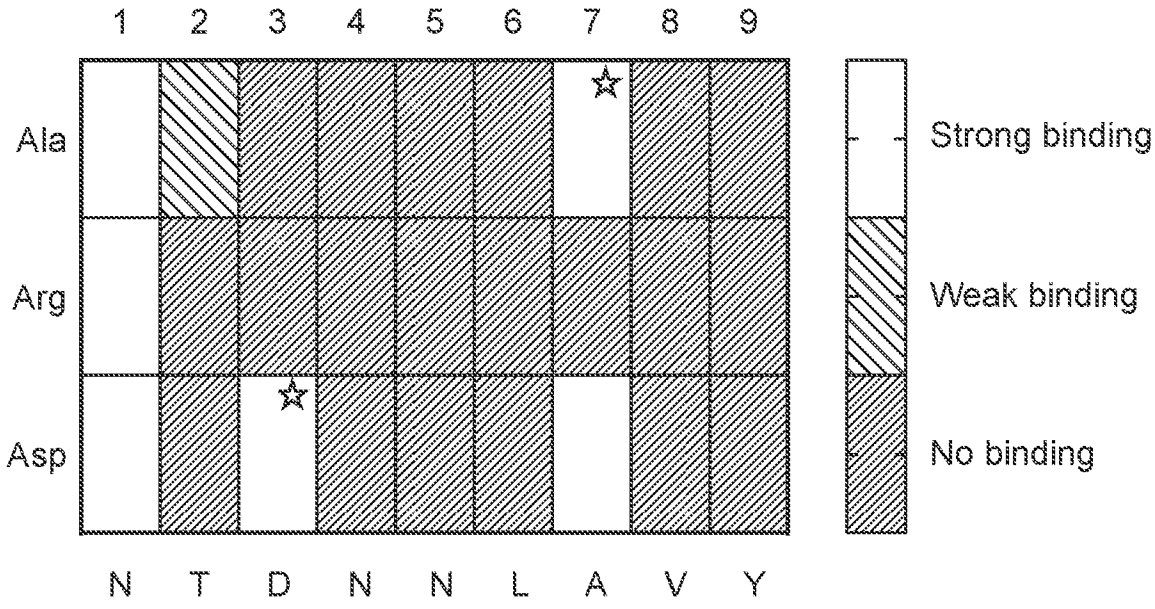


FIG. 17B

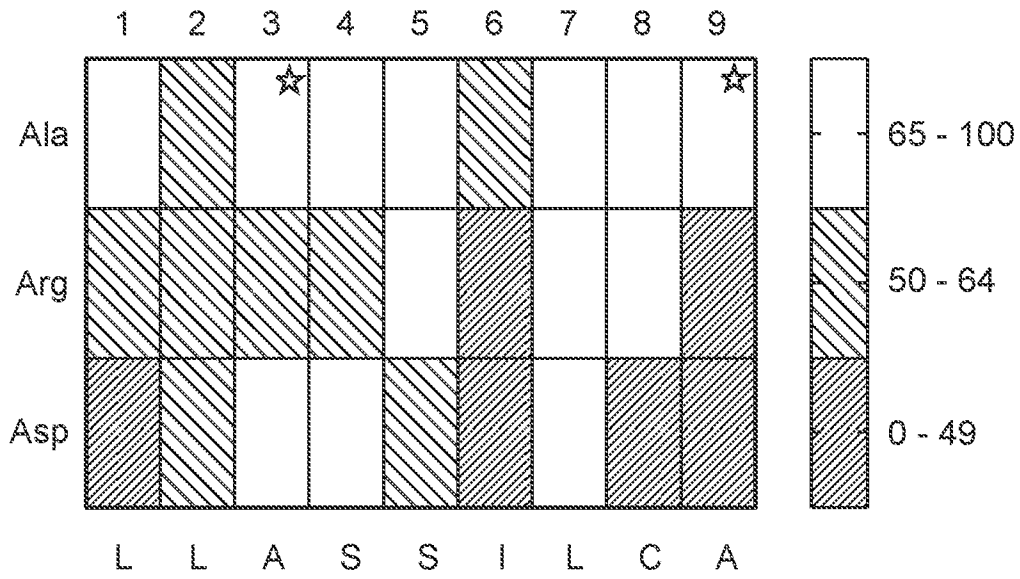


FIG. 18A

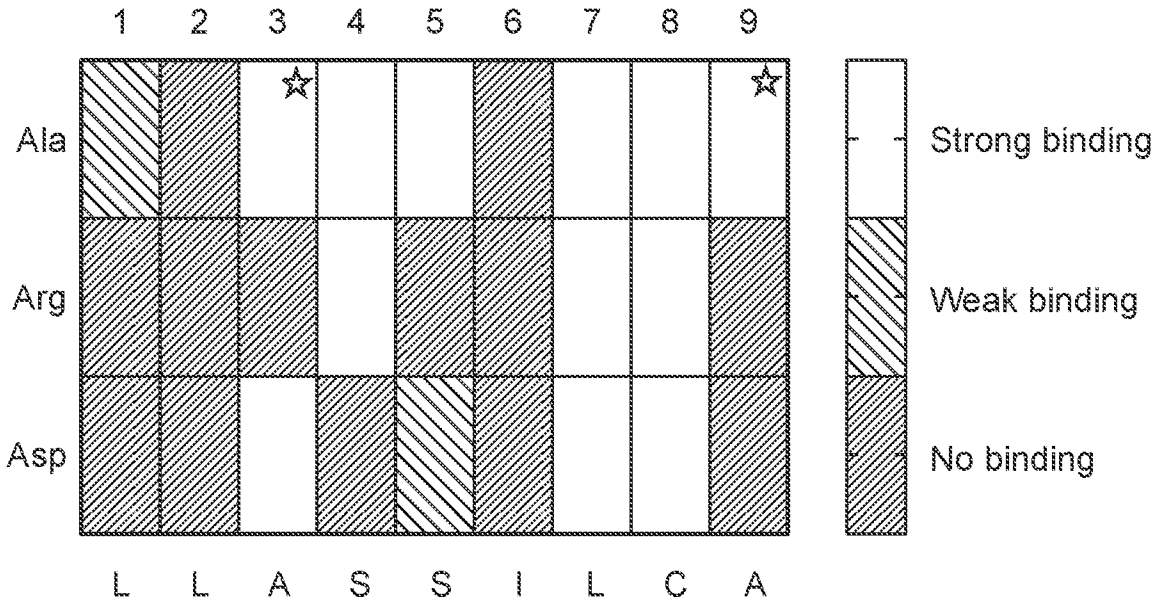
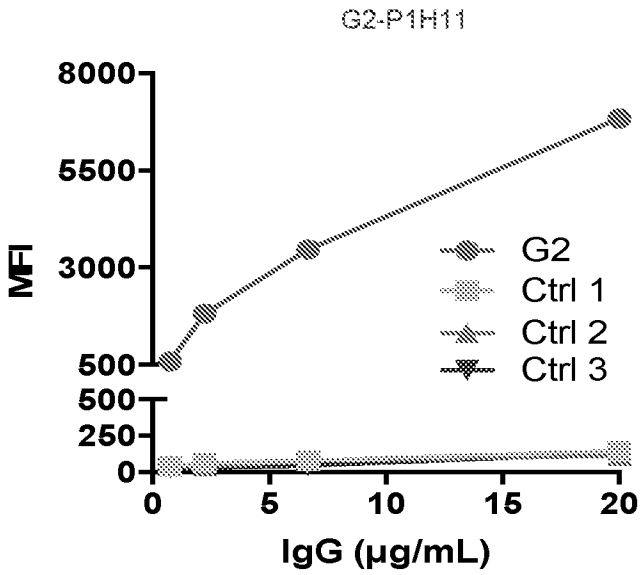


FIG. 18B

A


G2-P1H11
8000
5500
3000
500
500
250
0
MFI
0
5
10
15
20
IgG (µg/mL)
G2
Ctrl 1
Ctrl 2
Ctrl 3

