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## (57)

**ABSTRACT**

Disclosed is an isolated or purified T cell receptor (TCR) having antigenic specificity for an HLA-A11-restricted epitope of mutated Kirsten rat sarcoma viral oncogene homolog (KRAS) (KRAS<sub>7-16</sub>), Neuroblastoma RAS Viral (V-Ras) Oncogene Homolog (NRAS), or Harvey Rat Sarcoma Viral Oncogene Homolog (HRAS). Related polypeptides and proteins, as well as related nucleic acids, recombinant expression vectors, host cells, populations of cells, and pharmaceutical compositions are also provided. Also disclosed are methods of detecting the presence of cancer in a mammal and methods of treating or preventing cancer in a mammal.

**Specification includes a Sequence Listing.**

**ANTI-MUTATED KRAS T CELL RECEPTORS****CROSS-REFERENCE TO RELATED APPLICATIONS**

**[0001]** This patent application is a continuation of co-pending U.S. patent application Ser. No. 17/535,318, filed Nov. 24, 2021, which is a continuation of U.S. patent application Ser. No. 15/528,813, filed May 23, 2017, now U.S. Pat. No. 11,207,394, which is the U.S. national stage of PCT/US2015/062269, filed Nov. 24, 2015, which claims the benefit of U.S. Provisional Patent Application No. 62/084,654, filed Nov. 26, 2014 and U.S. Provisional Patent Application No. 62/171,321, filed Jun. 5, 2015, each of which is incorporated by reference in its entirety herein.

**STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT**

**[0002]** This invention was made with Government support under project number Z01BC011337-04 by the National Institutes of Health, National Cancer Institute. The Government has certain rights in the invention.

**INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY**

**[0003]** Incorporated by reference in its entirety herein is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 304,688 Byte Extensible Markup Language (XML) file named "772939\_ST26.xml," dated Apr. 17, 2025.

**BACKGROUND OF THE INVENTION**

**[0004]** Some cancers may have very limited treatment options, particularly when the cancer becomes metastatic and unresectable. Despite advances in treatments such as, for example, surgery, chemotherapy, and radiation therapy, the prognosis for many cancers, such as, for example, pancreatic, colorectal, lung, endometrial, ovarian, and prostate cancers, may be poor. Accordingly, there exists an unmet need for additional treatments for cancer.

**BRIEF SUMMARY OF THE INVENTION**

**[0005]** An embodiment of the invention provides an isolated or purified T cell receptor (TCR) having antigenic specificity for a mutated epitope, the mutated epitope (a) comprising VVVGADGVGK (SEQ ID NO: 2) or (b) consisting of VVVGAVGVGK (SEQ ID NO: 33) or VVGAVGVGK (SEQ ID NO: 35).

**[0006]** The invention further provides related polypeptides and proteins, as well as related nucleic acids, recombinant expression vectors, host cells, populations of cells, and pharmaceutical compositions relating to the TCRs of the invention.

**[0007]** Methods of detecting the presence of cancer in a mammal and methods of treating or preventing cancer in a mammal are further provided by the invention.

**DETAILED DESCRIPTION OF THE INVENTION**

**[0008]** Kirsten rat sarcoma viral oncogene homolog (KRAS), also referred to as GTPase KRas, V-Ki-Ras2 Kirsten rat sarcoma viral oncogene, or KRAS2, is a member of the small GTPase superfamily. There are two transcript

variants of KRAS: KRAS variant A and KRAS variant B. Hereinafter, references to "KRAS" (mutated or unmutated) refer to both variant A and variant B, unless specified otherwise. Without being bound to a particular theory or mechanism, it is believed that, when mutated, KRAS may be involved in signal transduction early in the oncogenesis of many human cancers. A single amino acid substitution may activate the mutation. When activated, mutated KRAS binds to guanosine-5'-triphosphate (GTP) and converts GTP to guanosine 5'-diphosphate (GDP). The mutated KRAS protein product may be constitutively activated. Mutated KRAS protein may be expressed in any of a variety of human cancers such as, for example, pancreatic (e.g., pancreatic carcinoma), colorectal, lung (e.g., lung adenocarcinoma), endometrial, ovarian (e.g., epithelial ovarian cancer), and prostate cancers.

**[0009]** An embodiment of the invention provides an isolated or purified TCR having antigenic specificity for mutated human KRAS (hereinafter, "mutated KRAS"). Hereinafter, references to a "TCR" also refer to functional portions and functional variants of the TCR, unless specified otherwise. The inventive TCR may have antigenic specificity for any mutated KRAS protein, polypeptide or peptide. In an embodiment of the invention, the TCR has antigenic specificity for a mutated KRAS protein comprising or consisting of the amino acid sequence of SEQ ID NO: 1, 32, 122, or 123. The mutated KRAS variant A protein amino acid sequences of each of SEQ ID NOS: 1 and 32 generally corresponds to positions 1-189 of the unmutated, wild-type (WT) KRAS protein variant A amino acid sequence of SEQ ID NO: 29 with the exception that in SEQ ID NOS: 1 and 32, the glycine at position 12 is substituted with aspartic acid or valine, respectively. The mutated KRAS variant B protein amino acid sequences of each of SEQ ID NOS: 122 and 123 generally corresponds to positions 1-188 of the unmutated. WT KRAS protein variant B amino acid sequence of SEQ ID NO: 121 with the exception that in SEQ ID NOS: 122 and 123, the glycine at position 12 is substituted with aspartic acid or valine, respectively. In a preferred embodiment of the invention, the TCR has antigenic specificity for a mutated KRAS7-16 peptide comprising or consisting of the amino acid sequence of VVVGADGVGK (SEQ ID NO: 2), or VVVGAVGVGK (SEQ ID NO: 33). The mutated KRAS peptide amino acid sequences of SEQ ID NOS: 2 and 33 generally correspond to positions 1-10 of the unmutated. WT KRAS7-16 peptide amino acid sequence of SEQ ID NO: 30 with the exception that in SEQ ID NOS: 2 and 33, the glycine at position 6 is substituted with aspartic acid or valine, respectively. In an embodiment of the invention, the TCR has antigenic specificity for a mutated KRAS8-16 peptide comprising or consisting of the amino acid sequence of VVGADGVGK (SEQ ID NO: 34) or VVGAVGVGK (SEQ ID NO: 35). The mutated KRAS peptide amino acid sequences of SEQ ID NOS: 34 and 35 generally correspond to positions 1-9 of the unmutated. WT KRAS8-16 peptide amino acid sequence of SEQ ID NO: 31 with the exception that in SEQ ID NOS: 34 and 35, the glycine at position 5 is substituted with aspartic acid or valine, respectively. In a preferred embodiment, the TCR has antigenic specificity for a mutated KRAS epitope, the mutated KRAS epitope (a) comprising VVVGADGVGK (SEQ ID NO: 2) or (b) consisting of VVVGAVGVGK (SEQ ID NO: 33) or VVGAVGVGK (SEQ ID NO: 35). In an especially preferred embodiment, the TCR has antigenic specificity for a mutated

KRAS epitope comprising VVVGADGVGK (SEQ ID NO: 2). In another preferred embodiment, the TCR has antigenic specificity for a mutated KRAS epitope consisting of VVVGAVGVGK (SEQ ID NO: 33) or VVGAVGVGK (SEQ ID NO: 35). The mutated KRAS amino acid sequences VVVGAVGVGK (SEQ ID NO: 33) and VVGAVGVGK (SEQ ID NO: 35) are also referred to herein as "KRAS G12V." The mutated KRAS amino acid sequences VVVGADGVGK (SEQ ID NO: 2) and VVGADGVGK (SEQ ID NO: 34) are also referred to herein as "KRAS G12D."

[0010] The mutated KRAS epitope amino acid sequences described herein are also found in two other mutated oncogenes in human cancer. Neuroblastoma RAS Viral (V-Ras) Oncogene Homolog (NRAS) and Harvey Rat Sarcoma Viral Oncogene Homolog (HRAS). The amino acid sequences of mutated human NRAS and mutated human HRAS contain the mutated human KRAS epitope sequences described herein. Accordingly, in an embodiment of the invention, the inventive TCRs also have antigenic specificity for mutated human NRAS and HRAS. Mutated human KRAS, mutated human NRAS, and mutated human HRAS are collectively referred to herein as "mutated target(s)."

[0011] In an embodiment of the invention, the inventive TCRs are able to recognize mutated target, e.g., mutated KRAS, in a major histocompatibility complex (MHC) class I-dependent manner. "MHC class I-dependent manner," as used herein, means that the TCR elicits an immune response upon binding to mutated target, e.g., mutated KRAS, within the context of an MHC class I molecule. The MHC class I molecule can be any MHC class I molecule known in the art, e.g., HLA-A molecules. In a preferred embodiment of the invention, the TCR has antigenic specificity for the mutated epitope, presented in the context of an HLA-A11 molecule.

[0012] The TCRs of the invention provide many advantages, including when expressed by cells used for adoptive cell transfer. Mutated KRAS, mutated NRAS, and mutated HRAS are expressed by cancer cells and are not expressed by normal, noncancerous cells. Without being bound to a particular theory or mechanism, it is believed that the inventive TCRs advantageously target the destruction of cancer cells while minimizing or eliminating the destruction of normal, non-cancerous cells, thereby reducing, for example, by minimizing or eliminating, toxicity. Moreover, the inventive TCRs may, advantageously, successfully treat or prevent one or more of mutated KRAS-positive cancers, mutated NRAS-positive cancers, and mutated HRAS-positive cancers that do not respond to other types of treatment such as, for example, chemotherapy, surgery, or radiation. Additionally, the inventive TCRs may provide highly avid recognition of one or more of mutated KRAS, mutated NRAS, and mutated HRAS, which may provide the ability to recognize unmanipulated tumor cells (e.g., tumor cells that have not been treated with interferon (IFN)- $\gamma$ , transfected with a vector encoding one or both of mutated KRAS and HLA-A11, pulsed with the mutated KRAS7-16 or KRAS8-16 peptide, or a combination thereof).

[0013] The phrase "antigenic specificity," as used herein, means that the TCR can specifically bind to and immunologically recognize mutated target, e.g., mutated KRAS, with high avidity. For example, a TCR may be considered to have "antigenic specificity" for mutated target if T cells expressing the TCR secrete at least about 200 pg/mL or more (e.g., 200 pg/mL or more, 300 pg/mL or more, 400 pg/mL

or more, 500 pg/mL or more, 600 pg/mL or more, 700 pg/mL or more, 1000 pg/mL or more, 5,000 pg/mL or more, 7,000 pg/mL or more, 10,000 pg/mL or more, 20,000 pg/mL or more, or a range defined by any two of the foregoing values) of IFN- $\gamma$  upon co-culture with (a) antigen-negative HLA-A11 $^{+}$  target cells pulsed with a low concentration of mutated target peptide (e.g., about 0.05 ng/ml to about 5 ng/ml, 0.05 ng/ml, 0.1 ng/ml, 0.5 ng/mL, 1 ng/mL, 5 ng/ml, or a range defined by any two of the foregoing values) or (b) antigen-negative HLA-A11 $^{+}$  target cells into which a nucleotide sequence encoding the mutated target has been introduced such that the target cell expresses the mutated target. Cells expressing the inventive TCRs may also secrete IFN- $\gamma$  upon co-culture with antigen-negative HLA-A11 $^{+}$  target cells pulsed with higher concentrations of mutated target peptide.

