## SUMMARY

**[0003a]** In one aspect, provided herein is a method of producing an *ex vivo* population of expanded antigen specific T cells, the method comprising:

(a) culturing T cells from a biological sample from a subject in a first cell culture medium comprising antigen presenting cells (APCs) to produce a first population of T cells, wherein the APCs present an epitope of a peptide antigen in complex with an MHC protein;

(b) culturing the first population of T cells in a second cell culture medium to produce a second population of T cells;

(c) enriching CD137 (4-1BB)-expressing T cells from the second population of T cells to produce a third population of T cells; and

expanding the third population of T cells in a third cell culture medium to obtain *ex vivo* population of expanded antigen specific T cells, wherein antigen specific T cells in the third population of T cells is at least ten-fold compared to antigen specific T cells in the first or the second population of T cells.

**[0003b]** In one aspect, provided herein is a method for producing an *ex vivo* population of expanded antigen specific therapeutic T cells, the method comprising:

(d) culturing T cells from a biological sample from a subject in a first cell culture medium comprising antigen presenting cells (APCs), wherein the APC's present an epitope of a peptide antigen in complex with an MHC protein;

(e) culturing the first population of T cells in a second cell culture medium to produce a second population of T cells; and

expanding the second population of T cells in a third cell culture medium in presence of an increasing concentration of a plurality of peptide antigens comprising the peptide antigen, thereby obtaining the *ex vivo* population of expanded antigen specific therapeutic T cells.

**[0003c]** In one aspect, provided herein is a pharmaceutical composition comprising a population of T cells comprising the *ex vivo* population of expended antigen-specific T cells as described herein and a therapeutically acceptable excipient.

**[0003d]** In one aspect, provided herein is a use of a composition comprising the *ex vivo* population of expanded antigen specific T cells as described herein in the manufacture of a medicament for treating cancer in a human subject.

**[0003e]** In one aspect, provided herein is a composition comprising the *ex vivo* population of expanded antigen specific T cells as described herein for use in therapy.

**[0004]** Provided herein is a method for producing a therapeutic population of T cells comprising: (a) culturing T cells from a biological sample from a subject in a first cell culture medium comprising antigen presenting cells (APCs) to produce a first population of T cells, wherein the APCs present an epitope of a peptide antigen in complex with an MHC protein; (b) optionally, culturing the first population of T cells in a second cell culture medium to produce a second population of T cells; (c) enriching CD137 (4-1BB)-expressing T cells and/or

CD69 expressing T cells from the first or second population of T cells to produce a third population of T cells; and (d) expanding the third population of T cells in a third cell culture medium to obtain a therapeutic population of T cells comprising antigen-specific T cells.

**[0005]** In some embodiments, the method comprises culturing the first population of T cells in a second cell culture medium to produce the second population of T cells, and enriching CD137 (4-1BB)-expressing T cells and/or CD69 expressing T cells from the second population of T cells to produce the third population of T cells.

**[0006]** Provided herein is a method for producing a therapeutic population of T cells comprising: (a) culturing T cells from a biological sample from a subject in a first cell culture medium comprising antigen presenting cells (APCs), wherein the APCs present an epitope of a peptide antigen in complex with an MHC protein; (b) culturing the first population of T cells in a second cell culture medium to produce a second population of T cells; (c) optionally, enriching CD137 (4-1BB)-expressing T cells and/or CD69 expressing T cells from the second population of T cells to produce a third population of T cells; and (d) expanding the second or third population of T cells in a third cell culture medium to obtain a therapeutic population of T cells comprising antigen-specific T cells; wherein the concentration of the peptide antigen in the third culture medium is at least 2-fold lower than the concentration of the peptide antigen in the first culture medium and/or second culture medium.

**[0007]** In some embodiments, the method comprises enriching CD137 (4-1BB)-expressing T cells and/or CD69 expressing T cells from the second population of T cells to produce a third population of T cells.

**[0008]** In some embodiments, enriching CD137 (4-1BB)-expressing T cells and/or CD69 expressing T cells from the second population of T cells begins 10, 11, 12, 13, 14, 15, 16, 17 or 18 days after beginning the culturing of the T cells from a biological sample from a subject in a first cell culture medium.

**[0009]** In some embodiments, the APCs (i) comprise a polynucleotide sequence encoding the peptide antigen, or (ii) are loaded with the epitope of a peptide antigen.

**[0010]** In some embodiments, the peptide antigen is directly added to the first cell culture medium.

**[0011]** In some embodiments, the first cell culture medium comprises a first concentration of the peptide antigen

**[0012]** In some embodiments, the method further comprises supplementing the first cell culture medium with an amount of the peptide antigen such that the first cell culture medium comprises a first concentration of the peptide antigen.

“conventional 5'-cap” refers to a naturally occurring RNA 5'-cap, to the 7-methylguanosine cap (m G). In the context of the present invention, the term “5'-cap” includes a 5'-cap analog that resembles the RNA cap structure and is modified to possess the ability to stabilize RNA and/or enhance translation of RNA if attached thereto, in vivo and/or in a cell. In some embodiments, mRNA is capped cotranscriptionally.

**[0373]** In some embodiments, the mRNA encoding one or more neoantigenic peptides comprise a 3’-UTR comprising a poly A tail. In some embodiments, the poly A tail is 100-200 bp long (SEQ ID NO: 184). In some embodiments, the poly A tail is longer than 20 nucleotides. In some embodiments, the poly A tail is longer than 50 nucleotides. In some embodiments, the poly A tail is longer than 60 nucleotides. In some embodiments, the poly A tail is longer than 70 nucleotides. In some embodiments, the poly A tail is longer than 80 nucleotides. In some embodiments, the poly A tail is longer than 90 nucleotides. In some embodiments, the poly A tail is longer than 100 nucleotides. In some embodiments, the poly A tail is longer than 110 nucleotides. In some embodiments, the poly A tail is longer than 120 nucleotides. In some embodiments, the poly A tail is longer than 130 nucleotides. In some embodiments, the poly A tail is longer than 140 nucleotides. In some embodiments, the poly A tail is longer than 150 nucleotides. In some embodiments, the poly A tail is longer than 160 nucleotides. In some embodiments, the poly A tail is longer than 170 nucleotides. In some embodiments, the poly A tail is longer than 180 nucleotides. In some embodiments, the poly A tail is longer than 190 nucleotides. In some embodiments, the poly A tail is longer than 200 nucleotides. In some embodiments, the poly A tail is longer than 210 nucleotides. In some embodiments, the poly A tail is longer than 220 nucleotides. In some embodiments, the poly A tail is longer than 230 nucleotides. In some embodiments, the poly A tail is longer than 100 nucleotides. In some embodiments, the poly A tail is longer than 240 nucleotides. In some embodiments, the poly A tail is longer than 100 nucleotides. In some embodiments, the poly A tail is about 250 nucleotides.

**[0374]** In some embodiments, the poly A tail comprises 100-250 adenosine units (SEQ ID NO: 185). In some embodiments, the poly A tail comprises 120-130 adenine units (SEQ ID NO: 186). In some embodiments, the poly A tail comprises 120 adenine units (SEQ ID NO: 187). In some embodiments, the poly A tail comprises 121 adenine units (SEQ ID NO: 188). In some embodiments, the poly A tail comprises 122 adenine units (SEQ ID NO: 189). In some embodiments, the poly A tail comprises 123 adenine units (SEQ ID NO: 190). In some embodiments, the poly A tail comprises 124 adenine units (SEQ ID NO: 191). In some embodiments, the poly A tail comprises 125 adenine units (SEQ ID NO: 192). In some embodiments, the poly A tail as 129 bases (SEQ ID NO: 193).