B

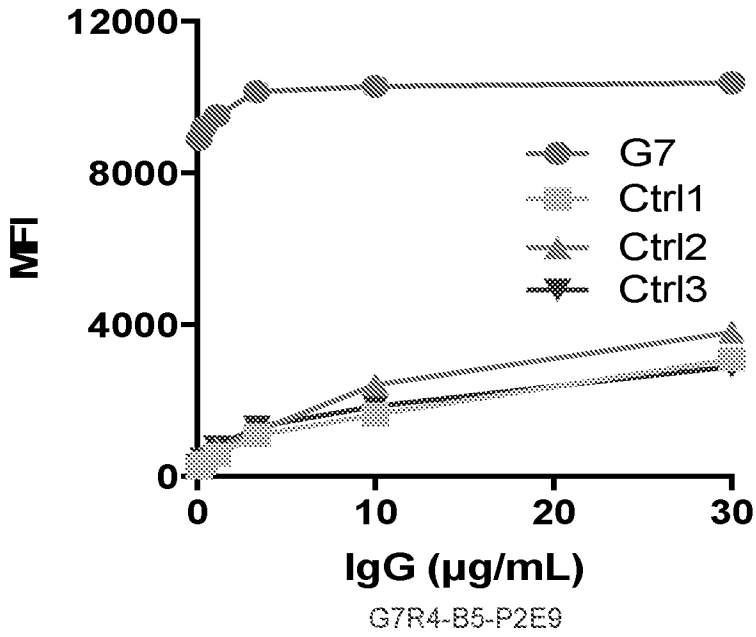

12000
8000
4000
0
MFI
0
10
20
30
IgG (µg/mL)
G7R4-B5-P2E9
G7
Ctrl1
Ctrl2
Ctrl3

FIG. 19

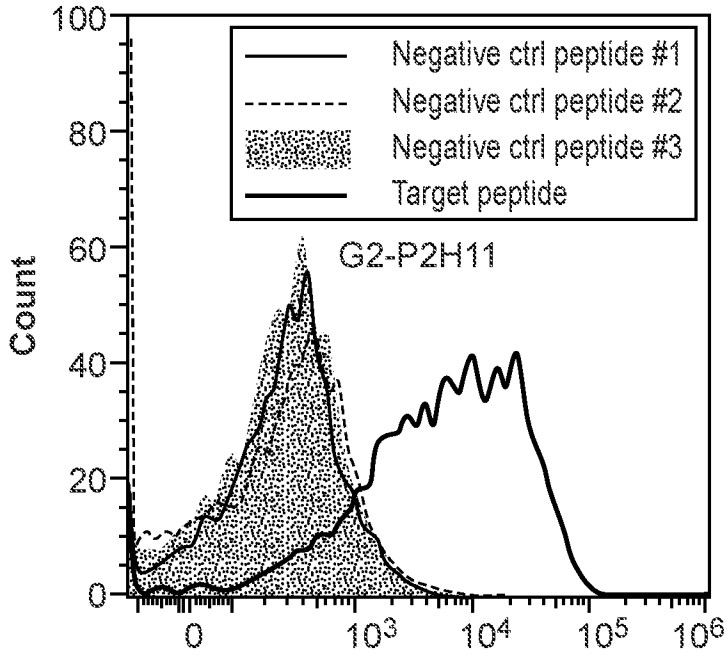


FIG. 20A

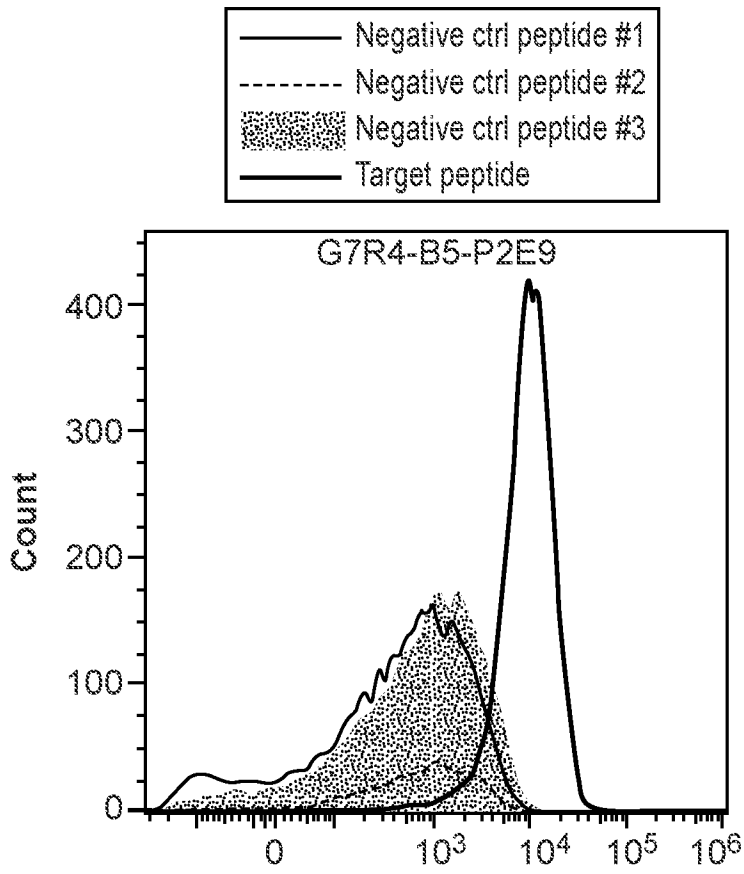


FIG. 20B

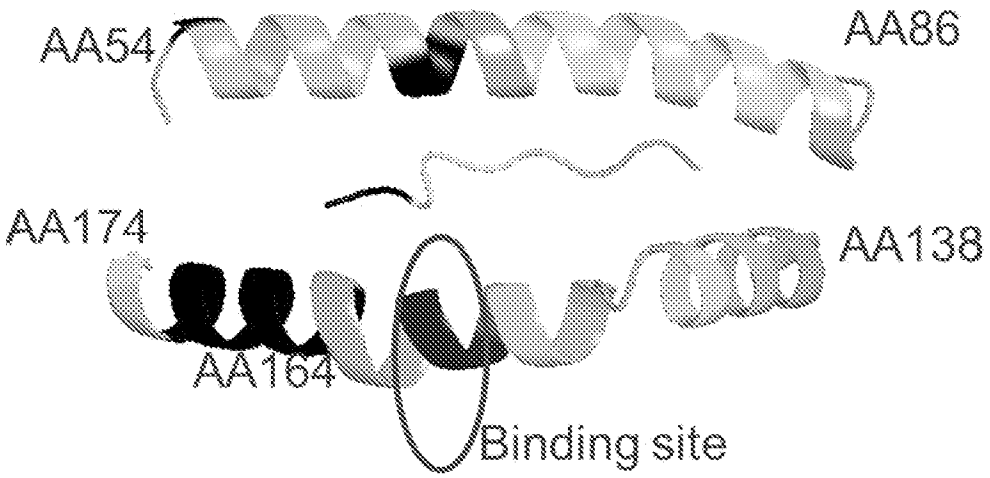


FIG. 21

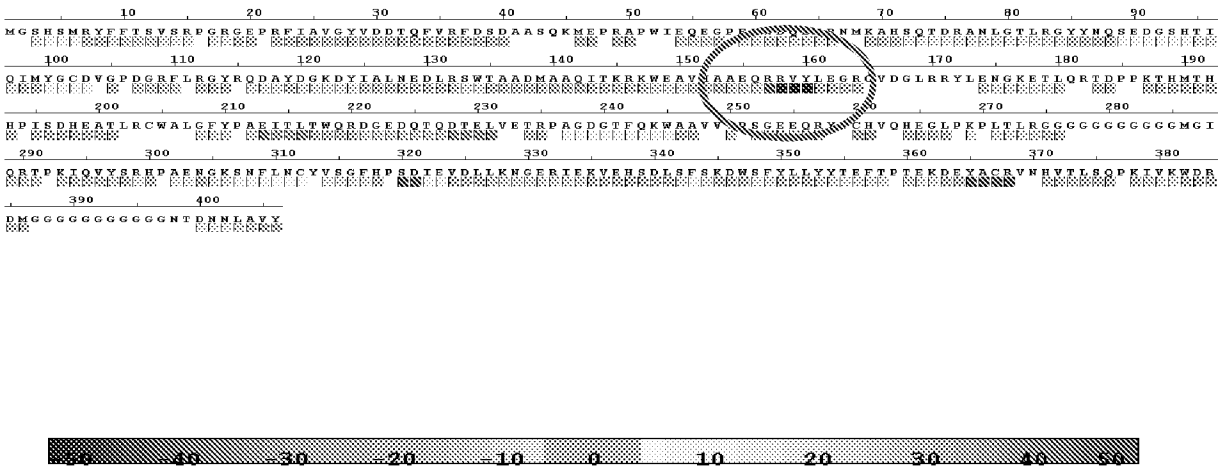


FIG. 22

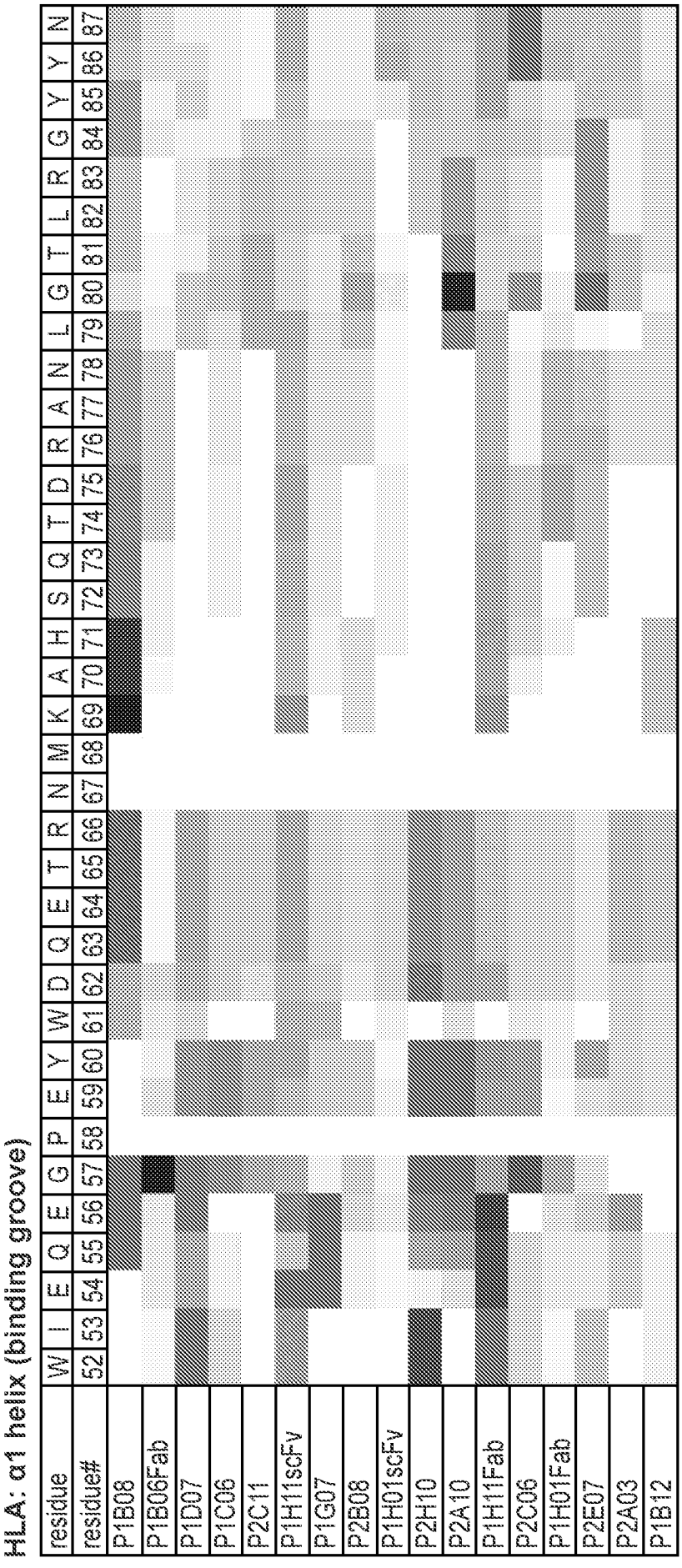

HLA: α1 helix (binding groove)
residue
residue#
W I E Q E G P E Y W D Q E T R N M K A H S Q T D R A N L G T L R G Y Y N
52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87
P1B08
P1B06Fab
P1D07
P1C06
P2C11
P1H11scFv
P1G07
P2B08
P1H01scFv
P2H10
P2A10
P1H11Fab
P2C06
P1H01Fab
P2E07
P2A03
P1B12