[0014] Alternatively or additionally, a TCR may be considered to have "antigenic specificity" for a mutated target if T cells expressing the TCR secrete at least twice as much IFN- $\gamma$  upon co-culture with (a) antigen-negative HLA-A11 $^{+}$  target cells pulsed with a low concentration of mutated target peptide or (b) antigen-negative HLA-A11 $^{+}$  target cells into which a nucleotide sequence encoding the mutated target has been introduced such that the target cell expresses the mutated target as compared to the amount of IFN- $\gamma$  expressed by a negative control. The negative control may be, for example, (i) T cells expressing the TCR, co-cultured with (a) antigen-negative HLA-A11 $^{+}$  target cells pulsed with the same concentration of an irrelevant peptide (e.g., some other peptide with a different sequence from the mutated target peptide) or (b) antigen-negative HLA-A11 $^{+}$  target cells into which a nucleotide sequence encoding an irrelevant peptide has been introduced such that the target cell expresses the irrelevant peptide, or (ii) untransduced T cells (e.g., derived from PBMC, which do not express the TCR) co-cultured with (a) antigen-negative HLA-A11 $^{+}$  target cells pulsed with the same concentration of mutated target peptide or (b) antigen-negative HLA-A11 $^{+}$  target cells into which a nucleotide sequence encoding the mutated target has been introduced such that the target cell expresses the mutated target. IFN- $\gamma$  secretion may be measured by methods known in the art such as, for example, enzyme-linked immunosorbent assay (ELISA).

[0015] Alternatively or additionally, a TCR may be considered to have "antigenic specificity" for a mutated target if at least twice as many of the numbers of T cells expressing the TCR secrete IFN- $\gamma$  upon co-culture with (a) antigen-negative HLA-A11 $^{+}$  target cells pulsed with a low concentration of mutated target peptide or (b) antigen-negative HLA-A11 $^{+}$  target cells into which a nucleotide sequence encoding the mutated target has been introduced such that the target cell expresses the mutated target as compared to the numbers of negative control T cells that secrete IFN- $\gamma$ . The concentration of peptide and the negative control may be as described herein with respect to other aspects of the invention. The numbers of cells secreting IFN- $\gamma$  may be measured by methods known in the art such as, for example, ELISPOT.

[0016] The invention provides a TCR comprising two polypeptides (i.e., polypeptide chains), such as an alpha ( $\alpha$ ) chain of a TCR, a beta ( $\beta$ ) chain of a TCR, a gamma ( $\gamma$ ) chain of a TCR, a delta ( $\delta$ ) chain of a TCR, or a combination thereof. The polypeptides of the inventive TCR can com-

prise any amino acid sequence, provided that the TCR has antigenic specificity for the mutated target, e.g., mutated KRAS.

[0017] In an embodiment of the invention, the TCR comprises two polypeptide chains, each of which comprises a variable region comprising a complementarity determining region (CDR) 1, a CDR2, and a CDR3 of a TCR. In an embodiment of the invention, the TCR comprises: (a) a first polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 3 (CDR1 of a chain of anti-KRAS G12D TCR), a CDR2 comprising the amino acid sequence of SEQ ID NO: 4 (CDR2 of  $\alpha$  chain of anti-KRAS G12D TCR), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 5 (CDR3 of a chain of anti-KRAS G12D TCR), and a second polypeptide chain comprising a CDR1 comprising the amino acid sequence of SEQ ID NO: 6 (CDR1 of  $\beta$  chain of anti-KRAS G12D TCR), a CDR2 comprising the amino acid sequence of SEQ ID NO: 7 (CDR2 of  $\beta$  chain of anti-KRAS G12D TCR), and a CDR3 comprising the amino acid sequence of SEQ ID NO: 8 (CDR3 of  $\beta$  chain of anti-KRAS G12D TCR); (b) a first polypeptide chain comprising an anti-KRAS G12V TCR  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 125, an anti-KRAS G12V TCR  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 126, an anti-KRAS G12V TCR  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 127, and a second polypeptide chain comprising an anti-KRAS G12V TCR  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 128, an anti-KRAS G12V TCR  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 129, and an anti-KRAS G12V TCR  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 130; (c) a first polypeptide chain comprising an anti-KRAS G12V TCR  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 137, an anti-KRAS G12V TCR  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 138, an anti-KRAS G12V TCR  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 139, and a second polypeptide chain comprising an anti-KRAS G12V TCR  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 140, an anti-KRAS G12V TCR  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 141, and an anti-KRAS G12V TCR  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 142; or (d) first polypeptide chain comprising an anti-KRAS G12D TCR  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 149, an anti-KRAS G12D TCR  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 150, an anti-KRAS G12D TCR  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 151, and a second polypeptide chain comprising an anti-KRAS G12D TCR  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 152, an anti-KRAS G12D TCR  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 153, and an anti-KRAS G12D TCR  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 154. In this regard, the inventive TCR can comprise any one or more of the amino acid sequences selected from the group consisting of SEQ ID NOS: 3-8; SEQ ID NOS: 6-8; SEQ ID NOS: 125-127; SEQ ID NOS: 128-130; SEQ ID NOS: 137-139; SEQ ID NOS: 140-142; SEQ ID NOS: 149-151; or SEQ ID NOS: 152-154. In an especially preferred embodi-

ment, the TCR comprises the amino acid sequences of (a) all of SEQ ID NOS: 3-8; (b) all of SEQ ID NOS: 125-130; (c) all of SEQ ID NOS: 137-142; (d) all of SEQ ID NOS: 149-154.

[0018] In an embodiment of the invention, the TCR comprises an amino acid sequence of a variable region of a TCR comprising the CDRs set forth above. In this regard, the TCR can comprise the amino acid sequence of SEQ ID NO: 9 (variable region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 10 (variable region of anti-KRAS G12D TCR  $\beta$  chain); both SEQ ID NOS: 9 and 10; SEQ ID NO: 131 (variable region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 132 (variable region of anti-KRAS G12V TCR  $\beta$  chain); both SEQ ID NOS: 131 and 132; SEQ ID NO: 143 (variable region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 144 (variable region of anti-KRAS G12V TCR  $\beta$  chain); both SEQ ID NOS: 143 and 144; SEQ ID NO: 155 (variable region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 156 (variable region of anti-KRAS G12D TCR  $\beta$  chain); or both SEQ ID NOS: 155 and 156. Preferably, the inventive TCR comprises the amino acid sequences of both SEQ ID NOS: 9 and 10; both SEQ ID NOS: 131 and 132; both SEQ ID NOS: 143 and 144; or both SEQ ID NOS: 155 and 156.

[0019] In an embodiment of the invention, the TCR further comprises an amino acid sequence of a constant region of a TCR. In this regard, the TCR can comprise the amino acid sequence of SEQ ID NO: 13 (constant region of anti-KRAS G12D TCR  $\alpha$  chain). SEQ ID NO: 14 (constant region of anti-KRAS G12D TCR  $\beta$  chain), both SEQ ID NOS: 13 and 14; SEQ ID NO: 135 (constant region of anti-KRAS G12V TCR  $\alpha$  chain). SEQ ID NO: 136 (constant region of anti-KRAS G12V TCR  $\beta$  chain), both SEQ ID NOS: 135 and 136; SEQ ID NO: 147 (constant region of anti-KRAS G12V TCR  $\alpha$  chain). SEQ ID NO: 148 (constant region of anti-KRAS G12V TCR  $\beta$  chain), both SEQ ID NOS: 147 and 148; SEQ ID NO: 159 (constant region of anti-KRAS G12D TCR  $\alpha$  chain). SEQ ID NO: 160 (constant region of anti-KRAS G12D TCR  $\beta$  chain), or both SEQ ID NOS: 159 and 160. Preferably, the inventive TCR comprises the amino acid sequences of both SEQ ID NOS: 13 and 14; both SEQ ID NOS: 135 and 136; both SEQ ID NOS: 147 and 148; both SEQ ID NOS: 159 and 160.

[0020] In an embodiment of the invention, the inventive TCR may comprise a combination of a variable region and a constant region. In this regard, the TCR can comprise: (a) an  $\alpha$  chain comprising the amino acid sequences of both SEQ ID NO: 9 (variable region of a chain) and SEQ ID NO: 13 (constant region of a chain); a  $\beta$  chain comprising the amino acid sequences of both SEQ ID NO: 10 (variable region of  $\beta$  chain) and SEQ ID NO: 14 (constant region of  $\beta$  chain); or the amino acid sequences of all of SEQ ID NOS: 9, 10, 13, and 14; (b) an  $\alpha$  chain comprising the amino acid sequences of both SEQ ID NO: 131 (variable region of a chain) and SEQ ID NO: 135 (constant region of a chain); a  $\beta$  chain comprising the amino acid sequences of both SEQ ID NO: 132 (variable region of  $\beta$  chain) and SEQ ID NO: 136 (constant region of  $\beta$  chain); or the amino acid sequences of all of SEQ ID NOS: 131, 132, 135, and 136; (c) an  $\alpha$  chain comprising the amino acid sequences of both SEQ ID NO: 143 (variable region of a chain) and SEQ ID NO: 147 (constant region of a chain); a  $\beta$  chain comprising the amino acid sequences of both SEQ ID NO: 144 (variable region of  $\beta$  chain) and SEQ ID NO: 148 (constant region of  $\beta$  chain).

$\beta$  chain); or the amino acid sequences of all of SEQ ID NOS: 143, 144, 147, and 148; or (d) an  $\alpha$  chain comprising the amino acid sequences of both SEQ ID NO: 155 (variable region of a chain) and SEQ ID NO: 159 (constant region of a chain); a  $\beta$  chain comprising the amino acid sequences of both SEQ ID NO: 156 (variable region of  $\beta$  chain) and SEQ ID NO: 160 (constant region of  $\beta$  chain); or the amino acid sequences of all of SEQ ID NOS: 155, 156, 159, and 160. Preferably, the inventive TCR comprises the amino acid sequences of (a) all of SEQ ID NOS: 9, 10, 13, and 14; (b) all of SEQ ID NOS: 131, 132, 135, and 136; (c) all of SEQ ID NOS: 143, 144, 147, and 148; or (d) all of SEQ ID NOS: 155, 156, 159, and 160.