**[0375]** In some embodiments, the coding sequence for two consecutive neoantigenic peptides are separated by a spacer or linker.

**[0376]** In some embodiments, the spacer or linker comprises up to 5000 nucleotide residues. An exemplary spacer sequence is GGCGGCAGCGGCGGCGGCGGCAGCGGCGGC (SEQ ID NO: 1). Another exemplary spacer sequence is GGCGGCAGCCTGGGCGGCGGCGGCAGCGGC (SEQ ID NO: 2). Another exemplary spacer sequence is GGCGTCGGCACC (SEQ ID NO: 3). Another exemplary spacer sequence is

CAGCTGGGCCTG (SEQ ID NO: 4). Another exemplary spacer is a sequence that encodes a lysine, such as AAA or AAG. Another exemplary spacer sequence is CAACTGGGATTG (SEQ ID NO: 5).

| | | |
|---|---|---|
| Sterility | BACT/ALERT® | negative |

**[0657]** Safety tests are conducted with rapid methods to minimize time to product release. The current manufacturing process is estimated at 26 calendar days, with an overall turnaround time of 5 to 6 weeks at the initial phase. Due to the nature of autologous therapies and the indication (oncology), manufacturing turnaround is critical.

**Example 2. Exemplary peptide antigen:MHCs**

**[0658]** Provided below are exemplary RAS peptide:MHCs that can be used in the methods described herein.

**[0659]** In some embodiments, a peptide comprises a RAS mutation according to Table 1 below.

**Table 1A**

| **Gene** | **Exemplary Protein Change** | **Mutation Sequence Context** (Mutated non-native residue underlined) | SEQ ID NO: | **Exemplary Diseases** |
|---|---|---|---|---|
| KRAS | G12C | MTEYKLVVVGA<u>C</u>GVGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE | 6 | BRCA (breast cancer), CESC (cervical squamous cell carcinoma and endocervical adenocarcinoma), CRC (colorectal cancer), HNSC (head-neck squamous cell carcinoma), LUAD (lung adenocarcinoma), PAAD (pancreatic adenocarcinoma), UCEC (uterine corpus endometrial carcinoma) |
| KRAS | G12D | MTEYKLVVVGA<u>D</u>GVGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE | 7 | BLCA (urothelial bladder carcinoma), BRCA, CESC, CRC, GBM (glioblastoma), HNSC, KIRP (kidney renal papillary cell carcinoma), LIHC (liver hepatocellular carcinoma), LUAD, PAAD, SKCM (skin cutaneous melanoma), UCEC |
| KRAS | G12R | MTEYKLVVVGA<u>R</u>GVGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE | 8 | PDAC, LUAD |

| | | | | |
|---|---|---|---|---|
| KRAS | G12V | MTEYKLVVVGAVGVGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE | 9 | BRCA, CESC, CRC, LUAD, PAAD, THCA (thyroid carcinoma, UCEC |
| KRAS | Q61H | AGGVGKSALTIQLIQNHFVDEYDPTIEDSYRK QVVIDGETCLLDILDTAGHEEYSAMRDQYMR TGEGFLCVFAINNTKSFEDIHHYREQIKRVKD SEDVPM | 10 | CRC, LUSC (lung squamous cell carcinoma), PAAD, SKCM, UCEC |

| | | | | |
|---|---|---|---|---|
| KRAS | Q61L | AGGVGKSALTIQLIQNHFVDEYDPTIEDSYRK QVVIDGETCLLDILDTAGLEEYSAMRDQYMR TGEGFLCVFAINNTKSFEDIHHYREQIKRVKD SEDVPM | 11 | CRC, GBM, HNSC, LUAD, SKCM, UCEC |

**[0660]** Table 1B below shows an exemplary pool of mutated RAS peptides used in the methods described herein.

**Table 1B**

| KRAS Mutation | Peptide name | Sequence | SEQ ID NO: | MS Validated HLA-I Alleles |
|---|---|---|---|---|
| G12D | AS2 | GADGVGKSA | 12 | C08:02 |
| | AS3 | GADGVGKSAL | 13 | B07:02, C08:02, C03:04 |
| | AS4 | VVVGADGVGK | 14 | A03:01, A11:01, A68:01 |
| | AL1 | KKKTEYKLVVVGADGVGKSALTIQL | 15 | N/A |
| G12V | BS1 | AVGVGKSAL | 16 | C01:02 |
| | BS2 | GAVGVGKSA | 17 | C03:03, C03:04 |
| | BS3 | GAVGVGKSAL | 18 | C03:03, C03:04 |
| | BS4 | VVGAVGVGK | 19 | A03:01, A11:01, A30:01, A68:01 |
| | BS5 | VVVGAVGVGK | 20 | A03:01, A11:01, A30:01, A68:01 |
| | BL1 | KKKKTEYKLVVVGAVGVGKSALTIQL | 21 | N/A |
| G12R | CS2 | GARGVGKSAL | 22 | B07:02 |
| | CS3 | VVVGARGVGK | 23 | A03:01, A11:01, A30:01, A68:01 |
| | CL1 | KKKTEYKLVVVGARGVGKSALTIQL | 24 | N/A |
| G12C | DS1 | VVVGACGVGK | 25 | A03:01, A11:01, A68:01 |
| | DL1 | KKKKTEYKLVVVGACGVGKSALTIQL | 26 | N/A |

**[0661]** In some embodiments, a peptide comprises a RAS Q61H mutation according to Table 2 below.

**Table 2**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| ILDTAGHEEY | 27 | HLA-A36:01 | 1 |
| ILDTAGHEEY | 27 | HLA-A01:01 | 2 |
| DTAGHEEYSAM | 28 | HLA-A26:01 | 3 |
| DTAGHEEYSAM | 28 | HLA-A25:01 | 4 |
| GHEEYSAM | 29 | HLA-B15:09 | 4 |
| DTAGHEEY | 30 | HLA-A26:01 | 5 |

| | | | |
|---|---|---|---|
| ILDTAGHEE | 31 | HLA-C08:02 | 5 |
| AGHEEYSAM | 32 | HLA-C01:02 | 6 |
| AGHEEYSAM | 32 | HLA-B46:01 | 6 |