FIG. 23

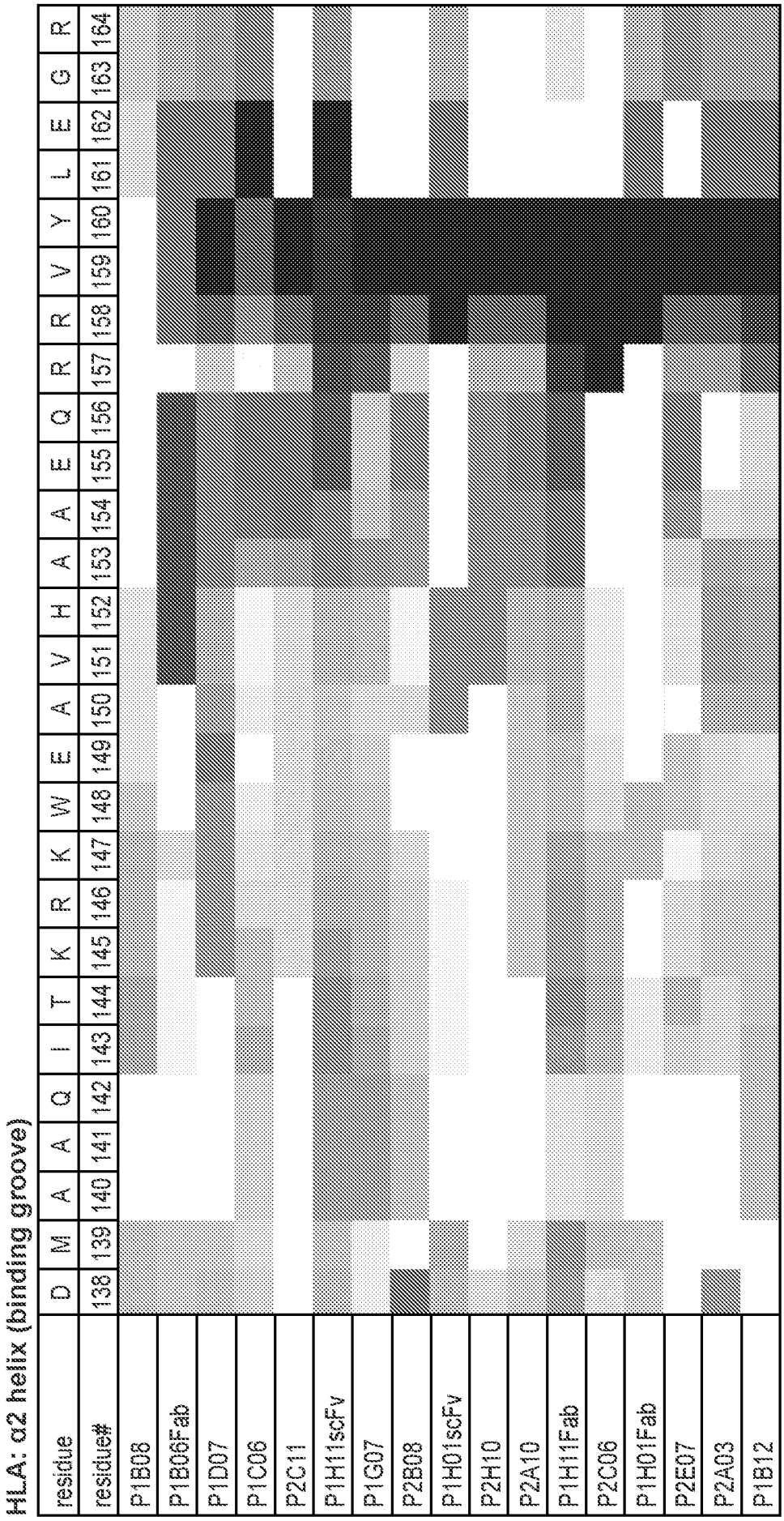

HLA: α2 helix (binding groove)
residue
residue#
D 138
M 139
A 140
A 141
Q 142
I 143
T 144
K 145
R 146
K 147
W 148
E 149
A 150
V 151
H 152
A 153
A 154
E 155
Q 156
R 157
R 158
V 159
Y 160
L 161
E 162
G 163
R 164
P1B08
P1B06Fab
P1D07
P1C06
P2C11
P1H11scFv
P1G07
P2B08
P1H01scFv
P2H10
P2A10
P1H11Fab
P2C06
P1H01Fab
P2E07
P2A03
P1B12
Change in % D
50
-50

FIG. 23 (Cont.)

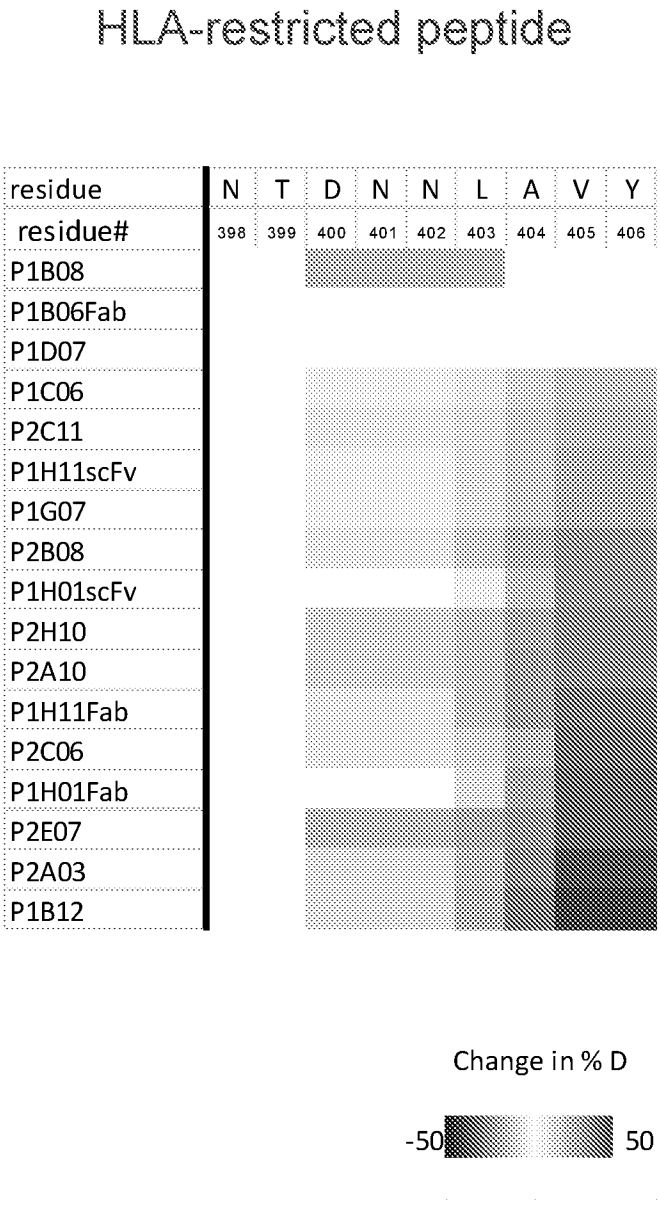

HLA-restricted peptide
residue
residue#
N T D N N L A V Y
398 399 400 401 402 403 404 405 406
P1B08
P1B06Fab
P1D07
P1C06
P2C11
P1H11scFv
P1G07
P2B08
P1H01scFv
P2H10
P2A10
P1H11Fab
P2C06
P1H01Fab
P2E07
P2A03
P1B12
Change in % D
-50
50

FIG. 24

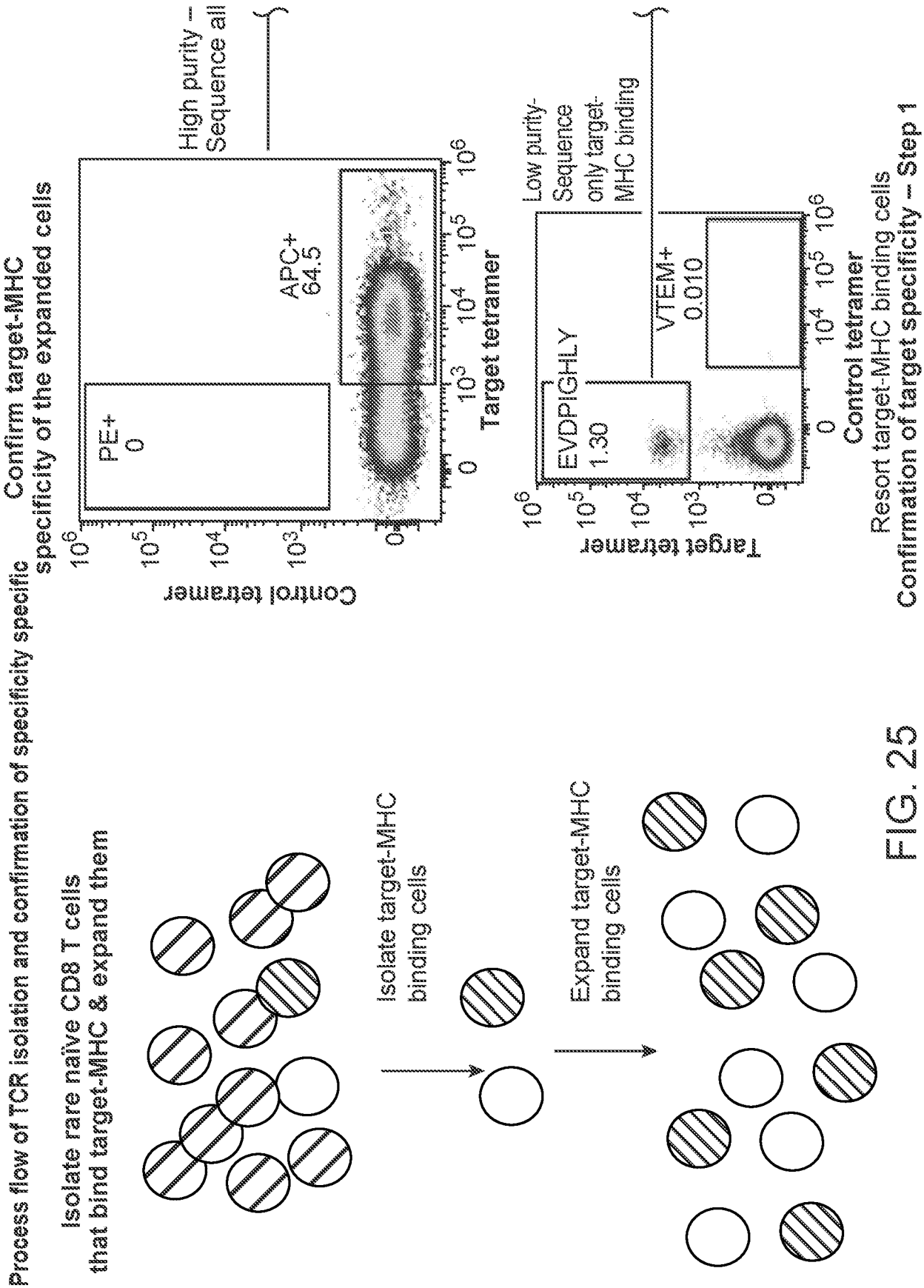

Process flow of TCR isolation and confirmation of specificity specific
Isolate rare naïve CD8 T cells
that bind target-MHC & expand them
Isolate target-MHC
binding cells
Expand target-MHC
binding cells
Confirm target-MHC
specificity of the expanded cells
Control tetramer
PE+
0
APC+
64.5
Target tetramer
High purity –
Sequence all
Target tetramer
EVDPIGHLY
1.30
VTEM+
0.010
Low purity-
Sequence
only target-
MHC binding
Control tetramer
Resort target-MHC binding cells
Confirmation of target specificity – Step 1