[0021] In an embodiment of the invention, the inventive TCR may comprise a combination of any of the CDR regions described herein and a constant region. In this regard, the TCR can comprise an  $\alpha$  chain comprising: (a) the amino acid sequences of all of SEQ ID NOS: 3-5 and 13; a  $\beta$  chain comprising the amino acid sequences of all of SEQ ID NOS: 6-8 and 14; or the amino acid sequences of all of SEQ ID NOS: 3-8 and 13-14; (b) the amino acid sequences of all of SEQ ID NOS: 125-127 and 135; a  $\beta$  chain comprising the amino acid sequences of all of SEQ ID NOS: 128-130 and 136; or the amino acid sequences of all of SEQ ID NOS: 125-130 and 135-136; (c) the amino acid sequences of all of SEQ ID NOS: 137-139 and 147; a  $\beta$  chain comprising the amino acid sequences of all of SEQ ID NOS: 140-142 and 148; or the amino acid sequences of all of SEQ ID NOS: 137-142 and 147-148; or (d) the amino acid sequences of all of SEQ ID NOS: 149-151 and 159; a  $\beta$  chain comprising the amino acid sequences of all of SEQ ID NOS: 152-154 and 160; or the amino acid sequences of all of SEQ ID NOS: 149-154 and 159-160.

[0022] In an embodiment of the invention, the inventive TCR can comprise an  $\alpha$  chain of a TCR and a  $\beta$  chain of a TCR. Each of the  $\alpha$  chain and  $\beta$  chain of the inventive TCR can independently comprise any amino acid sequence. In this regard, the  $\alpha$  chain of the inventive TCR can comprise the amino acid sequence of SEQ ID NO: 11 (anti-KRAS G12D TCR  $\alpha$  chain), SEQ ID NO: 133 (anti-KRAS G12V TCR  $\alpha$  chain), SEQ ID NO: 145 (anti-KRAS G12V TCR  $\alpha$  chain), or SEQ ID NO: 157 (anti-KRAS G12D TCR  $\alpha$  chain). An  $\alpha$  chain of this type can be paired with any  $\beta$  chain of a TCR. In this regard, the  $\beta$  chain of the inventive TCR can comprise the amino acid sequence of SEQ ID NO: 12 (anti-KRAS G12D TCR  $\beta$  chain), SEQ ID NO: 134 (anti-KRAS G12V TCR  $\beta$  chain), SEQ ID NO: 146 (anti-KRAS G12V TCR  $\beta$  chain), or SEQ ID NO: 158 (anti-KRAS G12D TCR  $\beta$  chain). The inventive TCR, therefore, can comprise the amino acid sequence of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 157, SEQ ID NO: 158, both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, or both SEQ ID NOS: 157 and 158. Preferably, the inventive TCR comprises the amino acid sequences of both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, or both SEQ ID NOS: 157 and 158.

[0023] In an embodiment of the invention, the inventive TCRs recognize mutated target, e.g., mutated KRAS, either (i) in the presence of CD4 and the absence of CD8 or (ii) in the presence of CD8 and the absence of CD4. In a preferred embodiment, a TCR comprising the amino acid sequences of (i) SEQ ID NOS: 125-130; (ii) SEQ ID NOS: 131-132; or

(iii) SEQ ID NOS: 133 and 134 recognizes mutated target, e.g., mutated KRAS, either (i) in the presence of CD4 and the absence of CD8 or (ii) in the presence of CD8 and the absence of CD4. Accordingly, these inventive TCRs may, advantageously recognize mutated target, e.g., mutated KRAS, when expressed by either CD4+ or CD8+ cells.

[0024] In an embodiment of the invention, the TCR is a murine TCR. As used herein, the term "murine," when referring to a TCR or any component of a TCR described herein (e.g., complementarity determining region (CDR), variable region, constant region,  $\alpha$  chain, and/or  $\beta$  chain), means a TCR (or component thereof) which is derived from a mouse, i.e., a TCR (or component thereof) that originated from or was, at one time, expressed by a mouse T cell. In an embodiment of the invention, a TCR comprising (i) all of SEQ ID NOS: 3-8; (ii) SEQ ID NOS: 9 and 10; (iii) SEQ ID NOS: 11 and 12; (iv) all of SEQ ID NOS: 3-8 and 13-14; (v) all of SEQ ID NOS: 9, 10, 13, and 14; (vi) all of SEQ ID NOS: 125-130; (vii) SEQ ID NOS: 131 and 132; (viii) SEQ ID NOS: 133 and 134; (ix) all of SEQ ID NOS: 125-130 and 135-136; (x) all of SEQ ID NOS: 131, 132, 135, and 136; (xi) all of SEQ ID NOS: 137-142; (xii) SEQ ID NOS: 143 and 144; (xiii) SEQ ID NOS: 145 and 146; (xiv) all of SEQ ID NOS: 137-142 and 147-148; (xv) all of SEQ ID NOS: 143, 144, 147, and 148; (xvi) all of SEQ ID NOS: 149-154; (xvii) SEQ ID NOS: 155 and 156; (xviii) SEQ ID NOS: 157 and 158; (xix) all of SEQ ID NOS: 149-154 and 159-160; or (xx) all of SEQ ID NOS: 155, 156, 159, and 160 is a murine TCR.

[0025] Included in the scope of the invention are functional variants of the inventive TCRs described herein. The term "functional variant," as used herein, refers to a TCR, polypeptide, or protein having substantial or significant sequence identity or similarity to a parent TCR, polypeptide, or protein, which functional variant retains the biological activity of the TCR, polypeptide, or protein of which it is a variant. Functional variants encompass, for example, those variants of the TCR, polypeptide, or protein described herein (the parent TCR, polypeptide, or protein) that retain the ability to specifically bind to mutated target, e.g., mutated KRAS for which the parent TCR has antigenic specificity or to which the parent polypeptide or protein specifically binds, to a similar extent, the same extent, or to a higher extent, as the parent TCR, polypeptide, or protein. In reference to the parent TCR, polypeptide, or protein, the functional variant can, for instance, be at least about 30%, 50%, 75%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or more identical in amino acid sequence to the parent TCR, polypeptide, or protein.

[0026] The functional variant can, for example, comprise the amino acid sequence of the parent TCR, polypeptide, or protein with at least one conservative amino acid substitution. Conservative amino acid substitutions are known in the art, and include amino acid substitutions in which one amino acid having certain physical and/or chemical properties is exchanged for another amino acid that has the same chemical or physical properties. For instance, the conservative amino acid substitution can be an acidic amino acid substituted for another acidic amino acid (e.g., Asp or Glu), an amino acid with a nonpolar side chain substituted for another amino acid with a nonpolar side chain (e.g., Ala, Gly, Val, Ile, Leu, Met, Phe, Pro, Trp, Val, etc.), a basic amino acid substituted for another basic amino acid (Lys, Arg, etc.), an amino acid with a polar side chain substituted for another amino acid with a polar side chain (Asn, Cys, Gln, Ser, Thr, Tyr, etc.), etc.

**[0027]** Alternatively or additionally, the functional variants can comprise the amino acid sequence of the parent TCR, polypeptide, or protein with at least one non-conservative amino acid substitution. In this case, it is preferable for the non-conservative amino acid substitution to not interfere with or inhibit the biological activity of the functional variant. Preferably, 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 TCR, polypeptide, or protein. In an embodiment of the invention, the functional variant is a substituted TCR, polypeptide, or protein comprising (i) the substituted CDR3 $\alpha$ , variable region of the  $\alpha$  chain, or full-length  $\alpha$  chain amino acid sequence of any one of SEQ ID NOs: 46-56 and 207, 70-80 and 208, and 94-104 and 209, respectively; (ii) the substituted CDR3B, variable region of the  $\beta$  chain, or full-length  $\beta$  chain amino acid sequence of any one of SEQ ID NOs: 57-69, 81-93, and 105-117, respectively; or (iii) a pair of any one of the amino acid sequences of (i) in combination with any one of the amino acid sequences of (ii).

**[0028]** For example, in an embodiment of the invention, a substituted TCR, polypeptide, or protein may comprise one or both of (a) a substituted CDR3 $\alpha$  amino acid sequence of any one of SEQ ID NOs: 46-56 and 207 (Table I) and (b) a substituted CDR3 $\beta$  amino acid sequence of any one of SEQ ID NOs: 57-69 (Table II). An embodiment of the invention provides a TCR, polypeptide, or protein having any one or more of the native, unsubstituted CDR1 $\alpha$ , CDR2 $\alpha$ , CDR1 $\beta$ , CDR2 $\beta$ , and CDR3 $\beta$  amino acid sequences described herein with respect to other aspects of the invention in combination with any one of the substituted CDR3 $\alpha$  amino acid sequences of SEQ ID NOs: 46-56 and 207. In this regard, an embodiment of the invention provides a substituted TCR comprising the amino acid sequences of all of SEQ ID NOs: 149-150, 207, and 152-154. Another embodiment of the invention provides a TCR, polypeptide, or protein having any one or more of the native, unsubstituted CDR1 $\alpha$ , CDR2 $\alpha$ , CDR3 $\alpha$ , CDR1 $\beta$ , and CDR2 $\beta$  amino acid sequences described herein with respect to other aspects of the invention in combination with any one of the substituted CDR3 $\beta$  amino acid sequences of SEQ ID NOs: 57-69.

TABLE I

Substituted CDR3 $\alpha$ -version 1	CXLRGNAGAKLTF Wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 46)
Substituted CDR3 $\alpha$ -version 2	CAXRGNAGAKLTF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 47)
Substituted CDR3 $\alpha$ -version 3	CALXGNAGAKLTF Wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 48)
Substituted CDR3 $\alpha$ -version 4	CALRXNAGAKLTF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 49)
Substituted CDR3 $\alpha$ -version 5	CALRGXAGAKLTF Wherein X is alanine, arginine, asparatic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 50)
Substituted CDR3 $\alpha$ -version 6	CALRGNXGAKLTF Wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 51)
Substituted CDR3 $\alpha$ -version 7	CALRGNAXAKLTF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 52)
Substituted CDR3 $\alpha$ -version 8	CALRGNAGXKLTF Wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 53)
Substituted CDR3 $\alpha$ -version 9	CALRGNAGAXLTF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 54)
Substituted CDR3 $\alpha$ -version 10	CALRGNAGAKXTF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 55)

TABLE I-continued

Substituted CDR3 $\alpha$ -version 11	CALRGNAGAKLXF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, tryptophan, tyrosine, or valine (SEQ ID NO: 56)
Substituted CDR3 $\alpha$ -version 12	CAADSSNTXYQNFYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 207). In a preferred embodiment, X is alanine in SEQ ID NO: 207.