| | | | |
|---|---|---|---|
| DTAGHEEY | 30 | HLA-A25:01 | 6 |
| DTAGHEEY | 30 | HLA-A01:01 | 6 |
| DTAGHEEY | 30 | HLA-B18:01 | 7 |
| DTAGHEEY | 30 | HLA-A36:01 | 7 |
| ILDTAGHEE | 31 | HLA-C05:01 | 7 |
| ILDTAGHEE | 31 | HLA-A02:07 | 7 |
| ILDTAGHEEY | 27 | HLA-A29:02 | 7 |
| ILDTAGHEEY | 27 | HLA-C08:02 | 7 |
| HEEYSAMRD | 33 | HLA-B49:01 | 8 |
| TAGHEEYSA | 34 | HLA-B35:03 | 8 |
| DTAGHEEYS | 35 | HLA-A68:02 | 9 |
| DTAGHEEYSAMR | 36 | HLA-A68:01 | 9 |
| GHEEYSAM | 29 | HLA-B39:01 | 9 |
| ILDTAGHEE | 31 | HLA-A01:01 | 9 |
| LDTAGHEEY | 37 | HLA-B53:01 | 9 |
| HEEYSAMRD | 33 | HLA-B41:01 | 10 |
| ILDTAGHEE | 31 | HLA-A36:01 | 10 |
| DTAGHEEY | 30 | HLA-B58:01 | 11 |
| LLDILDTAGH | 38 | HLA-A01:01 | 12 |
| TAGHEEYSAM | 39 | HLA-B35:03 | 12 |
| LDTAGHEEY | 37 | HLA-B35:01 | 13 |
| DILDTAGHE | 40 | HLA-A26:01 | 14 |
| DTAGHEEY | 30 | HLA-C12:03 | 14 |
| ILDTAGHEEY | 27 | HLA-C05:01 | 14 |
| AGHEEYSAM | 32 | HLA-A30:02 | 15 |
| DILDTAGHEEY | 41 | HLA-A25:01 | 15 |
| DTAGHEEY | 30 | HLA-C02:02 | 15 |
| ILDTAGHEE | 31 | HLA-C04:01 | 15 |
| DILDTAGH | 42 | HLA-A26:01 | 16 |
| ILDTAGHEE | 31 | HLA-A02:01 | 16 |
| LDTAGHEEY | 37 | HLA-A29:02 | 16 |
| ILDTAGHE | 43 | HLA-A01:01 | 17 |
| LDTAGHEEY | 37 | HLA-B18:01 | 17 |
| AGHEEYSAM | 32 | HLA-C14:03 | 18 |
| DILDTAGHEEY | 41 | HLA-A29:02 | 18 |

| | | | |
|---|---|---|---|
| DTAGHEEYS | 35 | HLA-A26:01 | 18 |
| ILDTAGHEEY | 27 | HLA-B15:01 | 18 |
| DTAGHEEYSA | 44 | HLA-A68:02 | 19 |
| ILDTAGHE | 43 | HLA-C05:01 | 19 |
| ILDTAGHEEY | 27 | HLA-A02:07 | 19 |
| ILDTAGHEEY | 27 | HLA-A30:02 | 19 |
| LDTAGHEEY | 37 | HLA-A36:01 | 19 |
| AGHEEYSAM | 32 | HLA-C14:02 | 20 |
| AGHEEYSAM | 32 | HLA-B15:03 | 20 |
| LLDILDTAGH | 38 | HLA-A02:07 | 20 |

**[0662]** In some embodiments, a peptide comprises a RAS Q61R mutation according to Table 3 below.

**Table 3**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| ILDTAGREEY | 45 | HLA-A36:01 | 1 |
| ILDTAGREEY | 45 | HLA-A01:01 | 2 |
| DTAGREEYSAM | 46 | HLA-A26:01 | 3 |
| DILDTAGR | 47 | HLA-A33:03 | 4 |
| DILDTAGR | 47 | HLA-A68:01 | 5 |
| DTAGREEY | 48 | HLA-A26:01 | 6 |
| DTAGREEYSAM | 46 | HLA-A25:01 | 6 |
| CLLDILDTAGR | 49 | HLA-A74:01 | 7 |
| DTAGREEY | 48 | HLA-A01:01 | 7 |
| REEYSAMRD | 50 | HLA-B41:01 | 7 |
| GREEYSAMR | 51 | HLA-B27:05 | 8 |
| ILDTAGREE | 52 | HLA-C08:02 | 8 |
| ILDTAGREEY | 45 | HLA-A29:02 | 8 |
| REEYSAMRD | 50 | HLA-B49:01 | 8 |
| AGREEYSAM | 53 | HLA-B46:01 | 9 |
| DTAGREEY | 48 | HLA-B18:01 | 9 |
| DTAGREEY | 48 | HLA-A25:01 | 9 |
| DTAGREEY | 48 | HLA-A36:01 | 9 |
| DILDTAGR | 47 | HLA-A74:01 | 10 |
| DILDTAGRE | 54 | HLA-A26:01 | 10 |
| ILDTAGREE | 52 | HLA-C05:01 | 10 |
| DILDTAGR | 47 | HLA-A26:01 | 11 |
| GREEYSAM | 55 | HLA-B39:01 | 11 |
| AGREEYSAM | 53 | HLA-B15:03 | 12 |
| GREEYSAM | 55 | HLA-C07:02 | 12 |
| ILDTAGREE | 52 | HLA-A01:01 | 12 |
| TAGREEYSA | 56 | HLA-B35:03 | 12 |

| | | | |
|---|---|---|---|
| ILDTAGREEY | 45 | HLA-A30:02 | 13 |
| DTAGREEYS | 57 | HLA-A68:02 | 14 |
| ILDTAGRE | 58 | HLA-A01:01 | 14 |
| CLLDILDTAGR | 49 | HLA-A31:01 | 15 |
| DTAGREEYSAMR | 59 | HLA-A68:01 | 15 |
| LLDILDTAGR | 60 | HLA-A01:01 | 15 |
| DTAGREEY | 48 | HLA-B58:01 | 16 |
| ILDTAGREEY | 45 | HLA-C08:02 | 16 |
| DILDTAGR | 47 | HLA-A31:01 | 17 |
| ILDTAGREE | 52 | HLA-C04:01 | 17 |
| ILDTAGREEY | 45 | HLA-A32:01 | 17 |
| LLDILDTAGR | 60 | HLA-A74:01 | 17 |
| TAGREEYSAM | 61 | HLA-B35:03 | 17 |
| DILDTAGREEY | 62 | HLA-A32:01 | 18 |
| ILDTAGRE | 58 | HLA-C05:01 | 18 |
| ILDTAGREE | 52 | HLA-A02:07 | 18 |
| REEYSAMRD | 50 | HLA-B40:01 | 18 |
| AGREEYSAM | 53 | HLA-B15:01 | 19 |
| AGREEYSAMR | 63 | HLA-A31:01 | 19 |
| ILDTAGRE | 58 | HLA-A36:01 | 19 |
| LDILDTAGR | 64 | HLA-A68:01 | 19 |
| LDTAGREEY | 65 | HLA-A29:02 | 19 |
| LDTAGREEY | 65 | HLA-B35:01 | 19 |
| REEYSAMRD | 50 | HLA-B45:01 | 19 |
| REEYSAMRDQY | 66 | HLA-A36:01 | 19 |
| DTAGREEY | 48 | HLA-C02:02 | 20 |

**[0663]** In some embodiments, a peptide comprises a RAS Q61K mutation according to Table 4 below.

**Table 4**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| ILDTAGKEEY | 67 | HLA-A36:01 | 1 |
| ILDTAGKEEY | 67 | HLA-A01:01 | 2 |
| DTAGKEEYSAM | 68 | HLA-A26:01 | 3 |
| CLLDILDTAGK | 69 | HLA-A03:01 | 4 |
| DTAGKEEY | 70 | HLA-A01:01 | 5 |
| DTAGKEEY | 70 | HLA-A26:01 | 5 |
| DTAGKEEYSAM | 68 | HLA-A25:01 | 5 |
| AGKEEYSAM | 71 | HLA-B46:01 | 6 |
| DILDTAGKE | 72 | HLA-A26:01 | 7 |
| KEEYSAMRD | 73 | HLA-B41:01 | 7 |
| DTAGKEEY | 70 | HLA-B18:01 | 8 |
| GKEEYSAM | 74 | HLA-B15:03 | 8 |
| ILDTAGKEE | 75 | HLA-C08:02 | 8 |
| ILDTAGKEEY | 67 | HLA-A29:02 | 8 |