FIG. 25

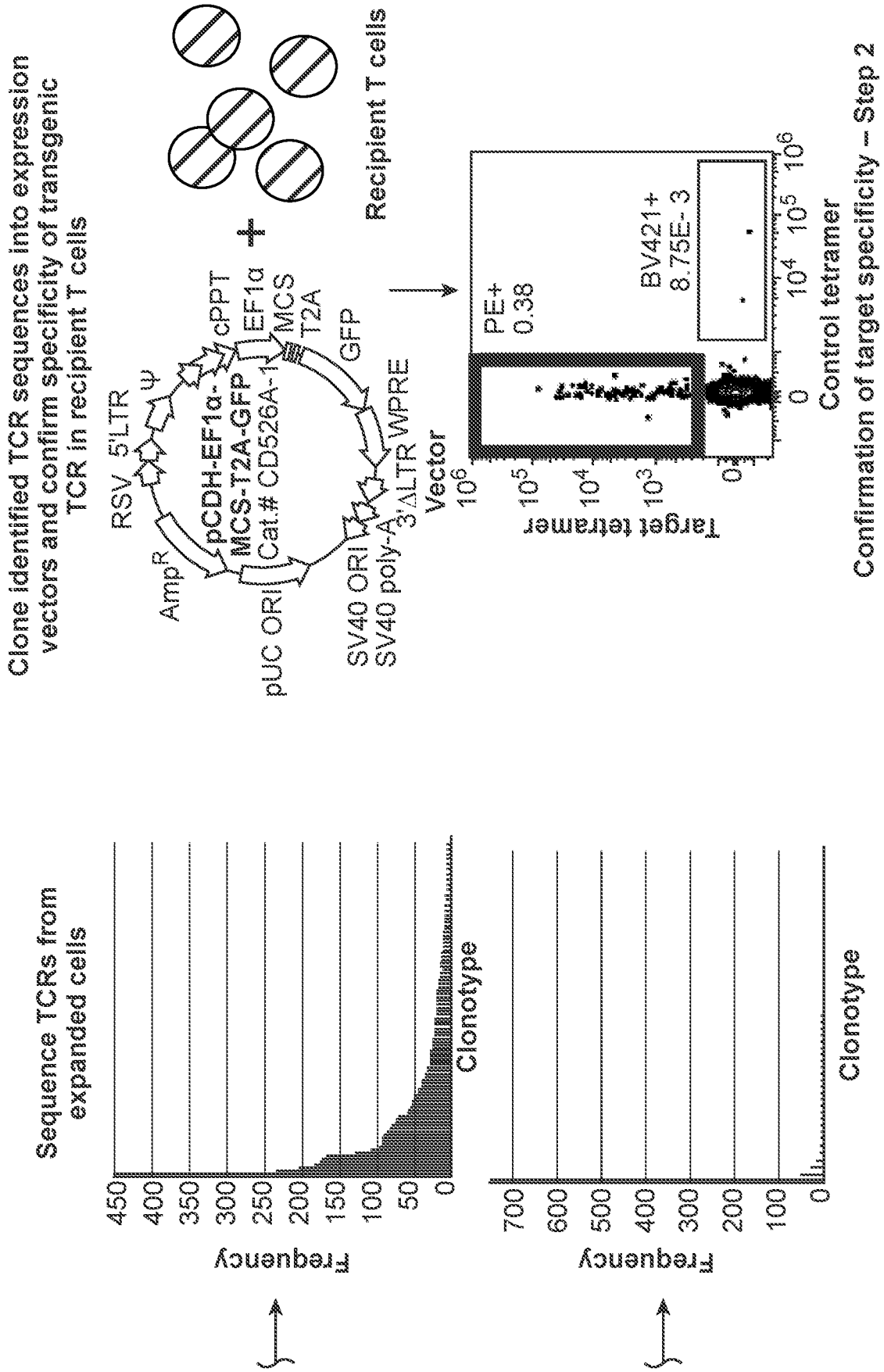

Sequence TCRs from expanded cells
Frequency
Clonotype
Clone identified TCR sequences into expression vectors and confirm specificity of transgenic TCR in recipient T cells
RSV 5'LTR
ψ
cPPT
EF1α
MCS
T2A
GFP
WPRE
3'ΔLTR
SV40 poly-A
SV40 ORI
pUC ORI
Amp^R
pCDH-EF1α-MCS-T2A-GFP
Cat.# CD526A-1
Vector
Recipient T cells
PE+
0.38
BV421+
8.75E-3
Target tetramer
Control tetramer
Confirmation of target specificity – Step 2

FIG. 25 (Cont.)

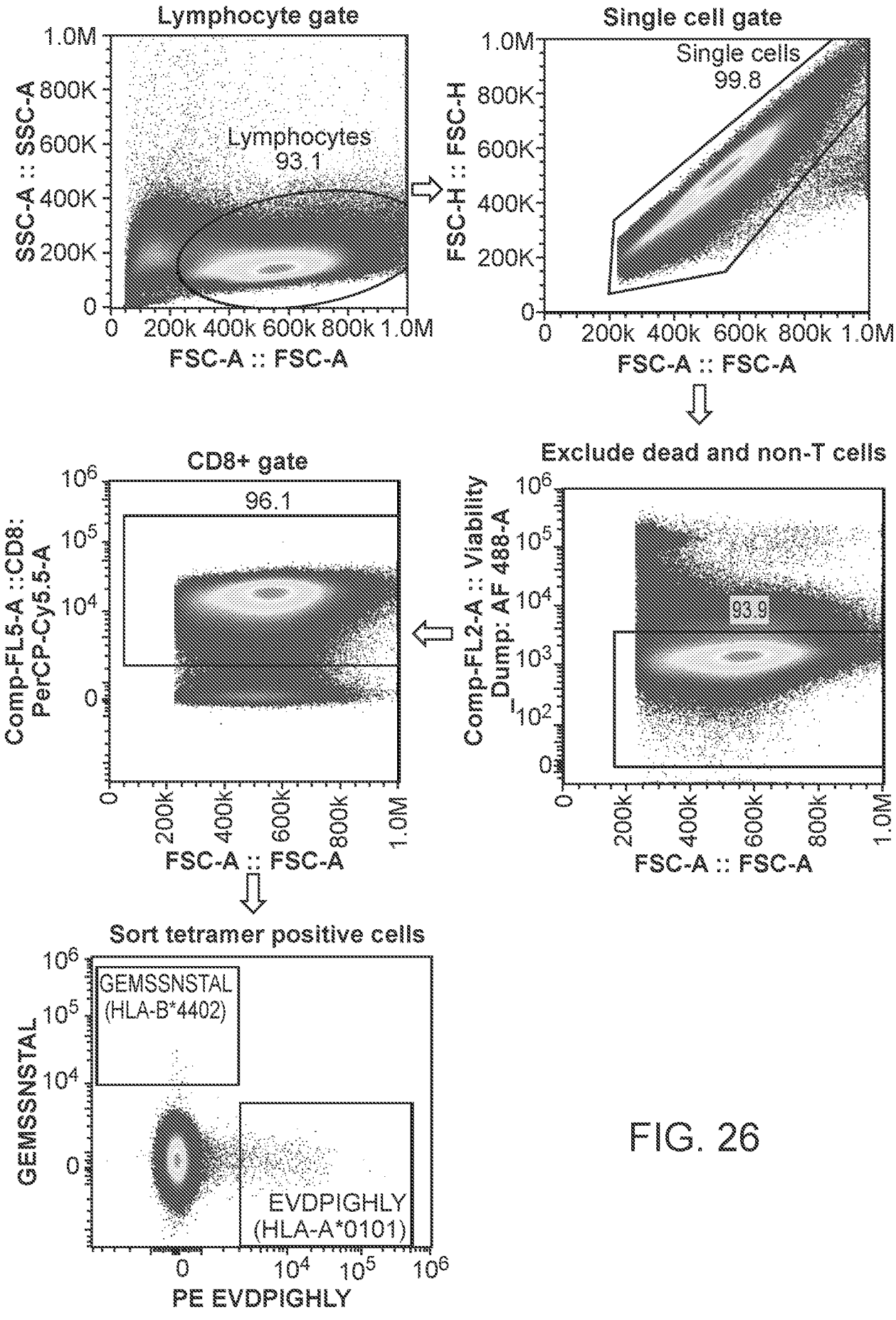

Lymphocyte gate
SSC-A :: SSC-A
Lymphocytes
93.1
FSC-A :: FSC-A
Single cell gate
FSC-H :: FSC-H
Single cells
99.8
FSC-A :: FSC-A
Exclude dead and non-T cells
Comp-FL2-A :: Viability _Dump: AF 488-A
93.9
FSC-A :: FSC-A
CD8+ gate
Comp-FL5-A ::CD8: PerCP-Cy5.5-A
96.1
FSC-A :: FSC-A
Sort tetramer positive cells
GEMSSNSTAL
GEMSSNSTAL (HLA-B*4402)
EVDPIGHLY (HLA-A*0101)
PE EVDPIGHLY