TABLE II

Substituted CDR3 $\beta$ -version 1	CXSSSRDWSAETLYF Wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 57)
Substituted CDR3 $\beta$ -version 2	CAXSSRDWSAETLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 58)
Substituted CDR3 $\beta$ -version 3	CASXSSRDWSAETLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 59)
Substituted CDR3 $\beta$ -version 4	CASSSXRDWSAETLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 60)
Substituted CDR3 $\beta$ -version 5	CASSSSRXWSAETLYF Wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 61)
Substituted CDR3 $\beta$ -version 6	CASSSSRXWSAETLYF Wherein X is alanine, arginine, asparagine, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 62)
Substituted CDR3 $\beta$ -version 7	CASSSSRDWSAETLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 63)
Substituted CDR3 $\beta$ -version 8	CASSSSRDWXSAETLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 64)
Substituted CDR3 $\beta$ -version 9	CASSSSRDWSXETLYF Wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 65)
Substituted CDR3 $\beta$ -version 10	CASSSSRDWSAYTLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 66)
Substituted CDR3 $\beta$ -version 11	CASSSSRDWSAEXLYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, tryptophan, tyrosine, or valine (SEQ ID NO: 67)
Substituted CDR3 $\beta$ -version 12	CASSSSRDWSAETXYF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine (SEQ ID NO: 68)

TABLE II-continued

Substituted CDR $\beta$ -version 13	CASSSRDWSAETLXF Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, or valine (SEQ ID NO: 69)
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**[0029]** In an embodiment of the invention, each of the substituted CDR3 $\alpha$  amino acid sequences of SEQ ID NOS: 46-56 does not comprise the native, unsubstituted CDR3 $\alpha$  amino acid sequence of SEQ ID NO: 5. In an embodiment of the invention, the substituted CDR3 $\alpha$  amino acid sequence of SEQ ID NO: 207 does not comprise the native, unsubstituted CDR3 $\alpha$  amino acid sequence of SEQ ID NO: 151. Similarly, in an embodiment of the invention, each of the substituted CDR3 $\beta$  amino acid sequences of SEQ ID NOS: 57-69 does not comprise the native, unsubstituted CDR3 $\beta$  amino acid sequence of SEQ ID NO: 8.

**[0030]** An embodiment of the invention provides a substituted TCR, polypeptide, or protein comprising one or both of (i) a substituted variable region of an  $\alpha$  chain comprising

the amino acid sequence of any one of SEQ ID NOS: 70-80 and 208 (Table III) and (ii) a substituted variable region of a  $\beta$  chain comprising the amino acid sequence of any one of SEQ ID NOS: 81-93 (Table IV). An embodiment of the invention provides a TCR, polypeptide, or protein having any of the native, unsubstituted variable regions of the  $\beta$  chain described herein with respect to other aspects of the invention in combination with any one of the substituted variable region  $\alpha$  chain amino acid sequences of SEQ ID NOS: 70-80 and 208. Another embodiment of the invention provides a TCR, polypeptide, or protein having any of the native, unsubstituted variable regions of the  $\alpha$  chain described herein with respect to other aspects of the invention in combination with any one of the substituted variable region  $\beta$  chain amino acid sequences of SEQ ID NOS: 81-93.

TABLE III

Substituted variable region $\alpha$ -version 1	SEQ ID NO: 70, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 2	SEQ ID NO: 71, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 3	SEQ ID NO: 72, wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 4	SEQ ID NO: 73, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 5	SEQ ID NO: 74, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 6	SEQ ID NO: 75, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 7	SEQ ID NO: 76, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 8	SEQ ID NO: 77, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 9	SEQ ID NO: 78, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine

TABLE III-continued

Substituted variable region $\alpha$ -version 10	SEQ ID NO: 79, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 11	SEQ ID NO: 80, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, tryptophan, tyrosine, or valine
Substituted variable region $\alpha$ -version 12	SEQ ID NO: 208, Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine. In a preferred embodiment, X is alanine in SEQ ID NO: 208.

TABLE IV

Substituted variable region $\beta$ -version 1	SEQ ID NO: 81, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 2	SEQ ID NO: 82, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 3	SEQ ID NO: 83, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 4	SEQ ID NO: 84, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 5	SEQ ID NO: 85, wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 6	SEQ ID NO: 86, wherein X is alanine, arginine, asparagine, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 7	SEQ ID NO: 87, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tyrosine, or valine
Substituted variable region $\beta$ -version 8	SEQ ID NO: 88, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 9	SEQ ID NO: 89, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 10	SEQ ID NO: 90, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine

TABLE IV-continued

Substituted variable region $\beta$ -version 11	SEQ ID NO: 91, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 12	SEQ ID NO: 92, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted variable region $\beta$ -version 13	SEQ ID NO: 93, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine

**[0031]** In an embodiment of the invention, each of the substituted variable region  $\alpha$  chain amino acid sequences of SEQ ID NOS: 70-80 does not comprise the native, unsubstituted variable region  $\alpha$  chain amino acid sequence of SEQ ID NO: 9. In an embodiment of the invention, the substituted variable region  $\alpha$  chain amino acid sequence of SEQ ID NO: 208 does not comprise the native, unsubstituted variable region  $\alpha$  chain amino acid sequence of SEQ ID NO: 155. Similarly, in an embodiment of the invention, each of the substituted variable region  $\beta$  chain amino acid sequences of SEQ ID NOS: 81-93 does not comprise the native, unsubstituted variable region  $\beta$  chain amino acid sequence of SEQ ID NO: 10.

**[0032]** An embodiment of the invention provides a substituted TCR, polypeptide, or protein comprising one or both

of (i) a substituted full length  $\alpha$  chain comprising the amino acid sequence of any one of SEQ ID NOS: 94-104 and 209 (Table V) and (ii) a substituted full length  $\beta$  chain comprising the amino acid sequence of any one of SEQ ID NOS: 105-117 (Table VI). An embodiment of the invention provides a TCR, polypeptide, or protein having any of the native, unsubstituted full-length  $\beta$  chain sequences described herein with respect to other aspects of the invention in combination with any one of the substituted full length  $\alpha$  chain amino acid sequences of SEQ ID NOS: 94-104 and 209. Another embodiment of the invention provides a TCR, polypeptide, or protein having any of the native, unsubstituted full-length  $\alpha$  chains described herein with respect to other aspects of the invention in combination with any one of the substituted full-length  $\beta$  chain sequences of SEQ ID NOS: 105-117.

TABLE V

Substituted full length $\alpha$ chain-version 1	SEQ ID NO: 94, wherein X is arginine, glutamic acid, asparagine, aspartic acid, cysteine, acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 2	SEQ ID NO: 95, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 3	SEQ ID NO: 96, wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 4	SEQ ID NO: 97, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 5	SEQ ID NO: 98, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 6	SEQ ID NO: 99, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain-version 7	SEQ ID NO: 100, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine

TABLE V-continued

Substituted full length $\alpha$ chain- version 8	SEQ ID NO: 101, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain- version 9	SEQ ID NO: 102, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain- version 10	SEQ ID NO: 103, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain- version 11	SEQ ID NO: 104, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\alpha$ chain- version 12	SEQ ID NO: 209, Wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine. In a preferred embodiment, X is alanine in SEQ ID NO: 209.

TABLE VI

Substituted full length $\beta$ chain- version 1	SEQ ID NO: 105, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 2	SEQ ID NO: 106, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 3	SEQ ID NO: 107, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 4	SEQ ID NO: 108, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 5	SEQ ID NO: 109, wherein X is alanine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 6	SEQ ID NO: 110, wherein X is alanine, arginine, asparagine, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 7	SEQ ID NO: 111, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tyrosine, or valine
Substituted full length $\beta$ chain- version 8	SEQ ID NO: 112, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, or valine

TABLE VI-continued

Substituted full length $\beta$ chain- version 9	SEQ ID NO: 113, wherein X is arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 10	SEQ ID NO: 114, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 11	SEQ ID NO: 115, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 12	SEQ ID NO: 116, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine
Substituted full length $\beta$ chain- version 13	SEQ ID NO: 117, wherein X is alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, or valine

**[0033]** In an embodiment of the invention, each of the substituted full length  $\alpha$  chain amino acid sequences of SEQ ID NOS: 94-104 does not comprise the native, unsubstituted full length  $\alpha$  chain amino acid sequence of SEQ ID NO: 11. In an embodiment of the invention, the substituted full length  $\alpha$  chain amino acid sequence of SEQ ID NO: 209 does not comprise the native, unsubstituted full length  $\alpha$  chain amino acid sequence of SEQ ID NO: 157. Similarly, in an embodiment of the invention, each of the substituted full length  $\beta$  chain amino acid sequences of SEQ ID NOS: 105-117 does not comprise the native, unsubstituted full length  $\beta$  chain amino acid sequence of SEQ ID NO: 12.

**[0034]** The TCR, polypeptide, or protein can consist essentially of the specified amino acid sequence or sequences described herein, such that other components of the TCR, polypeptide, or protein, e.g., other amino acids, do not materially change the biological activity of the TCR, polypeptide, or protein. In this regard, the inventive TCR, polypeptide, or protein can, for example, consist essentially of the amino acid sequence of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 209, both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, both SEQ ID NO: 157 and 158, or both SEQ ID NOS: 158 and 209. Also, for instance, the inventive TCRs, polypeptides, or proteins can consist essentially of the amino acid sequence (s) of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 143. SEQ ID NO: 144, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 208, both SEQ ID NOS: 9 and 10, both SEQ ID NOS: 131 and 132, both SEQ ID NO: 143 and 144, both SEQ ID NOS: 155 and 156, or both SEQ ID NOS: 156 and 208. Furthermore, the inventive TCRs, polypeptides, or proteins can consist essentially of the amino acid sequence of (a) SEQ ID NO: 3 (CDR1 of  $\alpha$  chain). SEQ ID NO: 4 (CDR2 of  $\alpha$  chain). SEQ ID NO: 5 (CDR3 of  $\alpha$  chain). SEQ ID NO: 6 (CDR1 of  $\beta$  chain). SEQ ID NO: 7 (CDR2 of  $\beta$  chain). SEQ ID NO: 8 (CDR3 of  $\beta$  chain), or any combination thereof, e.g., SEQ ID NOS: 3-5:6-8; or 3-8; (b) SEQ ID NO: 125 (CDR1 of  $\alpha$