| | | | |
|---|---|---|---|
| DTAGKEEYS | 76 | HLA-A68:02 | 9 |
| LDTAGKEEY | 77 | HLA-B53:01 | 9 |
| TAGKEEYSA | 78 | HLA-B35:03 | 9 |
| DILDTAGK | 79 | HLA-A68:01 | 10 |
| DTAGKEEY | 70 | HLA-A36:01 | 10 |
| KEEYSAMRD | 73 | HLA-B49:01 | 10 |
| LDTAGKEEY | 77 | HLA-C07:01 | 10 |
| DTAGKEEYSAMR | 80 | HLA-A68:01 | 11 |
| ILDTAGKEE | 75 | HLA-C05:01 | 11 |
| ILDTAGKEEY | 67 | HLA-C08:02 | 11 |
| LLDILDTAGK | 81 | HLA-A01:01 | 12 |
| AGKEEYSAM | 71 | HLA-A30:02 | 13 |
| DTAGKEEY | 70 | HLA-A25:01 | 13 |
| DTAGKEEYS | 76 | HLA-A26:01 | 13 |
| ILDTAGKE | 82 | HLA-C05:01 | 13 |
| LDTAGKEEY | 77 | HLA-B35:01 | 13 |
| AGKEEYSAMR | 83 | HLA-A31:01 | 14 |
| DILDTAGK | 79 | HLA-A33:03 | 14 |
| ILDTAGKE | 82 | HLA-A01:01 | 14 |
| ILDTAGKEE | 75 | HLA-A01:01 | 14 |
| ILDTAGKEE | 75 | HLA-A02:07 | 14 |
| TAGKEEYSAM | 84 | HLA-B35:03 | 14 |
| AGKEEYSAM | 71 | HLA-B15:01 | 15 |
| ILDTAGKEEY | 67 | HLA-A30:02 | 15 |
| LDTAGKEEY | 77 | HLA-B46:01 | 15 |
| DTAGKEEY | 70 | HLA-B58:01 | 16 |
| ILDTAGKEEY | 67 | HLA-C05:01 | 17 |
| AGKEEYSAM | 71 | HLA-A30:01 | 18 |
| AGKEEYSAM | 71 | HLA-B15:03 | 18 |
| DTAGKEEY | 70 | HLA-C02:02 | 18 |
| LDTAGKEEY | 77 | HLA-A29:02 | 18 |

**[0664]** In some embodiments, a peptide comprises a RAS Q61L mutation according to Table 5 below.

**Table 5**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| ILDTAGLEEY | 85 | HLA-A36:01 | 1 |
| ILDTAGLEEY | 85 | HLA-A01:01 | 2 |
| LLDILDTAGL | 86 | HLA-A02:07 | 3 |
| GLEEYSAMRDQY | 87 | HLA-A36:01 | 4 |
| DTAGLEEY | 88 | HLA-A25:01 | 5 |
| DTAGLEEY | 88 | HLA-A26:01 | 5 |
| DTAGLEEYSAM | 89 | HLA-A26:01 | 5 |
| DTAGLEEY | 88 | HLA-A01:01 | 6 |
| ILDTAGLEE | 90 | HLA-C08:02 | 6 |

| | | | |
|---|---|---|---|
| ILDTAGLEE | 90 | HLA-A01:01 | 6 |
| CLLDILDTAGL | 91 | HLA-A02:04 | 7 |
| ILDTAGLEE | 90 | HLA-A36:01 | 7 |
| LLDILDTAGL | 86 | HLA-A01:01 | 7 |
| DILDTAGL | 92 | HLA-B14:02 | 8 |
| DILDTAGLEEY | 93 | HLA-A25:01 | 8 |
| DTAGLEEYS | 94 | HLA-A68:02 | 8 |
| DTAGLEEYSAM | 89 | HLA-A25:01 | 8 |
| GLEEYSAMR | 95 | HLA-A74:01 | 8 |
| ILDTAGLE | 96 | HLA-A01:01 | 8 |
| DILDTAGLEEY | 93 | HLA-A26:01 | 9 |
| DTAGLEEY | 88 | HLA-A36:01 | 9 |
| ILDTAGLEEY | 85 | HLA-A29:02 | 9 |
| DILDTAGL | 92 | HLA-B08:01 | 10 |
| DTAGLEEY | 88 | HLA-B18:01 | 10 |
| ILDTAGLEE | 90 | HLA-A02:07 | 10 |
| LDTAGLEEY | 97 | HLA-B35:01 | 10 |
| CLLDILDTAGL | 91 | HLA-A02:01 | 11 |
| DTAGLEEY | 88 | HLA-C02:02 | 11 |
| ILDTAGLEE | 90 | HLA-C05:01 | 11 |
| ILDTAGLEEY | 85 | HLA-C08:02 | 11 |
| ILDTAGLEEY | 85 | HLA-A02:07 | 11 |
| LLDILDTAGL | 86 | HLA-C08:02 | 11 |
| DILDTAGL | 92 | HLA-A26:01 | 12 |
| LDTAGLEEY | 97 | HLA-B53:01 | 12 |
| DTAGLEEY | 88 | HLA-C03:02 | 13 |
| DTAGLEEY | 88 | HLA-B58:01 | 13 |
| ILDTAGLEEY | 85 | HLA-A30:02 | 13 |
| LLDILDTAGL | 86 | HLA-C05:01 | 13 |
| LLDILDTAGL | 86 | HLA-C04:01 | 13 |
| DTAGLEEYSAMR | 98 | HLA-A68:01 | 14 |
| ILDTAGLE | 96 | HLA-A36:01 | 15 |
| LLDILDTAGL | 86 | HLA-A02:01 | 15 |
| AGLEEYSAM | 99 | HLA-B15:03 | 16 |
| DTAGLEEYSA | 100 | HLA-A68:02 | 16 |
| GLEEYSAMRDQY | 87 | HLA-A01:01 | 16 |
| ILDTAGLE | 96 | HLA-C04:01 | 16 |
| ILDTAGLEEY | 85 | HLA-B15:01 | 16 |
| LDILDTAGL | 101 | HLA-B37:01 | 16 |
| AGLEEYSAM | 99 | HLA-A30:02 | 17 |
| AGLEEYSAM | 99 | HLA-B48:01 | 17 |
| AGLEEYSAMR | 102 | HLA-A31:01 | 17 |
| ILDTAGLEE | 90 | HLA-C04:01 | 17 |
| LDTAGLEEY | 97 | HLA-C03:02 | 17 |

| | | | |
|---|---|---|---|
| AGLEEYSAM | 99 | HLA-C14:02 | 18 |
| GLEEYSAMR | 95 | HLA-A31:01 | 18 |
| LEEYSAMRD | 103 | HLA-B41:01 | 18 |
| LLDILDTAGLE | 104 | HLA-A01:01 | 18 |
| AGLEEYSAM | 99 | HLA-C14:03 | 19 |
| LDILDTAGL | 101 | HLA-B40:02 | 19 |
| LDTAGLEEY | 97 | HLA-A29:02 | 19 |
| DILDTAGLE | 105 | HLA-A26:01 | 20 |
| DTAGLEEY | 88 | HLA-B15:01 | 20 |
| ILDTAGLEEY | 85 | HLA-A02:01 | 20 |
| LDTAGLEEY | 97 | HLA-A36:01 | 20 |
| LDTAGLEEY | 97 | HLA-B46:01 | 20 |
| DTAGLEEY | 88 | HLA-A68:02 | 21 |
| DTAGLEEY | 88 | HLA-C12:03 | 21 |
| ILDTAGLE | 96 | HLA-C05:01 | 21 |
| LDTAGLEEY | 97 | HLA-B18:01 | 21 |
| LEEYSAMRD | 103 | HLA-B49:01 | 21 |
| TAGLEEYSA | 106 | HLA-B54:01 | 21 |
| DILDTAGLEEY | 93 | HLA-A29:02 | 22 |
| GLEEYSAM | 107 | HLA-C05:01 | 22 |