FIG. 26

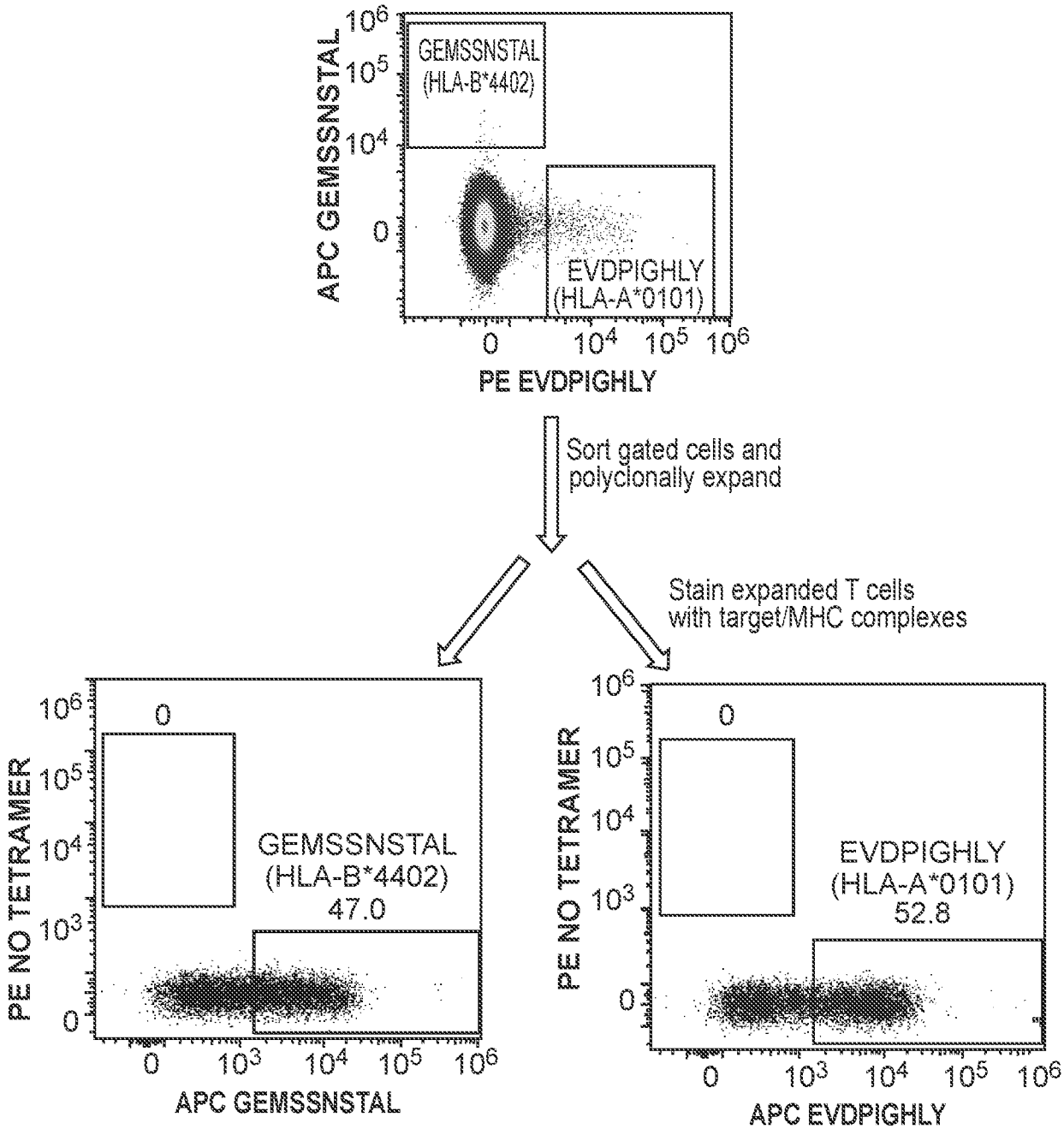

APC GEMSSNSTAL
GEMSSNSTAL
(HLA-B*4402)
EVDPIGHLY
(HLA-A*0101)
PE EVDPIGHLY
Sort gated cells and
polyclonally expand
Stain expanded T cells
with target/MHC complexes
PE NO TETRAMER
0
GEMSSNSTAL
(HLA-B*4402)
47.0
APC GEMSSNSTAL
PE NO TETRAMER
0
EVDPIGHLY
(HLA-A*0101)
52.8
APC EVDPIGHLY

FIG. 27

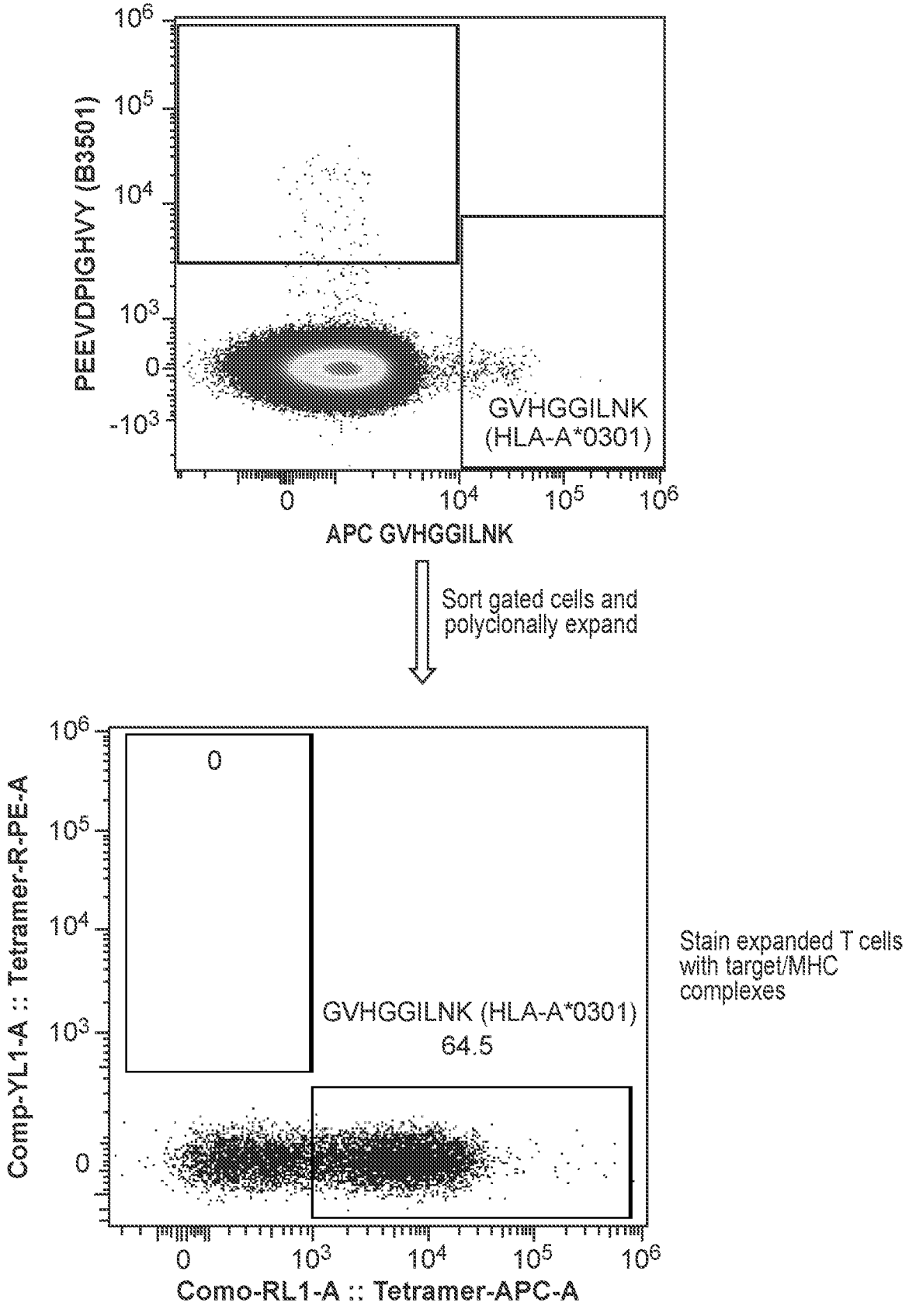

PEEVDPIGHVY (B3501)
APC GVHGGILNK
GVHGGILNK
(HLA-A*0301)
Sort gated cells and
polyclonally expand
Comp-YL1-A :: Tetramer-R-PE-A
Como-RL1-A :: Tetramer-APC-A
0
GVHGGILNK (HLA-A*0301)
64.5
Stain expanded T cells
with target/MHC
complexes