chain). SEQ ID NO: 126 (CDR2 of  $\alpha$  chain). SEQ ID NO: 127 (CDR3 of  $\alpha$  chain). SEQ ID NO: 128 (CDR1 of  $\beta$  chain). SEQ ID NO: 129 (CDR2 of  $\beta$  chain). SEQ ID NO: 130 (CDR3 of  $\beta$  chain), or any combination thereof, e.g., SEQ ID NOS: 125-127:128-130; or 125-130; (c) SEQ ID NO: 137 (CDR1 of  $\alpha$  chain). SEQ ID NO: 138 (CDR2 of  $\alpha$  chain). SEQ ID NO: 139 (CDR3 of  $\alpha$  chain). SEQ ID NO: 140 (CDR1 of  $\beta$  chain). SEQ ID NO: 141 (CDR2 of  $\beta$  chain). SEQ ID NO: 142 (CDR3 of  $\beta$  chain), or any combination thereof, e.g., SEQ ID NOS: 137-139:140-142; or 137-142; (d) SEQ ID NO: 149 (CDR1 of  $\alpha$  chain). SEQ ID NO: 150 (CDR2 of  $\alpha$  chain), SEQ ID NO: 151 (CDR3 of  $\alpha$  chain), SEQ ID NO: 152 (CDR1 of  $\beta$  chain), SEQ ID NO: 153 (CDR2 of  $\beta$  chain), SEQ ID NO: 154 (CDR3 of  $\beta$  chain), or any combination thereof, e.g., SEQ ID NOS: 149-151:152-154; or 149-154; or (e) SEQ ID NO: 149 (CDR1 of  $\alpha$  chain), SEQ ID NO: 150 (CDR2 of  $\alpha$  chain), SEQ ID NO: 207 (substituted CDR3 of  $\alpha$  chain), SEQ ID NO: 152 (CDR1 of  $\beta$  chain), SEQ ID NO: 153 (CDR2 of  $\beta$  chain), SEQ ID NO: 154 (CDR3 of  $\beta$  chain), or any combination thereof, e.g., SEQ ID NOS: 149-150 and 207: 152-154; or 149-150, 207, and 152-154.

**[0035]** Also provided by the invention is a polypeptide comprising a functional portion of any of the TCRs described herein. The term “polypeptide” as used herein includes oligopeptides and refers to a single chain of amino acids connected by one or more peptide bonds.

**[0036]** With respect to the inventive polypeptides, the functional portion can be any portion comprising contiguous amino acids of the TCR of which it is a part, provided that the functional portion specifically binds to mutated target, e.g., mutated KRAS. The term “functional portion” when used in reference to a TCR refers to any part or fragment of the TCR of the invention, which part or fragment retains the biological activity of the TCR of which it is a part (the parent TCR). Functional portions encompass, for example, those parts of a TCR that retain the ability to specifically bind to mutated target, e.g., mutated KRAS (e.g., in an HLA-A11-dependent manner), or detect, treat, or prevent cancer, to a similar extent, the same extent, or to a higher extent, as the

parent TCR. In reference to the parent TCR, the functional portion can comprise, for instance, about 10%, 25%, 30%, 50%, 68%, 80%, 90%, 95%, or more, of the parent TCR.

[0037] The functional portion can comprise additional amino acids at the amino or carboxy terminus of the portion, or at both termini, which additional amino acids are not found in the amino acid sequence of the parent TCR. Desirably, the additional amino acids do not interfere with the biological function of the functional portion, e.g., specifically binding to mutated target, e.g., mutated KRAS; and/or having the ability to detect cancer, treat or prevent cancer, etc. More desirably, the additional amino acids enhance the biological activity, as compared to the biological activity of the parent TCR or functional variant thereof.

[0038] The polypeptide can comprise a functional portion of either or both of the  $\alpha$  and  $\beta$  chains of the TCRs of the invention, such as a functional portion comprising one of more of CDR1, CDR2, and CDR3 of the variable region(s) of the  $\alpha$  chain and/or  $\beta$  chain of a TCR of the invention. In an embodiment of the invention, the polypeptide can comprise a functional portion comprising the amino acid sequence of (a) SEQ ID NO: 3 (CDR1 of  $\alpha$  chain), 4 (CDR2 of  $\alpha$  chain), 5 (CDR3 of  $\alpha$  chain), 6 (CDR1 of  $\beta$  chain), 7 (CDR2 of  $\beta$  chain), 8 (CDR3 of  $\beta$  chain), or a combination thereof; (b) SEQ ID NO: 125 (CDR1 of  $\alpha$  chain), 126 (CDR2 of  $\alpha$  chain), 127 (CDR3 of  $\alpha$  chain), 128 (CDR1 of  $\beta$  chain), 129 (CDR2 of  $\beta$  chain), 130 (CDR3 of  $\beta$  chain), or a combination thereof; (c) SEQ ID NO: 137 (CDR1 of  $\alpha$  chain), 138 (CDR2 of  $\alpha$  chain), 139 (CDR3 of  $\alpha$  chain), 140 (CDR1 of  $\beta$  chain), 141 (CDR2 of  $\beta$  chain), 142 (CDR3 of  $\beta$  chain), or a combination thereof; (d) SEQ ID NO: 149 (CDR1 of  $\alpha$  chain), 150 (CDR2 of  $\alpha$  chain), 151 (CDR3 of  $\alpha$  chain), 152 (CDR1 of  $\beta$  chain), 153 (CDR2 of  $\beta$  chain), 154 (CDR3 of  $\beta$  chain), or a combination thereof; or (e) SEQ ID NO: 149 (CDR1 of  $\alpha$  chain), 150 (CDR2 of  $\alpha$  chain), 207 (substituted CDR3 of  $\alpha$  chain), 152 (CDR1 of  $\beta$  chain), 153 (CDR2 of  $\beta$  chain), 154 (CDR3 of  $\beta$  chain), or a combination thereof. Preferably, the inventive polypeptide comprises a functional portion comprising the amino acid sequences of SEQ ID NOS: 3-5-6-8-125-127-128-130-137-139-140-142; 149-151-152-154; all of SEQ ID NOS: 3-8; all of SEQ ID NOS: 125-130; all of SEQ ID NOS: 137-142; all of SEQ ID NOS: 149-154; or all of SEQ ID NOS: 149-150, 207, and 152-154. More preferably, the polypeptide comprises a functional portion comprising the amino acid sequences of all of SEQ ID NOS: 3-8; all of SEQ ID NOS: 125-130; all of SEQ ID NOS: 137-142; all of SEQ ID NOS: 149-154; or all of SEQ ID NOS: 149-150, 207, and 152-154.

[0039] In an embodiment of the invention, the inventive polypeptide can comprise, for instance, the variable region of the inventive TCR or functional variant thereof comprising a combination of the CDR regions set forth above. In this regard, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 9 (variable region of  $\alpha$  chain), SEQ ID NO: 10 (variable region of  $\beta$  chain), SEQ ID NO: 131 (variable region of  $\alpha$  chain), SEQ ID NO: 132 (variable region of  $\beta$  chain), SEQ ID NO: 143 (variable region of  $\alpha$  chain), SEQ ID NO: 144 (variable region of  $\beta$  chain), SEQ ID NO: 155 (variable region of  $\alpha$  chain), SEQ ID NO: 156 (variable region of  $\beta$  chain), SEQ ID NO: 208 (substituted variable region of  $\alpha$  chain), both SEQ ID NOS: 9 and 10, both SEQ ID NOS: 131 and 132, both SEQ ID NOS: 143 and 144, both SEQ ID NO: 155 and 156, or both SEQ ID NOS: 208 and 156. Preferably, the polypeptide comprises the

amino acid sequences of both SEQ ID NOS: 9 and 10, both SEQ ID NOS: 131 and 132, both SEQ ID NOS: 143 and 144, both SEQ ID NO: 155 and 156, or both SEQ ID NOS: 208 and 156.

[0040] In an embodiment of the invention, the inventive polypeptide can further comprise the constant region of the inventive TCR or functional variant thereof set forth above. In this regard, the polypeptide can comprise the amino acid sequence of SEQ ID NO: 13 (constant region of  $\alpha$  chain), SEQ ID NO: 14 (constant region of  $\beta$  chain), SEQ ID NO: 135 (constant region of  $\alpha$  chain), SEQ ID NO: 136 (constant region of  $\beta$  chain), SEQ ID NO: 147 (constant region of  $\alpha$  chain), SEQ ID NO: 148 (constant region of  $\beta$  chain), SEQ ID NO: 159 (constant region of  $\alpha$  chain), SEQ ID NO: 160 (constant region of  $\beta$  chain), both SEQ ID NOS: 13 and 14, both SEQ ID NOS: 135 and 136, both SEQ ID NOS: 147 and 148, or both SEQ ID NOS: 159 and 160. Preferably, the polypeptide comprises the amino acid sequences of both SEQ ID NOS: 13 and 14, both SEQ ID NOS: 135 and 136, both SEQ ID NOS: 147 and 148, or both SEQ ID NOS: 159 and 160.

[0041] In an embodiment of the invention, the inventive polypeptide may comprise a combination of a variable region and a constant region of the inventive TCR or functional variant thereof. In this regard, the polypeptide can comprise: (a) the amino acid sequences of both SEQ ID NO: 9 (variable region of  $\alpha$  chain) and SEQ ID NO: 13 (constant region of  $\alpha$  chain), both SEQ ID NO: 10 (variable region of  $\beta$  chain) and SEQ ID NO: 14 (constant region of  $\beta$  chain), or all of SEQ ID NOS: 9, 10, 13, and 14; (b) the amino acid sequences of both SEQ ID NO: 131 (variable region of  $\alpha$  chain) and SEQ ID NO: 135 (constant region of  $\alpha$  chain), both SEQ ID NO: 132 (variable region of  $\beta$  chain) and SEQ ID NO: 136 (constant region of  $\beta$  chain), or all of SEQ ID NOS: 131, 132, 135, and 136; (c) the amino acid sequences of both SEQ ID NO: 143 (variable region of  $\alpha$  chain) and SEQ ID NO: 147 (constant region of  $\alpha$  chain), both SEQ ID NO: 144 (variable region of  $\beta$  chain) and SEQ ID NO: 148 (constant region of  $\beta$  chain), or all of SEQ ID NOS: 143, 144, 147, and 148; (d) the amino acid sequences of both SEQ ID NO: 155 (variable region of  $\alpha$  chain) and SEQ ID NO: 159 (constant region of  $\alpha$  chain), both SEQ ID NO: 156 (variable region of  $\beta$  chain) and SEQ ID NO: 160 (constant region of  $\beta$  chain), or all of SEQ ID NOS: 155, 156, 159, and 160; or (e) the amino acid sequences of both SEQ ID NO: 208 (substituted variable region of  $\alpha$  chain) and SEQ ID NO: 159 (constant region of  $\alpha$  chain), both SEQ ID NO: 156 (variable region of  $\beta$  chain) and SEQ ID NO: 160 (constant region of  $\beta$  chain), or all of SEQ ID NOS: 208, 156, 159, and 160. Preferably, the polypeptide comprises the amino acid sequences of all of SEQ ID NOS: 9, 10, 13, and 14; all of SEQ ID NOS: 131, 132, 135, and 136; all of SEQ ID NOS: 143, 144, 147, and 148; all of SEQ ID NOS: 155, 156, 159, and 160; or all of SEQ ID NOS: 208, 156, 159, and 160.