**[0665]** In some embodiments, a peptide comprises a RAS G12A mutation according to Table 6 below.

**Table 6**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| AAGVGKSAL | 108 | HLA-C03:04 | 1 |
| VVVGAAGVGK | 109 | HLA-A11:01 | 1 |
| VVGAAGVGK | 110 | HLA-A11:01 | 2 |
| TEYKLVVVGAA | 111 | HLA-B50:01 | 3 |
| VVGAAGVGK | 110 | HLA-A03:01 | 3 |
| VVVGAAGVGK | 109 | HLA-A68:01 | 3 |
| AAGVGKSAL | 108 | HLA-C08:02 | 4 |
| AAGVGKSAL | 108 | HLA-C08:01 | 4 |
| AAGVGKSAL | 108 | HLA-B46:01 | 4 |
| AAGVGKSAL | 108 | HLA-B81:01 | 5 |
| GAAGVGKSAL | 112 | HLA-B48:01 | 5 |
| LVVVGAAGV | 113 | HLA-A68:02 | 5 |
| AAGVGKSAL | 108 | HLA-C03:04 | 1 |
| VVVGAAGVGK | 109 | HLA-A11:01 | 1 |
| VVGAAGVGK | 110 | HLA-A11:01 | 2 |
| TEYKLVVVGAA | 111 | HLA-B50:01 | 3 |
| VVGAAGVGK | 110 | HLA-A03:01 | 3 |
| VVVGAAGVGK | 109 | HLA-A68:01 | 3 |
| AAGVGKSAL | 108 | HLA-C08:02 | 4 |
| AAGVGKSAL | 108 | HLA-C08:01 | 4 |

| | | | |
|---|---|---|---|
| AAGVGKSAL | 108 | HLA-B46:01 | 4 |
| AAGVGKSAL | 108 | HLA-B81:01 | 5 |
| AAGVGKSAL | 108 | HLA-C03:02 | 5 |
| AAGVGKSAL | 108 | HLA-C01:02 | 5 |
| GAAGVGKSAL | 112 | HLA-B48:01 | 5 |
| LVVVGAAGV | 113 | HLA-A68:02 | 5 |
| AAGVGKSAL | 108 | HLA-C03:03 | 6 |
| VVGAAGVGK | 110 | HLA-A68:01 | 6 |
| GAAGVGKSAL | 112 | HLA-B81:01 | 7 |
| VVVGAAGVGK | 109 | HLA-A03:01 | 7 |
| AAGVGKSAL | 108 | HLA-C05:01 | 8 |
| AAGVGKSAL | 108 | HLA-C12:03 | 8 |
| GAAGVGKSA | 114 | HLA-B46:01 | 8 |
| VVGAAGVGK | 110 | HLA-A30:01 | 8 |
| GAAGVGKSA | 114 | HLA-B55:01 | 9 |
| KLVVVGAAGV | 115 | HLA-A02:01 | 9 |
| AGVGKSAL | 116 | HLA-B08:01 | 10 |
| GAAGVGKSAL | 112 | HLA-C03:04 | 10 |
| AAGVGKSAL | 108 | HLA-C17:01 | 11 |
| GAAGVGKSAL | 112 | HLA-C03:03 | 11 |
| VVVGAAGV | 117 | HLA-A68:02 | 11 |
| YKLVVVGAA | 118 | HLA-B54:01 | 11 |
| AAGVGKSAL | 108 | HLA-B48:01 | 12 |
| AGVGKSAL | 116 | HLA-C03:04 | 12 |
| AGVGKSAL | 116 | HLA-C07:01 | 12 |
| VVVGAAGVGK | 109 | HLA-A30:01 | 12 |
| AAGVGKSA | 119 | HLA-B46:01 | 13 |
| KLVVVGAAGV | 115 | HLA-A02:07 | 13 |
| YKLVVVGAA | 118 | HLA-B50:01 | 13 |
| AAGVGKSAL | 108 | HLA-B07:02 | 14 |
| GAAGVGKSAL | 112 | HLA-A68:02 | 14 |
| VVGAAGVGK | 110 | HLA-A74:01 | 14 |
| AGVGKSAL | 116 | HLA-C08:01 | 15 |
| GAAGVGKSAL | 112 | HLA-C17:01 | 15 |
| GAAGVGKSAL | 112 | HLA-C08:01 | 16 |
| GAAGVGKSAL | 112 | HLA-B35:03 | 16 |
| AAGVGKSAL | 108 | HLA-C02:02 | 17 |
| AAGVGKSAL | 108 | HLA-B35:03 | 17 |
| AAGVGKSAL | 108 | HLA-C12:02 | 17 |
| AAGVGKSAL | 108 | HLA-C14:03 | 17 |
| GAAGVGKSA | 114 | HLA-B50:01 | 17 |
| AGVGKSAL | 116 | HLA-C03:02 | 18 |
| GAAGVGKSA | 114 | HLA-C03:04 | 18 |
| LVVVGAAGV | 113 | HLA-B55:01 | 18 |

| | | | |
|---|---|---|---|
| TEYKLVVVGAA | 111 | HLA-B41:01 | 18 |
| AGVGKSAL | 116 | HLA-C01:02 | 19 |
| GAAGVGKSA | 114 | HLA-B54:01 | 19 |
| GAAGVGKSAL | 112 | HLA-B07:02 | 19 |
| VGAAGVGKSA | 120 | HLA-B55:01 | 19 |
| AGVGKSAL | 116 | HLA-B48:01 | 20 |
| AGVGKSALTI | 121 | HLA-B49:01 | 20 |
| VVVGAAGV | 117 | HLA-B55:01 | 20 |

**[0666]** In some embodiments, a peptide comprises a RAS G12C mutation according to Table 7 below.

**Table 7**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| VVVGACGVGK | 25 | HLA-A11:01 | 1 |
| VVGACGVGK | 122 | HLA-A03:01 | 2 |
| VVGACGVGK | 122 | HLA-A11:01 | 3 |
| VVVGACGVGK | 25 | HLA-A68:01 | 4 |
| VVGACGVGK | 122 | HLA-A68:01 | 5 |
| VVVGACGVGK | 25 | HLA-A03:01 | 5 |
| VVGACGVGK | 122 | HLA-A30:01 | 6 |
| ACGVGKSAL | 123 | HLA-B81:01 | 7 |
| ACGVGKSAL | 123 | HLA-C01:02 | 7 |
| ACGVGKSAL | 123 | HLA-C14:03 | 8 |
| ACGVGKSAL | 123 | HLA-C03:04 | 9 |
| VVVGACGVGK | 25 | HLA-A30:01 | 9 |
| ACGVGKSAL | 123 | HLA-C14:02 | 10 |
| CGVGKSAL | 124 | HLA-B08:01 | 10 |
| KLVVVGACGV | 125 | HLA-A02:01 | 10 |
| ACGVGKSAL | 123 | HLA-B07:02 | 11 |
| GACGVGKSAL | 126 | HLA-B48:01 | 12 |
| GACGVGKSAL | 126 | HLA-C03:03 | 13 |
| ACGVGKSAL | 123 | HLA-B48:01 | 14 |
| ACGVGKSAL | 123 | HLA-B40:01 | 14 |
| YKLVVVGAC | 127 | HLA-B48:01 | 14 |
| YKLVVVGAC | 127 | HLA-B15:03 | 14 |
| GACGVGKSA | 128 | HLA-B46:01 | 15 |
| GACGVGKSAL | 126 | HLA-C03:04 | 15 |
| GACGVGKSAL | 126 | HLA-C01:02 | 15 |
| LVVVGACGV | 129 | HLA-A68:02 | 15 |
| CGVGKSAL | 124 | HLA-C03:04 | 16 |
| GACGVGKSAL | 126 | HLA-C08:02 | 16 |
| VVGACGVGK | 122 | HLA-A74:01 | 16 |