FIG. 28

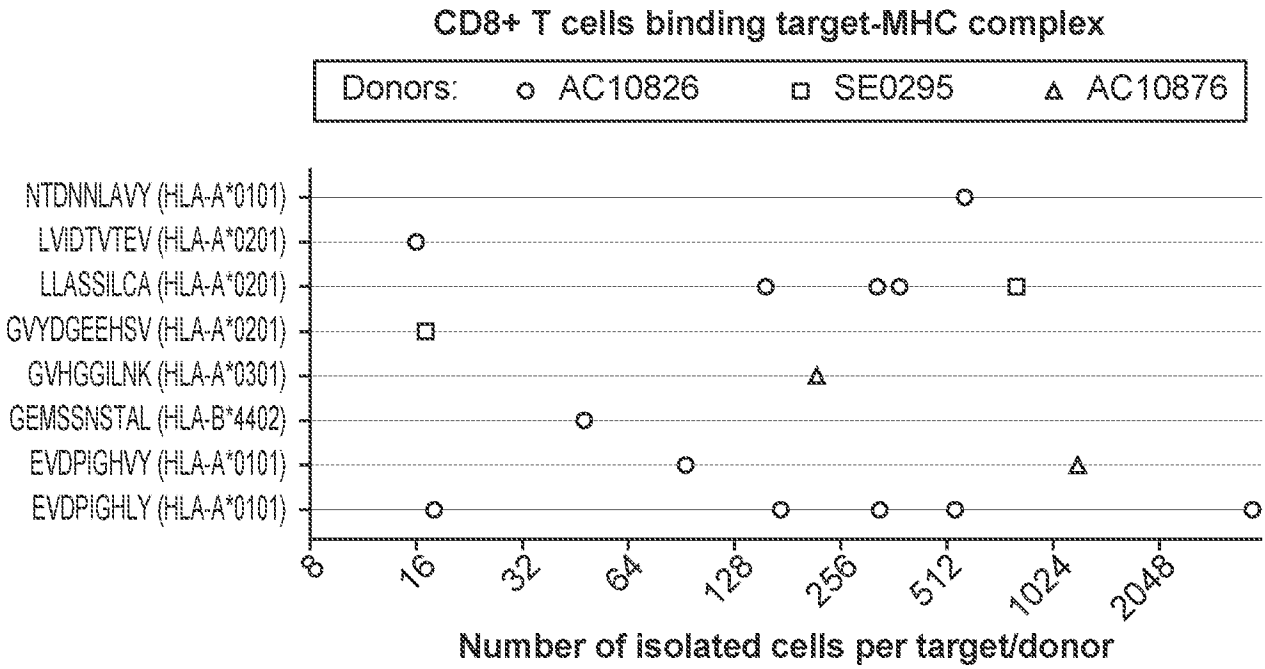


FIG. 29A

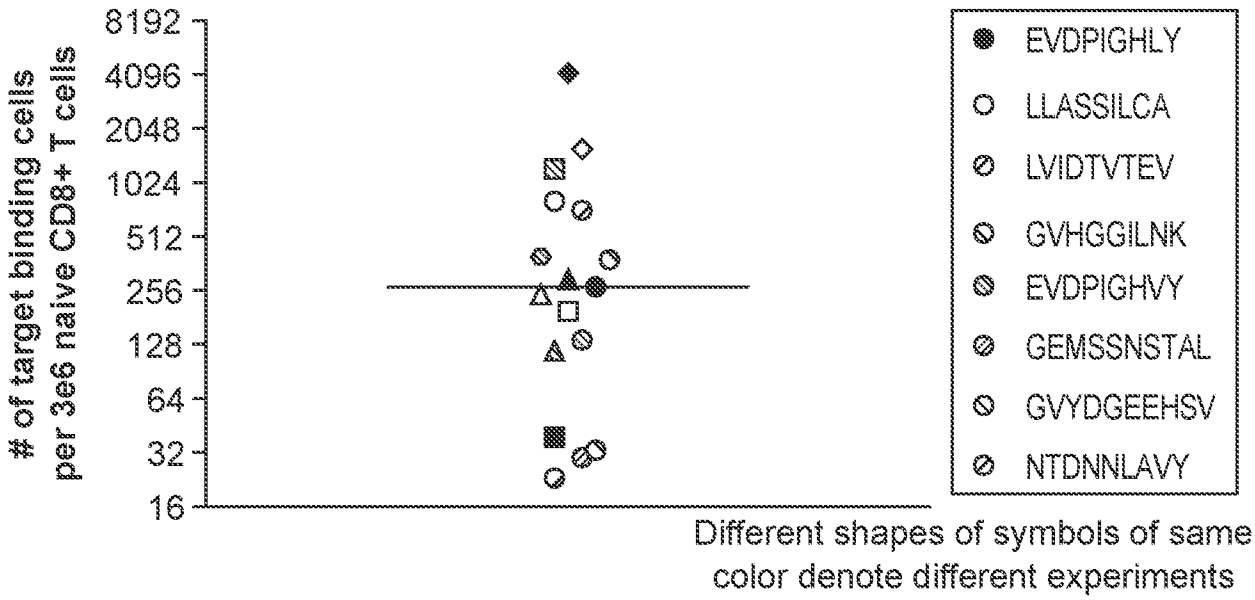


FIG. 29B

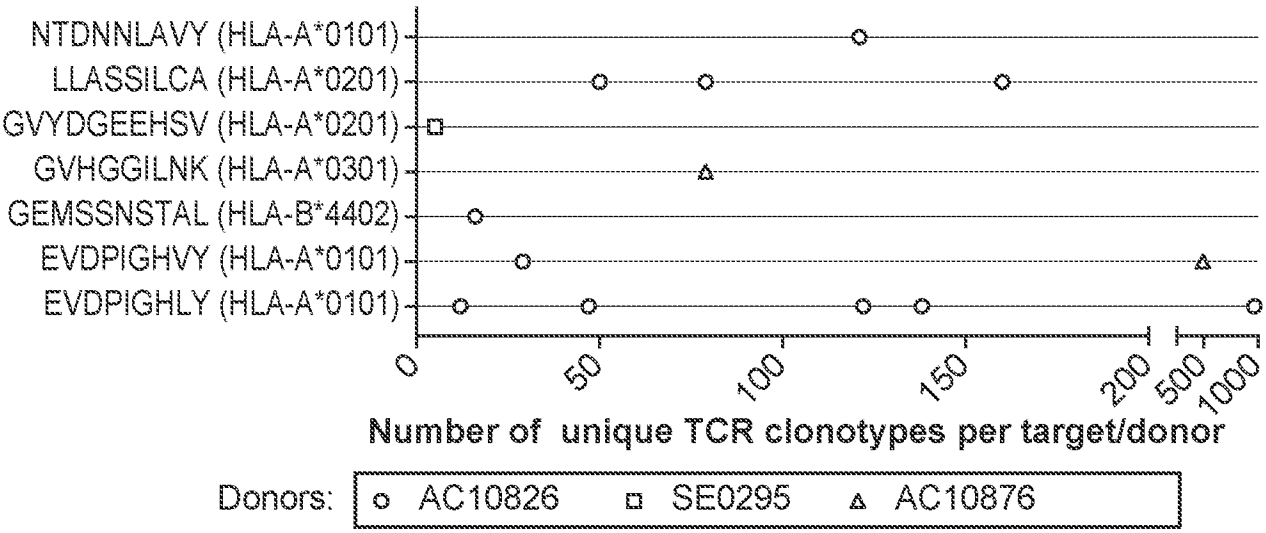


FIG. 30A

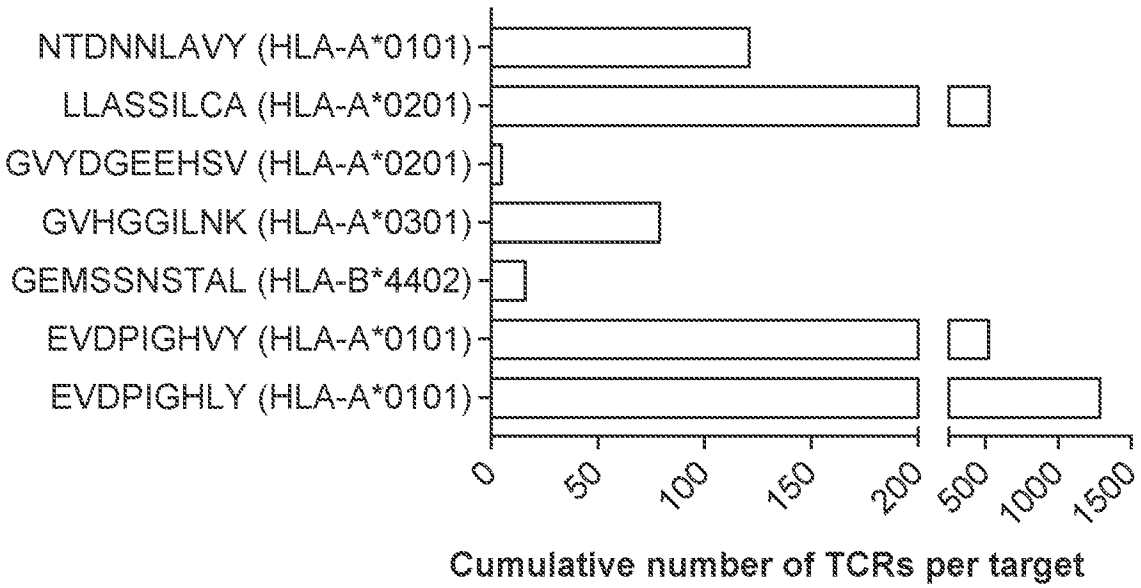


FIG. 30B

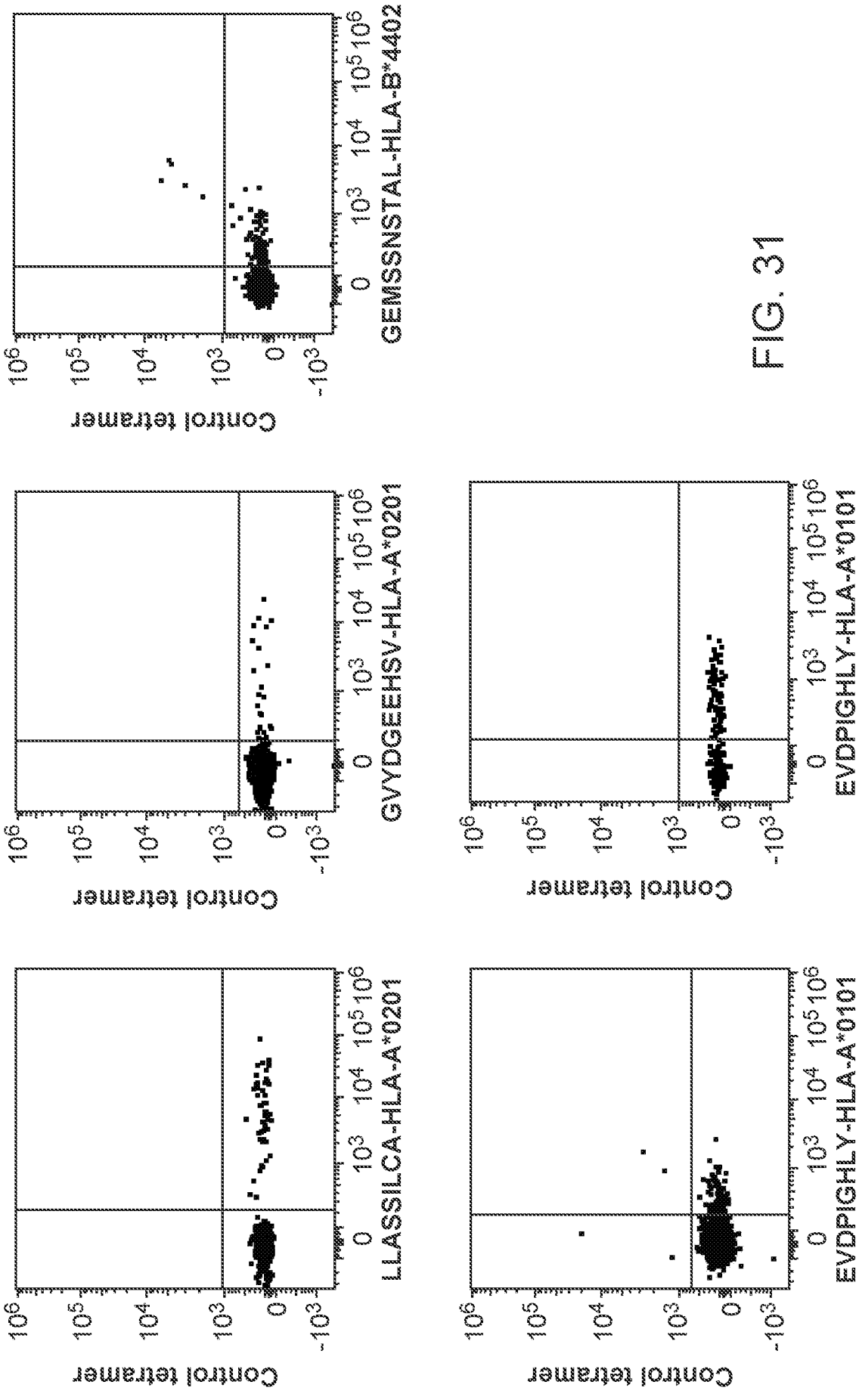

GEMSSNSTAL-HLA-B*4402
GVYDGEEHSV-HLA-A*0201
EVDPIGHLY-HLA-A*0101
LLASSILCA-HLA-A*0201
EVDPIGHLY-HLA-A*0101
Control tetramer
10^6
10^5
10^4
10^3
0
-10^3

FIG. 31

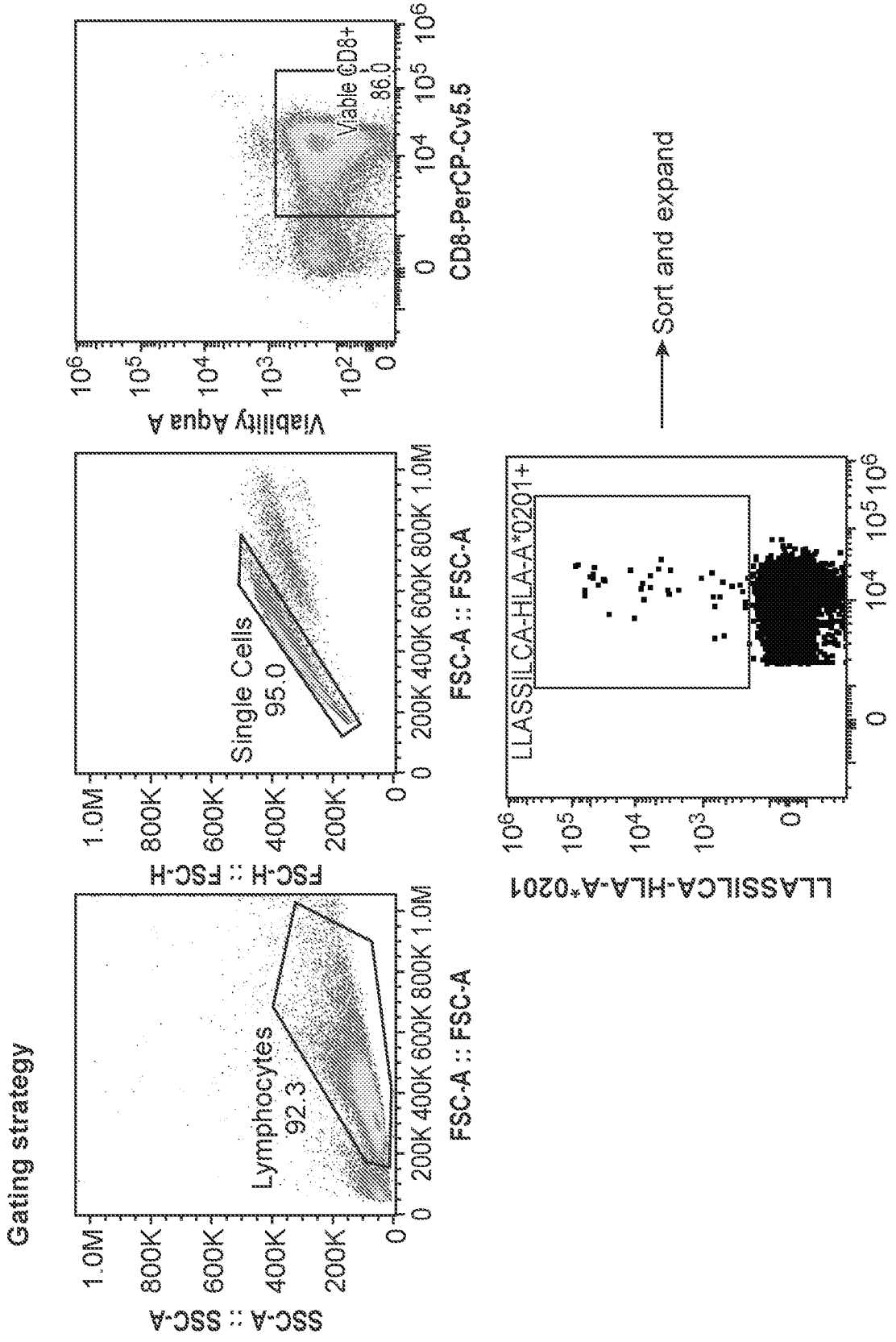

Gating strategy
SSC-A :: SSC-A
FSC-A :: FSC-A
Lymphocytes
92.3
FSC-H :: FSC-H
FSC-A :: FSC-A
Single Cells
95.0
Viability Aqua A