[0042] In an embodiment of the invention, the inventive polypeptide may comprise a combination of any of the CDR regions described herein and a constant region of the inventive TCR. In this regard, the polypeptide can comprise the amino acid sequences of all of SEQ ID NOS: 3-5 and 13, all of SEQ ID NOS: 6-8 and 14, all of SEQ ID NOS: 3-8 and 13-14; all of SEQ ID NOS: 125-127 and 135, all of SEQ ID NOS: 128-130 and 136, all of SEQ ID NOS: 125-130 and 135-136, all of SEQ ID NOS: 137-139 and 147, all of SEQ ID NOS: 140-142 and 148, all of SEQ ID NOS: 137-142 and

147-148, all of SEQ ID NOS: 149-151 and 159, all of SEQ ID NOS: 149-150, 207, and 159, all of SEQ ID NOS: 152-154 and 160, all of SEQ ID NOS: 149-154 and 159-160, or all of SEQ ID NOS: 149-150, 207, 152-154, and 159-160. Preferably, the polypeptide comprises the amino acid sequences of all of SEQ ID NOS: 3-8 and 13-14, all of SEQ ID NOS: 125-130 and 135-136, all of SEQ ID NOS: 137-142 and 147-148, all of SEQ ID NOS: 149-154 and 159-160, or all of SEQ ID NOS: 149-150, 207, 152-154, and 159-160.

**[0043]** In an embodiment of the invention, the inventive polypeptide can comprise the entire length of an  $\alpha$  or  $\beta$  chain of the TCR described herein. In this regard, the inventive polypeptide can comprise the amino acid sequence of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 157, SEQ ID NO: 209, SEQ ID NO: 158, both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, both SEQ ID NOS: 157 and 158, or both SEQ ID NOS: 209 and 158. Preferably, the polypeptide comprises the amino acid sequences of both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, both SEQ ID NOS: 157 and 158, or both SEQ ID NOS: 209 and 158.

**[0044]** The invention further provides a protein comprising at least one of the polypeptides described herein. By “protein” is meant a molecule comprising one or more polypeptide chains.

**[0045]** In an embodiment, the protein of the invention can comprise a first polypeptide chain comprising the amino acid sequences of SEQ ID NOS: 3-5 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOS: 6-8; a first polypeptide chain comprising the amino acid sequences of SEQ ID NOS: 125-127 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOS: 128-130; a first polypeptide chain comprising the amino acid sequences of SEQ ID NOS: 137-139 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOS: 140-142; a first polypeptide chain comprising the amino acid sequences of SEQ ID NOS: 149-151 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOS: 152-154; or a first polypeptide chain comprising the amino acid sequences of SEQ ID NOS: 149-150 and 207 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NOS: 152-154. Alternatively or additionally, the protein of the invention can comprise a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 9 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 10; a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 131 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 132; a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 143 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 144; a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 155 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 156; or a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 208 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 156. The protein can, for example, comprise (a) a first polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 9 and 13 or all of SEQ ID NOS: 3-5 and 13 and a second polypeptide chain comprising

the amino acid sequences of both SEQ ID NOS: 10 and 14 or all of SEQ ID NOS: 6-8 and 14; (b) a first polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 131 and 135 or all of SEQ ID NOS: 125-127 and 135 and a second polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 132 and 136 or all of SEQ ID NOS: 128-130 and 136; (c) a first polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 143 and 147 or all of SEQ ID NOS: 137-139 and 147 and a second polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 144 and 148 or all of SEQ ID NOS: 140-142 and 148; (d) a first polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 155 and 159 or all of SEQ ID NOS: 149-151 and 159 and a second polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 156 and 160 or all of SEQ ID NOS: 152-154 and 160; or (e) a first polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 208 and 159 or all of SEQ ID NOS: 149-150, 207 and 159 and a second polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 156 and 160 or all of SEQ ID NOS: 152-154 and 160. Alternatively or additionally, the protein of the invention can comprise (a) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 11 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 12; (b) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 133 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 134; (c) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 145 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 146; (d) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 157 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 158; or (e) a first polypeptide chain comprising the amino acid sequence of SEQ ID NO: 209 and a second polypeptide chain comprising the amino acid sequence of SEQ ID NO: 158. In this instance, the protein of the invention can be a TCR. Alternatively, if, for example, the protein comprises a single polypeptide chain comprising the amino acid sequences of both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, both SEQ ID NOS: 157 and 158, or if the first and/or second polypeptide chain(s) of the protein further comprise(s) other amino acid sequences, e.g., an amino acid sequence encoding an immunoglobulin or a portion thereof, then the inventive protein can be a fusion protein. In this regard, the invention also provides a fusion protein comprising at least one of the inventive polypeptides described herein along with at least one other polypeptide. The other polypeptide can exist as a separate polypeptide of the fusion protein, or can exist as a polypeptide, which is expressed in frame (in tandem) with one of the inventive polypeptides described herein. The other polypeptide can encode any peptidic or proteinaceous molecule, or a portion thereof, including, but not limited to an immunoglobulin. CD3, CD4, CD8, an MHC molecule, a CD1 molecule, e.g., CD1a, CD1b, CD1c, CD1d, etc.

**[0046]** The fusion protein can comprise one or more copies of the inventive polypeptide and/or one or more copies of the other polypeptide. For instance, the fusion protein can comprise 1, 2, 3, 4, 5, or more, copies of the inventive polypeptide and/or of the other polypeptide. Suit-

able methods of making fusion proteins are known in the art, and include, for example, recombinant methods.

[0047] In some embodiments of the invention, the TCRs, polypeptides, and proteins of the invention may be expressed as a single protein comprising a linker peptide linking the  $\alpha$  chain and the  $\beta$  chain. In this regard, the TCRs, polypeptides, and proteins of the invention comprising both SEQ ID NOS: 11 and 12, both SEQ ID NOS: 133 and 134, both SEQ ID NOS: 145 and 146, both SEQ ID NOS: 157 and 158, both SEQ ID NOS: 209 and 158, both SEQ ID NO: 9 and 10, both SEQ ID NOS: 131 and 132, both SEQ ID NOS: 143 and 144, both SEQ ID NOS: 155 and 156, both SEQ ID NOS: 208 and 156, all of SEQ ID NOS: 3-8, all of SEQ ID NOS: 125-130, all of SEQ ID NOS: 137-142, all of SEQ ID NOS: 149-154, all of SEQ ID NOS: 9, 10, 13, and 14, all of SEQ ID NOS: 131, 132, 135, and 136, all of SEQ ID NOS: 143, 144, 147, and 148, all of SEQ ID NOS: 155, 156, 159, and 160, all of SEQ ID NOS: 208, 156, 159, and 160, all of SEQ ID NOS: 3-8 and 13-14, all of SEQ ID NOS: 125-130 and 135-136, all of SEQ ID NOS: 137-142 and 147-148, all of SEQ ID NOS: 149-154 and 159-160, or all of SEQ ID NOS: 149-150, 207, 152-154, and 159-160 may further comprise a linker peptide. The linker peptide may advantageously facilitate the expression of a recombinant TCR, polypeptide, and/or protein in a host cell. The linker peptide may comprise any suitable amino acid sequence. In an embodiment of the invention, the TCR, polypeptide, or protein comprises a self-cleaving, viral linker peptide. For example, the linker peptide may comprise SEQ ID NO: 28. Upon expression of the construct including the linker peptide by a host cell, the linker peptide may be cleaved, resulting in separated  $\alpha$  and  $\beta$  chains. In an embodiment of the invention, the TCR, polypeptide, or protein may comprise an amino acid sequence comprising a full-length  $\alpha$  chain, a full-length  $\beta$  chain, and a linker peptide positioned between the  $\alpha$  and  $\beta$  chains (for example, the amino acid sequence of SEQ ID NO: 45 (anti-KRAS G12D TCR), SEQ ID NO: 162 (anti-KRAS G12D TCR), SEQ ID NO: 201 (anti-KRAS G12V TCR), or SEQ ID NO: 203 (anti-KRAS G12V TCR)).

[0048] The protein of the invention can be a recombinant antibody comprising at least one of the inventive polypeptides described herein. As used herein, “recombinant antibody” refers to a recombinant (e.g., genetically engineered) protein comprising at least one of the polypeptides of the invention and a polypeptide chain of an antibody, or a portion thereof. The polypeptide of an antibody, or portion thereof, can be a heavy chain, a light chain, a variable or constant region of a heavy or light chain, a single chain variable fragment (scFv), or an Fc, Fab, or F(ab)<sub>2</sub>' fragment of an antibody, etc. The polypeptide chain of an antibody, or portion thereof, can exist as a separate polypeptide of the recombinant antibody. Alternatively, the polypeptide chain of an antibody, or portion thereof, can exist as a polypeptide, which is expressed in frame (in tandem) with the polypeptide of the invention. The polypeptide of an antibody, or portion thereof, can be a polypeptide of any antibody or any antibody fragment, including any of the antibodies and antibody fragments described herein.

[0049] The TCRs, polypeptides, and proteins of the invention (including functional variants thereof) can be of any length, i.e., can comprise any number of amino acids, provided that the TCRs, polypeptides, or proteins (or functional variants thereof) retain their biological activity, e.g.,

the ability to specifically bind to mutated target, e.g., mutated KRAS; detect cancer in a mammal; or treat or prevent cancer in a mammal, etc. For example, the polypeptide can be in the range of from about 50 to about 5000 amino acids long, such as 50, 70, 75, 100, 125, 150, 175, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more amino acids in length. In this regard, the polypeptides of the invention also include oligopeptides.

[0050] The TCRs, polypeptides, and proteins of the invention of the invention can comprise synthetic amino acids in place of one or more naturally-occurring amino acids. Such synthetic amino acids are known in the art, and include, for example, aminocyclohexane carboxylic acid, norleucine,  $\alpha$ -amino n-decanoic acid, homoserine, S-acetylaminomethyl-cysteine, trans-3- and trans-4-hydroxyproline, 4-amino-naphenylalanine, 4-nitrophenylalanine, 4-chlorophenylalanine, 4-carboxyphenylalanine,  $\beta$ -phenylserine  $\beta$ -hydroxyphenylalanine, phenylglycine,  $\alpha$ -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-hydroxylsine, ornithine,  $\alpha$ -aminocyclopentane carboxylic acid,  $\alpha$ -aminocyclohexane carboxylic acid,  $\alpha$ -aminocycloheptane carboxylic acid, ox-(2-amino-2-norbornane)-carboxylic acid,  $\alpha,\gamma$ -diaminobutyric acid,  $\alpha,\beta$ -diaminopropionic acid, homophenylalanine, and  $\alpha$ -tert-butylglycine.