**[0667]** In some embodiments, a peptide comprises a RAS G12D mutation according to Table 8 below.

**Table 8**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| GADGVGKSAL | 13 | HLA-C08:02 | 1 |
| GADGVGKSAL | 13 | HLA-C05:01 | 2 |
| VVVGADGVGK | 14 | HLA-A11:01 | 3 |
| DGVGKSAL | 130 | HLA-B14:02 | 4 |
| VVGADGVGK | 131 | HLA-A11:01 | 4 |
| VVGADGVGK | 131 | HLA-A03:01 | 5 |
| DGVGKSAL | 130 | HLA-B08:01 | 6 |
| VVVGADGVGK | 14 | HLA-A68:01 | 6 |
| GADGVGKSAL | 13 | HLA-C03:03 | 7 |
| VVGADGVGK | 131 | HLA-A30:01 | 7 |
| ADGVGKSAL | 132 | HLA-B37:01 | 8 |
| GADGVGKSAL | 13 | HLA-C08:01 | 8 |
| VVGADGVGK | 131 | HLA-A68:01 | 8 |
| GADGVGKSA | 12 | HLA-C08:02 | 9 |
| GADGVGKSAL | 13 | HLA-B35:03 | 9 |
| GADGVGKS | 133 | HLA-C05:01 | 10 |
| GADGVGKSA | 12 | HLA-C05:01 | 10 |
| ADGVGKSAL | 132 | HLA-C07:01 | 11 |
| VVVGADGVGK | 14 | HLA-A03:01 | 11 |
| ADGVGKSAL | 132 | HLA-B40:02 | 12 |
| ADGVGKSAL | 132 | HLA-B46:01 | 13 |
| GADGVGKSAL | 13 | HLA-C03:04 | 13 |
| ADGVGKSAL | 132 | HLA-B81:01 | 14 |
| GADGVGKSAL | 13 | HLA-C17:01 | 14 |
| VVVGADGVGK | 14 | HLA-A30:01 | 14 |
| GADGVGKSA | 12 | HLA-B35:03 | 15 |
| GADGVGKSA | 12 | HLA-B46:01 | 15 |
| GADGVGKSAL | 13 | HLA-B48:01 | 15 |
| KLVVVGADGV | 134 | HLA-A02:01 | 15 |
| LVVVGADGV | 135 | HLA-A68:02 | 15 |
| VGADGVGKSA | 136 | HLA-B55:01 | 15 |
| VVGADGVGK | 131 | HLA-A74:01 | 16 |
| GADGVGKSA | 12 | HLA-B53:01 | 17 |
| KLVVVGADGV | 134 | HLA-A02:07 | 17 |
| VGADGVGK | 137 | HLA-A68:01 | 17 |
| YKLVVVGAD | 138 | HLA-B48:01 | 17 |
| ADGVGKSAL | 132 | HLA-C14:03 | 18 |
| DGVGKSALTI | 139 | HLA-B51:01 | 18 |
| VGADGVGK | 137 | HLA-A11:01 | 18 |

**[0668]** In some embodiments, a peptide comprises a RAS G12R mutation according to Table 9 below.

**Table 9**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| VVGARGVGK | 140 | HLA-A03:01 | 1 |
| EYKLVVVGAR | 141 | HLA-A33:03 | 2 |
| VVVGARGVGK | 23 | HLA-A11:01 | 3 |
| ARGVGKSAL | 142 | HLA-C07:02 | 4 |
| ARGVGKSAL | 142 | HLA-B39:01 | 5 |
| ARGVGKSAL | 142 | HLA-C07:01 | 5 |
| VVGARGVGK | 140 | HLA-A11:01 | 5 |
| VVVGARGVGK | 23 | HLA-A68:01 | 5 |
| GARGVGKSA | 143 | HLA-B46:01 | 6 |
| ARGVGKSAL | 142 | HLA-B27:05 | 7 |
| GARGVGKSA | 143 | HLA-B55:01 | 7 |
| RGVGKSAL | 144 | HLA-C07:01 | 8 |
| VVGARGVGK | 140 | HLA-A30:01 | 9 |
| ARGVGKSAL | 142 | HLA-B38:01 | 10 |
| ARGVGKSAL | 142 | HLA-B14:02 | 10 |
| VVGARGVGK | 140 | HLA-A68:01 | 10 |
| VVVGARGVGK | 23 | HLA-A03:01 | 11 |
| GARGVGKSAL | 22 | HLA-B48:01 | 12 |
| RGVGKSAL | 144 | HLA-B48:01 | 12 |
| RGVGKSALTI | 145 | HLA-A23:01 | 12 |
| ARGVGKSAL | 142 | HLA-C06:02 | 13 |
| GARGVGKSA | 143 | HLA-A30:01 | 13 |
| GARGVGKSAL | 22 | HLA-B81:01 | 13 |
| VVVGARGVGK | 23 | HLA-A30:01 | 13 |
| GARGVGKSAL | 22 | HLA-B07:02 | 14 |
| LVVVGARGV | 146 | HLA-C06:02 | 14 |
| RGVGKSAL | 144 | HLA-B81:01 | 14 |
| VVGARGVGK | 140 | HLA-A74:01 | 15 |
| KLVVVGARGV | 147 | HLA-A02:01 | 16 |
| LVVVGARGV | 146 | HLA-B55:01 | 16 |
| YKLVVVGAR | 148 | HLA-A33:03 | 16 |
| KLVVVGAR | 149 | HLA-A74:01 | 17 |
| KLVVVGARGV | 147 | HLA-B13:02 | 17 |
| RGVGKSAL | 144 | HLA-C01:02 | 17 |
| LVVVGARGV | 146 | HLA-A68:02 | 18 |
| VVVGARGV | 150 | HLA-B55:01 | 18 |
| ARGVGKSAL | 142 | HLA-B15:09 | 19 |
| ARGVGKSAL | 142 | HLA-C14:03 | 20 |
| GARGVGKSA | 143 | HLA-B54:01 | 20 |
| VVVGARGV | 150 | HLA-B52:01 | 20 |