CD8-PerCP-Cy5.5
Viable CD8+
86.0
Sort and expand
LLASSILCA-HLA-A*0201
CD8
LLASSILCA-HLA-A*0201+

FIG. 32

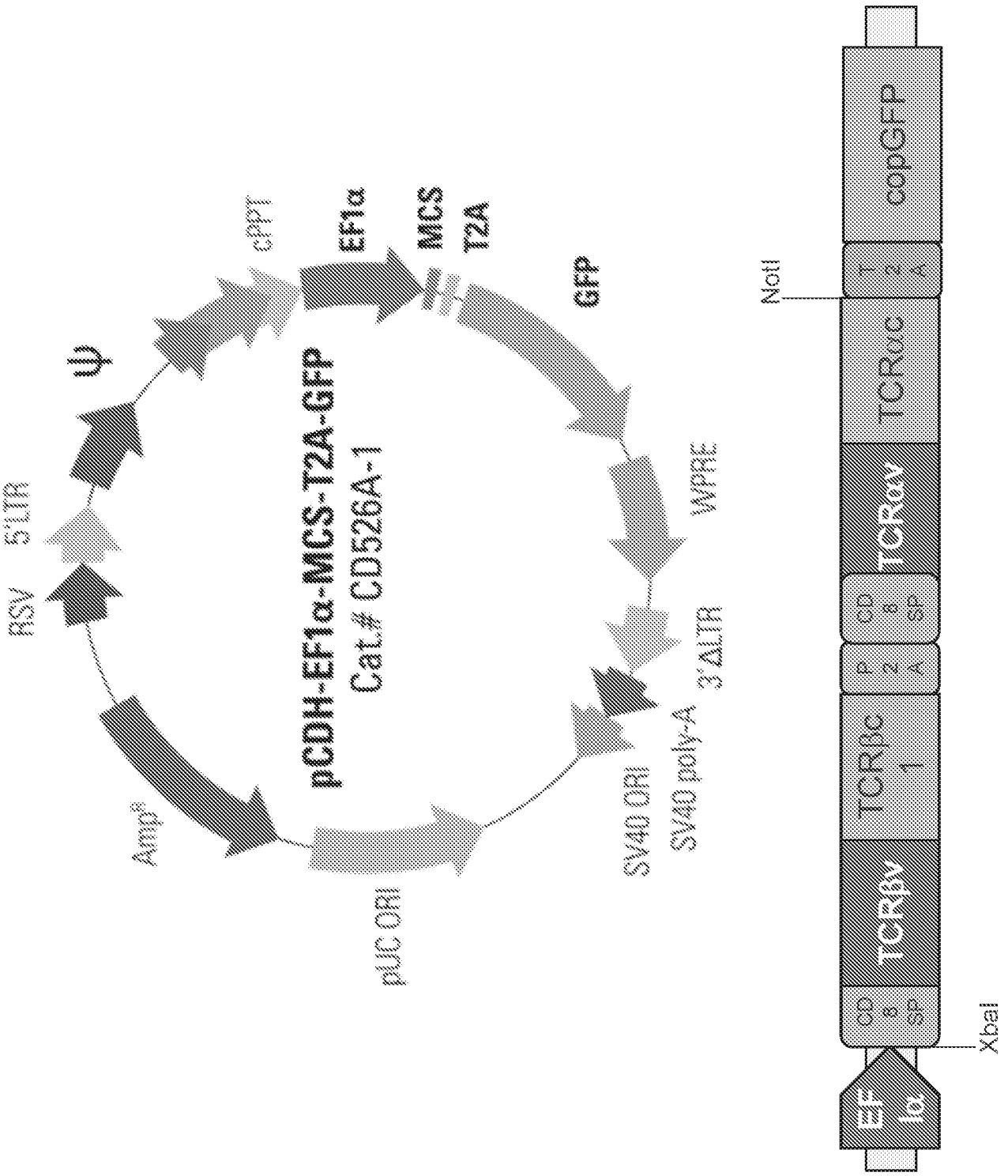

pCDH-EF1α-MCS-T2A-GFP
Cat.# CD526A-1
RSV 5'LTR
Ψ
cPPT
EF1α
MCS
T2A
GFP
WPRE
3'ΔLTR
SV40 poly-A
SV40 ORI
pUC ORI
Amp^R
NotI
XbaI
EF 1α
CD 3 SP
TCRβV
TCRβC 1
P 2 A
CD 3 SP
TCRαV
TCRαC
T 2 A
copGFP

FIG. 33

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/46997

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - A61K 39/00, C07K 16/28 (2018.01)
CPC - C07K 2317/34, C07K 2317/21, C07K 14/70539, C07K 2319/73, C07K 2319/74