[0051] The TCRs, polypeptides, and proteins of the invention (including functional variants thereof) can be glycosylated, amidated, carboxylated, phosphorylated, esterified, N-acylated, cyclized via, e.g., a disulfide bridge, or converted into an acid addition salt and/or optionally dimerized or polymerized, or conjugated.

[0052] The TCR, polypeptide, and/or protein of the invention can be obtained by methods known in the art such as, for example, de novo synthesis. Also, polypeptides and proteins can be recombinantly produced using the nucleic acids described herein using standard recombinant methods. See, for instance, Green and Sambrook, *Molecular Cloning: A Laboratory Manual*, 4th ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (2012). Alternatively, the TCRs, polypeptides, and/or proteins described herein (including functional variants thereof) can be commercially synthesized by companies, such as Synpep (Dublin, CA), Peptide Technologies Corp. (Gaithersburg, MD), and Multiple Peptide Systems (San Diego, CA). In this respect, the inventive TCRs, polypeptides, and proteins can be synthetic, recombinant, isolated, and/or purified.

[0053] Included in the scope of the invention are conjugates, e.g., bioconjugates, comprising any of the inventive TCRs, polypeptides, or proteins, nucleic acids, recombinant expression vectors, host cells, populations of host cells, and antibodies, or antigen binding portions thereof. Conjugates, as well as methods of synthesizing conjugates in general, are known in the art.

[0054] An embodiment of the invention provides a nucleic acid comprising a nucleotide sequence encoding any of the TCRs, polypeptides, or proteins described herein. “Nucleic acid,” as used herein, includes “polynucleotide,” “oligonucleotide,” and “nucleic acid molecule,” and generally means a polymer of DNA or RNA, which can be single-stranded or double-stranded, synthesized or obtained (e.g., isolated and/or purified) from natural sources, which can contain natural, non-natural or altered nucleotides, and

which can contain a natural, non-natural or altered inter-nucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified oligonucleotide. In an embodiment, the nucleic acid comprises complementary DNA (cDNA). It is generally preferred that the nucleic acid does not comprise any insertions, deletions, inversions, and/or substitutions. However, it may be suitable in some instances, as discussed herein, for the nucleic acid to comprise one or more insertions, deletions, inversions, and/or substitutions.

[0055] Preferably, the nucleic acids of the invention are recombinant. As used herein, the term "recombinant" refers to (i) molecules that are constructed outside living cells by joining natural or synthetic nucleic acid segments to nucleic acid molecules that can replicate in a living cell, or (ii) molecules that result from the replication of those described in (i) above. For purposes herein, the replication can be in vitro replication or in vivo replication.

[0056] The nucleic acids can be constructed based on chemical synthesis and/or enzymatic ligation reactions using procedures known in the art. See, for example, Green and Sambrook et al., *supra*. For example, a nucleic acid can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed upon hybridization (e.g., phosphorothioate derivatives and acridine substituted nucleotides). Examples of modified nucleotides that can be used to generate the nucleic acids include, but are not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxy hydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxy methylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N<sup>6</sup>-substituted adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxy carboxymethyluracil, 5-methoxyuracil, 2-methylthio-N<sup>6</sup>-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. Alternatively, one or more of the nucleic acids of the invention can be purchased from companies, such as Macromolecular Resources (Fort Collins, CO) and Synthegen (Houston, TX).

[0057] The nucleic acid can comprise any nucleotide sequence which encodes any of the TCRs, polypeptides, or proteins described herein. In an embodiment of the invention, the nucleic acid may comprise the nucleotide sequence of (a) SEQ ID NO: 22 (CDR1 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 23 (CDR2 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 24 (CDR3 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 25 (CDR1 of anti-KRAS G12D TCR  $\beta$  chain); the nucleotide sequence of SEQ ID NO: 26 (CDR2 of anti-KRAS G12D TCR  $\beta$  chain); or the nucleotide sequence of SEQ ID NO: 27 (CDR3 of anti-KRAS G12D TCR  $\beta$  chain); (b) SEQ ID NO: 164 (CDR1 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleo-

tide sequence of SEQ ID NO: 165 (CDR2 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 166 (CDR3 of anti-KRAS G12D TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 167 (CDR1 of anti-KRAS G12D TCR  $\beta$  chain); the nucleotide sequence of SEQ ID NO: 168 (CDR2 of anti-KRAS G12D TCR  $\beta$  chain); or the nucleotide sequence of SEQ ID NO: 169 (CDR3 of anti-KRAS G12D TCR  $\beta$  chain); (c) SEQ ID NO: 177 (CDR1 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 178 (CDR2 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 179 (CDR3 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 180 (CDR1 of anti-KRAS G12V TCR  $\beta$  chain); the nucleotide sequence of SEQ ID NO: 181 (CDR2 of anti-KRAS G12V TCR  $\beta$  chain); or the nucleotide sequence of SEQ ID NO: 182 (CDR3 of anti-KRAS G12V TCR  $\beta$  chain); or (d) SEQ ID NO: 189 (CDR1 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 190 (CDR2 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 191 (CDR3 of anti-KRAS G12V TCR  $\alpha$  chain); the nucleotide sequence of SEQ ID NO: 192 (CDR1 of anti-KRAS G12V TCR  $\beta$  chain); the nucleotide sequence of SEQ ID NO: 193 (CDR2 of anti-KRAS G12V TCR  $\beta$  chain); or the nucleotide sequence of SEQ ID NO: 194 (CDR3 of anti-KRAS G12V TCR  $\beta$  chain). Preferably, the nucleic acid comprises the nucleotide sequences of all of SEQ ID NOS: 22-24; all of SEQ ID NOS: 25-27; all of SEQ ID NOS: 22-27; all of SEQ ID NOS: 164-166; all of SEQ ID NOS: 167-169; all of SEQ ID NOS: 164-169; all of SEQ ID NOS: 177-179; all of SEQ ID NOS: 180-182; all of SEQ ID NOS: 177-182; all of SEQ ID NOS: 189-191; all of SEQ ID NOS: 192-194; SEQ ID NOS: 189-194. In an especially preferred embodiment, the nucleic acid comprises the nucleotide sequences of all of SEQ ID NOS: 22-27; all of SEQ ID NOS: 164-169; all of SEQ ID NOS: 177-182; or all of SEQ ID NOS: 189-194. In an embodiment of the invention, the nucleic acid may comprise the nucleotide sequence of (a) SEQ ID NO: 15 (variable region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 16 (variable region of anti-KRAS G12D TCR  $\beta$  chain); or both SEQ ID NOS: 15 and 16; (b) SEQ ID NO: 170 (variable region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 171 (variable region of anti-KRAS G12D TCR  $\beta$  chain); or both SEQ ID NOS: 170 and 171; (c) SEQ ID NO: 183 (variable region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 184 (variable region of anti-KRAS G12V TCR  $\beta$  chain); or both SEQ ID NOS: 183 and 184; (d) SEQ ID NO: 195 (variable region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 196 (variable region of anti-KRAS G12V TCR  $\beta$  chain); or both SEQ ID NOS: 195 and 196. Preferably, the nucleic acid comprises the nucleotide sequences of both SEQ ID NOS: 15 and 16; both SEQ ID NOS: 170 and 171; both SEQ ID NOS: 183 and 184; or both SEQ ID NOS: 195 and 196. In another embodiment of the invention, the nucleic acid may comprise the nucleotide sequence of (a) SEQ ID NO: 17 (full-length anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 18 (full length anti-KRAS G12D TCR  $\beta$  chain); or both of SEQ ID NOS: 17 and 18; (b) SEQ ID NO: 172 (full-length anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 173 (full length anti-KRAS G12D TCR  $\beta$  chain); or both of SEQ ID NOS: 172 and 173; (c) SEQ ID NO: 185 (full-length anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 186 (full length anti-KRAS G12V TCR  $\beta$  chain); or both of SEQ ID NOS: 185 and 186; or (d) SEQ ID NO: 197 (full-length

anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 198 (full length anti-KRAS G12V TCR  $\beta$  chain); or both of SEQ ID NOs: 197 and 198. Preferably, the nucleic acid comprises the nucleotide sequences of both of SEQ ID NOs: 17 and 18; both SEQ ID NOs: 172 and 173; both SEQ ID NOs: 185 and 186; or both SEQ ID NOs: 197 and 198.

[0058] In an embodiment of the invention, the nucleic acid further comprises a nucleotide sequence that encodes the constant region of a TCR  $\alpha$  or  $\beta$  chain. In this regard, any of the nucleic acids described herein may further comprise the nucleotide sequence of (a) SEQ ID NO: 19 (constant region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 20 (constant region of anti-KRAS G12D TCR  $\beta$  chain); or both SEQ ID NOs: 19 and 20; (b) SEQ ID NO: 174 (constant region of anti-KRAS G12D TCR  $\alpha$  chain); SEQ ID NO: 175 (constant region of anti-KRAS G12D TCR  $\beta$  chain); or both SEQ ID NOs: 174 and 175; (c) SEQ ID NO: 187 (constant region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 188 (constant region of anti-KRAS G12V TCR  $\beta$  chain); or both SEQ ID NOs: 187 and 188; or (d) SEQ ID NO: 199 (constant region of anti-KRAS G12V TCR  $\alpha$  chain); SEQ ID NO: 200 (constant region of anti-KRAS G12V TCR  $\beta$  chain); or both SEQ ID NOs: 199 and 200. Preferably, the nucleic acid comprises the nucleotide sequence of both SEQ ID NOs: 15 and 19; both SEQ ID NOs: 16 and 20; all of SEQ ID NOs: 15-16 and 19-20; all of SEQ ID NOs: 22-24 and 19; all of SEQ ID NOs: 25-27 and 20; all of SEQ ID NOs: 22-27 and 19-20; both SEQ ID NO: 170 and 174; both SEQ ID NOs: 171 and 175; all of SEQ ID NOs: 170-171 and 174-175; all of SEQ ID NOs: 164-166 and 174; all of SEQ ID NOs: 167-169 and 175; all of SEQ ID NOs: 164-169 and 174-175; both of SEQ ID NOs: 183 and 187; both of SEQ ID NOs: 184 and 188; all of SEQ ID NOs: 183-184 and 187-188; SEQ ID NO: 177-179 and 187; all of SEQ ID NOs: 180-182 and 188; all of SEQ ID NOs: 177-182 and 187-188; both of SEQ ID NOs: 195 and 199; both of SEQ ID NOs: 196 and 200; all of SEQ ID NOs: 195-196 and 199-200; all of SEQ ID NOs: 189-191 and 199; all of SEQ ID NOs: 192-194 and 200; or all of SEQ ID NOs: 189-194 and 199-200. In an especially preferred embodiment, the nucleic acid comprises the nucleotide sequences of all of SEQ ID NOs: 15-16 and 19-20; all of SEQ ID NOs: 22-27 and 19-20; all of SEQ ID NOs: 170-171 and 174-175; all of SEQ ID NOs: 164-169 and 174-175; all of SEQ ID NOs: 183-184 and 187-188; all of SEQ ID NOs: 177-182 and 187-188; all of SEQ ID NOs: 195-196 and 199-200; or all of SEQ ID NOs: 189-194 and 199-200.