**[0669]** In some embodiments, a peptide comprises a RAS G12S mutation according to Table 10 below.

**Table 10**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| VVVGASGVGK | 151 | HLA-A11:01 | 1 |
| VVGASGVGK | 152 | HLA-A11:01 | 2 |
| VVGASGVGK | 152 | HLA-A03:01 | 3 |
| VVVGASGVGK | 151 | HLA-A68:01 | 4 |
| ASGVGKSAL | 153 | HLA-C03:04 | 5 |
| ASGVGKSAL | 153 | HLA-B46:01 | 5 |
| VVGASGVGK | 152 | HLA-A68:01 | 6 |
| VVVGASGVGK | 151 | HLA-A03:01 | 6 |
| ASGVGKSAL | 153 | HLA-C01:02 | 7 |
| GASGVGKSAL | 154 | HLA-B48:01 | 7 |
| ASGVGKSAL | 153 | HLA-C07:01 | 8 |
| ASGVGKSAL | 153 | HLA-C08:02 | 9 |
| GASGVGKSAL | 154 | HLA-B81:01 | 9 |
| SGVGKSAL | 155 | HLA-B08:01 | 9 |
| ASGVGKSAL | 153 | HLA-C03:03 | 10 |
| ASGVGKSAL | 153 | HLA-C03:02 | 10 |
| SGVGKSAL | 155 | HLA-B14:02 | 10 |
| VVGASGVGK | 152 | HLA-A30:01 | 10 |
| ASGVGKSAL | 153 | HLA-C08:01 | 11 |
| VVVGASGVGK | 151 | HLA-A30:01 | 11 |
| GASGVGKSAL | 154 | HLA-B35:03 | 12 |
| SGVGKSAL | 155 | HLA-C07:01 | 12 |
| ASGVGKSAL | 153 | HLA-B81:01 | 13 |
| GASGVGKSA | 156 | HLA-B55:01 | 13 |
| GASGVGKSAL | 154 | HLA-C03:03 | 13 |
| KLVVVGASGV | 157 | HLA-A02:01 | 13 |
| LVVVGASGV | 158 | HLA-A68:02 | 13 |
| SGVGKSAL | 155 | HLA-C01:02 | 13 |
| ASGVGKSA | 159 | HLA-B46:01 | 14 |
| ASGVGKSAL | 153 | HLA-C15:02 | 14 |
| GASGVGKSAL | 154 | HLA-C08:01 | 15 |
| SGVGKSAL | 155 | HLA-C03:04 | 15 |
| ASGVGKSAL | 153 | HLA-C05:01 | 16 |
| GASGVGKSAL | 154 | HLA-C03:04 | 16 |
| VVGASGVGK | 152 | HLA-A74:01 | 16 |
| ASGVGKSAL | 153 | HLA-B48:01 | 17 |
| GASGVGKSAL | 154 | HLA-C01:02 | 17 |
| SGVGKSAL | 155 | HLA-C03:02 | 17 |
| SGVGKSALTI | 160 | HLA-A23:01 | 17 |
| VGASGVGKSA | 161 | HLA-B55:01 | 18 |
| ASGVGKSAL | 153 | HLA-C12:03 | 19 |
| ASGVGKSAL | 153 | HLA-B57:03 | 19 |
| KLVVVGASGV | 157 | HLA-A02:07 | 19 |

| | | | |
|---|---|---|---|
| SGVGKSAL | 155 | HLA-B81:01 | 19 |
| ASGVGKSAL | 153 | HLA-C17:01 | 20 |
| KLVVVGASG | 162 | HLA-A32:01 | 20 |

**[0670]** In some embodiments, a peptide comprises a RAS G12V mutation according to Table 11 below.

**Table 11**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| VVGAVGVGK | 19 | HLA-A03:01 | 1 |
| VVGAVGVGK | 19 | HLA-A11:01 | 2 |
| VVVGAVGVGK | 20 | HLA-A11:01 | 2 |
| VVVGAVGVGK | 20 | HLA-A68:01 | 3 |
| VVGAVGVGK | 19 | HLA-A68:01 | 4 |
| LVVVGAVGV | 163 | HLA-A68:02 | 5 |
| VVGAVGVGK | 19 | HLA-A30:01 | 5 |
| AVGVGKSAL | 16 | HLA-B81:01 | 6 |
| KLVVVGAVGV | 164 | HLA-A02:01 | 6 |
| AVGVGKSAL | 16 | HLA-B46:01 | 7 |
| GAVGVGKSAL | 18 | HLA-C03:03 | 7 |
| GAVGVGKSAL | 18 | HLA-B48:01 | 7 |
| VVVGAVGVGK | 20 | HLA-A03:01 | 7 |
| AVGVGKSAL | 16 | HLA-C03:04 | 8 |
| GAVGVGKSAL | 18 | HLA-C03:04 | 8 |
| KLVVVGAVGV | 164 | HLA-A02:07 | 9 |
| VGVGKSAL | 165 | HLA-B08:01 | 9 |
| VVVGAVGV | 166 | HLA-A68:02 | 9 |
| AVGVGKSAL | 16 | HLA-C08:02 | 10 |
| AVGVGKSAL | 16 | HLA-B07:02 | 10 |
| GAVGVGKSAL | 18 | HLA-B35:03 | 10 |
| AVGVGKSAL | 16 | HLA-C08:01 | 11 |
| AVGVGKSAL | 16 | HLA-C01:02 | 11 |
| GAVGVGKSA | 17 | HLA-B55:01 | 11 |
| GAVGVGKSAL | 18 | HLA-B81:01 | 11 |
| GAVGVGKSAL | 18 | HLA-C08:01 | 11 |
| KLVVVGAVGV | 164 | HLA-B13:02 | 11 |
| VGVGKSAL | 165 | HLA-C03:04 | 11 |
| AVGVGKSAL | 16 | HLA-A32:01 | 12 |
| GAVGVGKSA | 17 | HLA-B46:01 | 12 |
| VGVGKSAL | 165 | HLA-C03:02 | 12 |
| VGVGKSALTI | 167 | HLA-A23:01 | 12 |
| GAVGVGKSA | 17 | HLA-B54:01 | 13 |
| VGVGKSAL | 165 | HLA-C01:02 | .3 |
| AVGVGKSAL | 16 | HLA-B48:01 | 14 |
| AVGVGKSAL | 16 | HLA-C03:03 | 14 |
| AVGVGKSAL | 16 | HLA-B42:01 | 14 |

| | | | |
|---|---|---|---|
| LVVVGAVGV | 163 | HLA-B55:01 | 14 |
| VGVGKSAL | 165 | HLA-C08:01 | 14 |
| VVGAVGVGK | 19 | HLA-A74:01 | 14 |
| AVGVGKSAL | 16 | HLA-C05:01 | 15 |
| AVGVGKSAL | 16 | HLA-C03:02 | 15 |
| GAVGVGKSA | 17 | HLA-C03:04 | 15 |
| KLVVVGAVGV | 164 | HLA-A02:04 | 15 |
| LVVVGAVGV | 163 | HLA-A02:07 | 15 |
| VGVGKSAL | 165 | HLA-B14:02 | 15 |
| VVVGAVGVGK | 20 | HLA-A30:01 | 15 |
| VVGAVGVGK | 19 | HLA-B81:01 | 16 |
| VVVGAVGV | 166 | HLA-B55:01 | 16 |
| AVGVGKSAL | 16 | HLA-C14:03 | 17 |
| AVGVGKSAL | 16 | HLA-B15:01 | 17 |
| LVVVGAVGV | 163 | HLA-B54:01 | 17 |
| AVGVGKSA | 168 | HLA-B55:01 | 18 |
| AVGVGKSAL | 16 | HLA-C17:01 | 18 |
| GAVGVGKSA | 17 | HLA-B50:01 | 19 |
| GAVGVGKSAL | 18 | HLA-C17:01 | 19 |
| YKLVVVGAV | 169 | HLA-A02:04 | 19 |
| GAVGVGKSAL | 18 | HLA-B35:01 | 20 |
| VVGAVGVGK | 19 | HLA-A31:01 | 20 |
| YKLVVVGAV | 169 | HLA-B51:01 | 20 |