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y --- A	US 2007/0196369 A1 (HOOGENBOOM et al.) 23 August 2007 (23.08.2007) abstract, para [0007], [0009], [0010], [0074], [0105]	1-5, 79-82 --- 6
Y	PARET et al. CXorf61 is a target for T cell based immunotherapy of triple-negative breast cancer. Oncotarget, 22 September 2015, Vol. 6, No. 28, pp 25356-25367, abstract, supplemental Table S2	1-5, 79-82
A	US 2012/0058906 A1 (SMIDER et al.) 8 March 2012 (08.03.2012) abstract, para [0020], SEQ ID NO: 1527	6

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
25 November 2018	20 DEC 2018

Name and mailing address of the ISA/US	Authorized officer:
Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/46997

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 7-13, 16-78, 83-96, 101-114, 116-117, 120-123, 132-150, 154-178
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of Item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

---------- see extra sheet ----------

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-6 and 79-82, limited to SEQ ID NO: 25 and peptide sequence LLASSILCA

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/46997

Continuation of Box No. III, Observations where unity of invention is lacking:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I+: Claims 1-6, 14-15, and 79-82 directed to an isolated antigen binding protein (ABP) that specifically binds to a human leukocyte antigen (HLA)-PEPTIDE target, wherein the HLA-PEPTIDE target comprises a HLA-restricted peptide complexed with an HLA Class I molecule, wherein the HLA restricted peptide is located in the peptide binding groove of an .alpha.1/.alpha.2 heterodimer portion of the HLA Class I molecule. The ABP composition will be searched to the extent that the HLA Class I molecule bound by said ABP is HLA subtype A *02:01 and the HLA-restricted peptide consists of the sequence LLASSILCA, and the ABP comprises a CDR-H3 comprising a sequence set forth in SEQ ID NO: 3025. It is believed that claims 1-6 and 79-82, limited to an isolated antigen binding protein (ABP) encompass this first named invention, and thus these claims will be searched without fee to the extent that the ABP binds to HLA-A *02:01 that comprises the peptide LLASSILCA bound to the peptide binding groove of an .alpha.1/.alpha.2 heterodimer. Additional ABP will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected ABP. Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be an ABP that binds to HLA subtype HLA-A *01:01 and the HLA-restricted peptide consists of the sequence NTDNNLAVY (claims 1-4, 14-15 and 79-82).

Group II+: Claims 97-100, 115, 118-119, 124-131,151-153, directed to an isolated HLA-PEPTIDE target, that comprises an HLA-restricted peptide complexed with an HLA Class I molecule, located in in the peptide binding groove of an .alpha.1/.alpha.2 heterodimer portion the HLA Class I molecule and a kit for expressing said HLA-PEPTIDE target in a cell. Group II+ will be searched upon payment of additional fees. The isolated HLA-PEPTIDE target may be searched, for example, to the extent that the HLA Class I molecule is HLA subtype B *35:01 and the HLA-restricted peptide encompasses the sequence FPVQATIDF. It is believed that claims 97, 100, 115, (118-119)(in part), (124-131)(in part), 151-153, limited to an isolated HLA subtype B *35:01 and HLA-restricted peptide comprising the sequence FPVQATIDF read on this exemplary invention. [Note: HLA subtype B *35:01 with the sequence FPVQATIDF is the first named HLA-PEPTIDE target of Table A that is not also listed on Table B or Table C, see claim 97]. Additional HLA-PEPTIDE targets will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected recombinant polypeptide. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first named invention to be searched. An exemplary election would be a HLA Class I molecule having HLA subtype A *02:01 a HLA-restricted peptide with the sequence LLASSILCA, (97-100, 115, 118-119 and 124-131, 151-153).

The inventions listed as Groups I+ and II+ do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

No technical features are shared between the HLA-restricted peptides and HLA Class I polypeptide sequences of Groups I+ and II+, accordingly, these groups lack unity a priori.

Common Technical Features

The inventions of Group I+ share the technical feature of a ABP that binds to a HLA-PEPTIDE complex comprising an HLAA class I molecule and a HLA-restricted peptide bound to said HLA-A molecule. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is anticipated by US 2007/0196369 A1 to Hoogenboom et al (hereinafter 'Hoogenboom'). Hoogenboom teaches said antigen binding complexes (abstract "Disclosed are protein ligands comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, wherein the proteins bind a complex comprising an MHC and a peptide, do not substantially bind the MHC in the absence of the bound peptide, and do not substantially bind the peptide in the absence of the MHC", para [0074] "In one embodiment, the MHC component of the complex can be a class I MHC. ... For example, the allele is A*0201.").

The inventions of Group I+ share the technical feature of a Heavy chain CDR-3 that binds the specific HLA-A type I polypeptide when bound with a specific HLA-restricted peptide. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is mad eobvious by Hoogenboom. Hoogenboom teaches ABP specific to each HLA-PEPTIDE complex (abstract "Disclosed are protein ligands comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, wherein the proteins bind a complex comprising an MHC and a peptide, do not substantially bind the MHC in the absence of the bound peptide, and do not substantially bind the peptide in the absence of the MHC") that comprise specific CDRs in VH and VL (para [0105] "the protein ligand is an antibody. As used herein, the term "antibody" refers to a protein comprising at least one, and preferably two, heavy (H) chain variable regions (abbreviated herein as VH), and at least one and preferably two light (L) chain variable regions (abbreviated herein as VL). The VH and VL regions can be further subdivided into regions of hypervariability, termed "complementarity determining regions" ("CDR"), interspersed with regions that are more conserved, termed "framework regions" (FR). ... Each VH and VL is composed of three CDR's and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4."). Based on Hoogenboom's teaching, it would have been obvious to an artisan of ordinary skill to specify specific CDR sequences from a characterized ABP comprising a VH, such as CDR-3 from VH, because said CDRs are known in the art to give specificity to binding domains comprising VH and VL.

********** See Next Extra Sheet to continue **********

Previous Extra Sheet continued:

The inventions of Group I+, and II+ share the technical feature of an isolated HLA-PEPTIDE complex comprising an HLA A class I molecule and a HLA-restricted peptide located in in the peptide binding groove of an .alpha.1/.alpha.2 heterodimer portion the HLA Class I molecule and a host cell comprising . However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is anticipated by US 2013/0315935 A1 to Proimunne Limited (hereinafter 'Proimmune'). Proimunne teaches said HLA-PEPTIDE complexes (para [0025] "the present invention comprises an oligomeric receptor-ligand pair member complex", para [0048] Preferably peptides derived from the receptor-ligand pair member peptides or functional part thereof in the oligomeric receptor-ligand pair member complex are derived from the extra-cellular part of the MHC class I" para [0049] "More preferably the oligomeric receptor-ligand pair member complex further comprises a peptide bound to the MHC portions of the complex in the groove formed by the MHC .alpha.1 and .alpha.2 domains for class I complexes", para [0124] "these receptor-ligand pair monomer and the oligomeric core may be produced separately and allowed to associate in vitro.", para [0125] "MHC-peptide complexes can be obtained with very high peptide homogeneity, e.g. greater than 95% or even greater than 99%").

The inventions of Group II+ share the technical feature of an isolated HLA-PEPTIDE target, e.g, a cell line or tumor cell line comprising a heterologous HLA-PEPTIDE target complexed with an HLA Class I molecule, located in in the peptide binding groove of an .alpha.1/.alpha.2 heterodimer portion the HLA Class I molecule. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is anticipated by US 2013/0111617 A1 Regeneron Pharmaceuticals, Inc. (hereinafter 'Regeneron'). Proimmune teaches expressing said HLA complex (para [0124] "The oligomeric receptor-ligand pair member proteins, their respective polypeptide subunits, where applicable, and the chimeric proteins, respectively, may be coexpressed and assembled as oligomeric complexes in the same cell", see above for composition of HLA-peptide complex.). Proimunne does not expressly teach a host cell comprising (expressing on surface), however, Regeneron teaches host cells expressing said MHC class I HLA-A complexes (Fig. 1 shows the heterologous HLA- molecule, the dot id the HLA restricted peptide, para [0009] "A biological system for generating or identifying peptides that associate with human MHC class I proteins and chimeras thereof ... Humanized rodent cells that express human or humanized MHC and .beta.2 microglobulin molecules are also provided.", para [0077] "a cell displaying the chimeric MHC I protein, e.g., HLA-A2/H-2K protein, is a nucleated cell. In various aspects, the cell is an antigen-presenting cell (APC). Although most cells in the body can present an antigen in the context of MHC I, some nonlimiting examples of antigen presenting cells include macrophages, dendritic cells, and B cells. Other antigen presenting cells, including professional and nonprofessional APCs, are known in the art, and are encompassed herein. In some embodiments, the cell displaying the chimeric MHC I protein is a tumor cell, and a peptide fragment presented by the chimeric protein is derived from a tumor.", para [0013] "The human MHC I polypeptide may be HLA-A polypeptide, e.g., HLA-A2.1").

The inventions of Group II+ share the technical feature of a kit and polynucleotides for expression of the HLA A class I molecule in a host cell and a cell cuture system, including a medium comprising an HLA-restricted peptide. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is made obvious by Regeneron (para [0099] a method for making a chimeric human HLA class I/non-human MHC class I molecule is provided, comprising expressing in a single cell a chimeric HLA-A/H-2K protein from a nucleotide construct, wherein the nucleotide construct comprises a cDNA sequence that encodes an .alpha.1, .alpha.2, and .alpha.3 domain of an HLA-A protein and a transmembrane and cytoplasmic domain of a non-human H-2K protein, e.g., mouse H-2K protein. In one embodiment, the nucleotide construct is a viral vector") and an in vitro cell system for evaluating peptides (para [0002] "Also provided are methods for identifying and evaluating peptides in the context of a humanized cellular immune system in vitro", para [0009] "A biological system for generating or identifying peptides that associate with human MHC class I protein ... cells that express human or humanized MHC and .beta.2 microglobulin molecules are also provided. In vivo and in vitro systems are provided that comprise humanized rodent cells"). Although Regeneron does not recite a kit for expression of said expression system, it would be obvious to an artisan of ordinary skill to provide Regeneron's vectors and/or cells in the form of a kit. Regeneron does not expressly teach cultuing cell with a desired HLA restricted peptide, however, it would be obvious to culture Regeneron's cells with a peptide being evealuated.

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the inventions.

Groups I+ and II+ therefore lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.