**[0671]** In some embodiments, a peptide comprises a RAS G13C mutation according to Table 12 below.

**Table 12**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| VVVGAGCVGK | 170 | HLA-A11:01 | 1 |
| VVGAGCVGK | 171 | HLA-A11:01 | 2 |
| AGCVGKSAL | 172 | HLA-C01:02 | 3 |
| VVGAGCVGK | 171 | HLA-A03:01 | 4 |
| VVVGAGCVGK | 170 | HLA-A68:01 | 4 |
| CVGKSALTI | 173 | HLA-B13:02 | 5 |
| VVGAGCVGK | 171 | HLA-A68:01 | 5 |
| VVGAGCVGK | 171 | HLA-A30:01 | 6 |
| AGCVGKSAL | 172 | HLA-B48:01 | 7 |
| AGCVGKSAL | 172 | HLA-C03:04 | 8 |
| GCVGKSALTI | 174 | HLA-B49:01 | 8 |
| AGCVGKSAL | 172 | HLA-C08:02 | 9 |
| VVVGAGCVGK | 170 | HLA-A03:01 | 9 |
| KLVVVGAGC | 175 | HLA-A30:02 | 10 |
| GCVGKSAL | 176 | HLA-C07:01 | 11 |
| VVGAGCVGK | 171 | HLA-A74:01 | 12 |
| AGCVGKSAL | 172 | HLA-C14:03 | 13 |

| | | | |
|---|---|---|---|
| KLVVVGAGC | 175 | HLA-B15:01 | 14 |

**[0672]** In some embodiments, a peptide comprises a RAS G13D mutation according to Table 13 below.

**Table 13**

| Peptide | SEQ ID NO: | Allele | Rank of Binding Potential |
|---|---|---|---|
| AGDVGKSAL | 177 | HLA-C08:02 | 1 |
| AGDVGKSAL | 177 | HLA-C05:01 | 2 |
| VVGAGDVGK | 178 | HLA-A11:01 | 3 |
| VVVGAGDVGK | 179 | HLA-A11:01 | 3 |
| VVVGAGDVGK | 179 | HLA-A68:01 | 4 |
| GAGDVGKSA | 180 | HLA-B46:01 | 5 |
| GAGDVGKSAL | 181 | HLA-B48:01 | 5 |
| VVGAGDVGK | 178 | HLA-A68:01 | 5 |
| VVGAGDVGK | 178 | HLA-A03:01 | 5 |
| AGDVGKSAL | 177 | HLA-C03:04 | 6 |
| AGDVGKSAL | 177 | HLA-C04:01 | 6 |
| AGDVGKSAL | 177 | HLA-C01:02 | 6 |
| DVGKSALTI | 182 | HLA-B13:02 | 6 |
| DVGKSALTI | 182 | HLA-A25:01 | 6 |
| GDVGKSAL | 183 | HLA-C07:01 | 6 |
| GDVGKSAL | 183 | HLA-B40:02 | 7 |
| GDVGKSAL | 183 | HLA-B37:01 | 8 |
| AGDVGKSAL | 177 | HLA-B48:01 | 9 |
| DVGKSALTI | 182 | HLA-B51:01 | 10 |
| VVGAGDVGK | 178 | HLA-A30:01 | 10 |
| GAGDVGKSAL | 181 | HLA-C08:01 | 11 |
| GAGDVGKSAL | 181 | HLA-B81:01 | 11 |
| AGDVGKSAL | 177 | HLA-C08:01 | 12 |
| GAGDVGKSAL | 181 | HLA-C03:04 | 12 |
| DVGKSALTI | 182 | HLA-B53:01 | 13 |
| AGDVGKSAL | 177 | HLA-B07:02 | 14 |
| AGDVGKSAL | 177 | HLA-B46:01 | 14 |
| DVGKSALTI | 182 | HLA-A26:01 | 14 |
| VVGAGDVGK | 178 | HLA-A74:01 | 14 |
| GAGDVGKSA | 180 | HLA-B54:01 | 15 |
| DVGKSALTI | 182 | HLA-B38:01 | 16 |
| GAGDVGKSAL | 181 | HLA-C03:03 | 16 |
| VVVGAGDVGK | 179 | HLA-A03:01 | 16 |

**[0673]** In some embodiments, a peptide comprises a mutated RAS peptide according to Table 14 below.

**Table 14**

| Epitope | SEQ ID NO: | MHC protein encoded by allele |
|---|---|---|
| GACGVGKSA | 128 | C03:04 |

| | | |
|---|---|---|
| GAVGVGKSA | 17 | C03:03 |

**Example 3. Method for enrichment and expansion of antigen-specific T cells**.

**[0674]** In this example, a method for increasing the yield of antigen specific T cells is described. An overview of an examplary manufacturing process used to produce large number of KRAS neoantigen-specific T cells is presented in **FIG. 1A**, **FIG. 1B** and **FIG. 2**. In brief, peripheral blood mononuclear cells (PBMCs) derived from leukaphereses from healthy donors or patients were processed to deplete specific cell subsets on day 0. KRAS neoantigen peptides were added on day 1 to the cell culture, and maturation cytokines were added after a period of time. On day 0, human serum was added to the culture. On days 5, 7, 9 and 12, culture maintenance was performed, which entailed addition or changing of media and/or addition of cytokines. On day 13, the KRAS neoantigen peptides were spiked into the culture, which upregulated activation markers on the T cells. On day 14, antigen-specific T cells were enriched by antibody labeling and capturing of the cells expressing one or more of the activation markers. The process on days 13 and 14 are termed the "enrichment process."

*Enrichment of antigen specific T cells*

**[0675]** **FIGs. 3** and **4** demonstrate the schematic workflow and results from the feasibility of enrichment at research scale and large-scale runs using the CliniMACS system. For large scale runs, at least 10^9 cells were available to set up the runs. The naïve T cell induction protocol described above is used in large vessels, and the cells are pooled on day 14 after peptide pulsing and were run through the CliniMACS. **FIG. 4** shows results from the studies on feasibility of enrichment. Both the methods tested using MACS buffer yielded viable cells after enrichment which was considerably higher over historical small scale data. Multiple CliniMACS protcols were tested, which have different pressures and flow rates through the magnetic column (e.g., manufacturer specified protocols named Method 2.1, Method 3.2, etc.), and the enrichment was relatively similar. Method 2.1 was selected for further testing. Different running buffers were tested for passing through the CliniMACS columns, including MACS buffer and AIM-V, and the results were relatively similar.

**[0676]** After the initial stimulation of naïve T cells, the peptide pulse on day 13 can be used to, for example, upregulate cell surface activation markers that can be used to label and enrich antigen-specific T cells. Alternative methods, such as addition of antigen-expressing cells or scaffolds can function in a similar manner. **FIG. 5** shows the upregulation of four different cell surface activation markers (CD39, PD-1, CD137 (4-1BB), and CD69) after peptide pulse on day 13 and analysis on day 14. **FIGs. 5 and 6** demonstrates data that an overnight peptide pulse ( up to 24 hours) upregulates specific activation markers on antigen responsive T cells. Of the activation markers shown, 4-1BB (CD137) and CD69 showed great promise (**FIG. 6**). CD137 and CD69 were more substantially increased on multimer positive cells relative to multimer negative cells. Particularly, as shown in **FIG. 5**, CD137 enrichment and peptide spike with 2 uM peptide had a remarkable effect on enriching antigen-specific (multimer positive) T cells (data from lower right compared to the upper right flow cytometry results), exceeding that of CD69. **FIG. 7** shows that KRAS neoantigen-specific CD8+ T cells were enriched using either CD137 or CD69 using this method. Pre-enrichment frequencies were increased on average greater than 10-fold and antigen-specific responses that were not detectable prior to enrichment became detectable after