[0059] Any of the nucleic acids described herein may further comprise a nucleotide sequence encoding a linker peptide. The nucleotide sequence encoding the linker peptide may comprise any suitable nucleotide sequence. For example, the nucleotide sequence encoding a linker peptide may comprise the nucleotide sequence of SEQ ID NO: 44.

[0060] In an embodiment of the invention, a nucleic acid comprising the nucleotide sequence of all of SEQ ID NOs: 22-24; all of SEQ ID NOs: 25-27; all of SEQ ID NOs: 22-27; both SEQ ID NOs: 15 and 16; both SEQ ID NOs: 17 and 18; both SEQ ID NOs: 15 and 19; both SEQ ID NOs: 16 and 20; all of SEQ ID NOs: 15-16 and 19-20; all of SEQ ID NOs: 22-24 and 19; all of SEQ ID NOs: 25-27 and 20; all of SEQ ID NOs: 22-27 and 19-20; all of SEQ ID NOs: 164-169; both SEQ ID NOs: 170 and 171; both SEQ ID NOs: 172 and 173; all of SEQ ID NOs: 164-169 and 174-175; all of SEQ ID NOs: 170-171 and 174-175; all of SEQ ID NOs: 177-

182; both of SEQ ID NO: 183-184; both of SEQ ID NOs: 185-186; all of SEQ ID NOs: 177-182 and 187-188; all of SEQ ID NOs: 183-184 and 187-188; all of SEQ ID NOs: 189-194; both of SEQ ID NOs: 195-196; both of SEQ ID NOs: 197-198; all of SEQ ID NOs: 189-194 and 199-200; or all of SEQ ID NOs: 195-196 and 199-200 encodes a murine TCR.

[0061] The invention also provides a nucleic acid comprising a nucleotide sequence which is complementary to the nucleotide sequence of any of the nucleic acids described herein or a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of any of the nucleic acids described herein.

[0062] The nucleotide sequence which hybridizes under stringent conditions preferably hybridizes under high stringency conditions. By "high stringency conditions" is meant that the nucleotide sequence specifically hybridizes to a target sequence (the nucleotide sequence of any of the nucleic acids described herein) in an amount that is detectably stronger than non-specific hybridization. High stringency conditions include conditions which would distinguish a polynucleotide with an exact complementary sequence, or one containing only a few scattered mismatches from a random sequence that happened to have a few small regions (e.g., 3-10 bases) that matched the nucleotide sequence. Such small regions of complementarity are more easily melted than a full-length complement of 14-17 or more bases, and high stringency hybridization makes them easily distinguishable. Relatively high stringency conditions would include, for example, low salt and/or high temperature conditions, such as provided by about 0.02-0.1 M NaCl or the equivalent, at temperatures of about 50-70° C. Such high stringency conditions tolerate little, if any, mismatch between the nucleotide sequence and the template or target strand, and are particularly suitable for detecting expression of any of the inventive TCRs. It is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide.

[0063] The invention also provides a nucleic acid comprising a nucleotide sequence that is at least about 70% or more, e.g., about 80%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to any of the nucleic acids described herein. In this regard, the nucleic acid may consist essentially of any of the nucleotide sequences described herein.

[0064] The nucleic acids of the invention can be incorporated into a recombinant expression vector. In this regard, the invention provides a recombinant expression vector comprising any of the nucleic acids of the invention. In an embodiment of the invention, the recombinant expression vector comprises a nucleotide sequence encoding the  $\alpha$  chain, the  $\beta$  chain, and linker peptide. For example, in an embodiment, the recombinant expression vector comprises the nucleotide sequence of SEQ ID NO: 21 (encoding  $\alpha$  and  $\beta$  chains SEQ ID NOs: 11 and 12 with a linker positioned between them); SEQ ID NO: 163 (encoding  $\alpha$  and  $\beta$  chains SEQ ID NOs: 157 and 158 with a linker positioned between them); SEQ ID NO: 202 (encoding  $\alpha$  and  $\beta$  chains SEQ ID NOs: 145 and 146 with a linker positioned between them); or SEQ ID NO: 176 (encoding  $\alpha$  and  $\beta$  chains SEQ ID NOs: 133 and 134 with a linker positioned between them).

**[0065]** For purposes herein, the term “recombinant expression vector” means a genetically-modified oligonucleotide or polynucleotide construct that permits the expression of an mRNA, protein, polypeptide, or peptide by a host cell, when the construct comprises a nucleotide sequence encoding the mRNA, protein, polypeptide, or peptide, and the vector is contacted with the cell under conditions sufficient to have the mRNA, protein, polypeptide, or peptide expressed within the cell. The vectors of the invention are not naturally-occurring as a whole. However, parts of the vectors can be naturally-occurring. The inventive recombinant expression vectors can comprise any type of nucleotide, including, but not limited to DNA and RNA, which can be single-stranded or double-stranded, synthesized or obtained in part from natural sources, and which can contain natural, non-natural or altered nucleotides. The recombinant expression vectors can comprise naturally-occurring, non-naturally-occurring internucleotide linkages, or both types of linkages. Preferably, the non-naturally occurring or altered nucleotides or internucleotide linkages does not hinder the transcription or replication of the vector.

**[0066]** The recombinant expression vector of the invention can be any suitable recombinant expression vector, and can be used to transform or transfect any suitable host cell. Suitable vectors include those designed for propagation and expansion or for expression or both, such as plasmids and viruses. The vector can be selected from the group consisting of 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  $\lambda$ GT10,  $\lambda$ GT11,  $\lambda$ ZapII (Stratagene),  $\lambda$ EMBL4, and  $\lambda$ NM1149, also can be used. Examples of plant expression vectors include pBI01, pBI101.2, pBI101.3, pBI121 and pBIN19 (Clontech). Examples of animal expression vectors include pEUK-Cl, pMAM and pMAMneo (Clontech). Preferably, the recombinant expression vector is a viral vector, e.g., a retroviral vector. In an especially preferred embodiment, the recombinant expression vector is an MSGV1 vector.

**[0067]** The recombinant expression vectors of the invention can be prepared using standard recombinant DNA techniques described in, for example, Green and Sambrook et al., supra. Constructs of expression vectors, which are circular or linear, can be prepared to contain a replication system functional in a prokaryotic or eukaryotic host cell. Replication systems can be derived, e.g., from ColE1, 2 $\mu$  plasmid,  $\lambda$ , SV40, bovine papillomavirus, and the like.

**[0068]** Desirably, the recombinant expression vector comprises regulatory sequences, such as transcription and translation initiation and termination codons, which are specific to the type of host cell (e.g., bacterium, fungus, plant, or animal) into which the vector is to be introduced, as appropriate and taking into consideration whether the vector is DNA- or RNA-based.

**[0069]** The recombinant expression vector can include one or more marker genes, which allow for selection of transformed or transfected host cells. Marker genes include biocide resistance, e.g., resistance to antibiotics, heavy metals, etc., complementation in an auxotrophic host cell to provide prototrophy, and the like. Suitable marker genes for the inventive expression vectors include, for instance, neomycin/G418 resistance genes, hygromycin resistance genes,

histidinol resistance genes, tetracycline resistance genes, and ampicillin resistance genes.

**[0070]** The recombinant expression vector can comprise a native or nonnative promoter operably linked to the nucleotide sequence encoding the TCR, polypeptide, or protein, or to the nucleotide sequence which is complementary to or which hybridizes to the nucleotide sequence encoding the TCR, polypeptide, or protein. The selection of promoters, e.g., strong, weak, inducible, tissue-specific and developmental-specific, is within the ordinary skill of the artisan. Similarly, the combining of a nucleotide sequence with a promoter is also within the skill of the artisan. The promoter can be a non-viral promoter or a viral promoter, e.g., a cytomegalovirus (CMV) promoter, an SV40 promoter, an RSV promoter, and a promoter found in the long-terminal repeat of the murine stem cell virus.

**[0071]** The inventive recombinant expression vectors can be designed for either transient expression, for stable expression, or for both. Also, the recombinant expression vectors can be made for constitutive expression or for inducible expression.

**[0072]** Further, the recombinant expression vectors can be made to include a suicide gene. As used herein, the term “suicide gene” refers to a gene that causes the cell expressing the suicide gene to die. The suicide gene can be a gene that confers sensitivity to an agent, e.g., a drug, upon the cell in which the gene is expressed, and causes the cell to die when the cell is contacted with or exposed to the agent. Suicide genes are known in the art and include, for example, the Herpes Simplex Virus (HSV) thymidine kinase (TK) gene, cytosine deaminase, purine nucleoside phosphorylase, and nitroreductase.

**[0073]** Another embodiment of the invention further provides a host cell comprising any of the recombinant expression vectors described herein. As used herein, the term “host cell” refers to any type of cell that can contain the inventive recombinant expression vector. The host cell can be a eukaryotic cell, e.g., plant, animal, fungi, or algae, or can be a prokaryotic cell, e.g., bacteria or protozoa. The host cell can be a cultured cell or a primary cell, i.e., isolated directly from an organism, e.g., a human. The host cell can be an adherent cell or a suspended cell, i.e., a cell that grows in suspension. Suitable host cells are known in the art and include, for instance, DH5 $\alpha$  *E. coli* cells, Chinese hamster ovarian cells, monkey VERO cells, COS cells, HEK293 cells, and the like. For purposes of amplifying or replicating the recombinant expression vector, the host cell is preferably a prokaryotic cell, e.g., a DH5 $\alpha$  cell. For purposes of producing a recombinant TCR, polypeptide, or protein, the host cell is preferably a mammalian cell. Most preferably, the host cell is a human cell. While the host cell can be of any cell type, can originate from any type of tissue, and can be of any developmental stage, the host cell preferably is a peripheral blood lymphocyte (PBL) or a peripheral blood mononuclear cell (PBMC). More preferably, the host cell is a T cell.

**[0074]** For purposes herein, the T cell can be any T cell, such as a cultured T cell, e.g., a primary T cell, or a T cell from a cultured T cell line, e.g., Jurkat, SupT1, etc., or a T cell obtained from a mammal. If obtained from a mammal, the T cell can be obtained from numerous sources, including but not limited to blood, bone marrow, lymph node, the thymus, or other tissues or fluids. T cells can also be enriched for or purified. Preferably, the T cell is a human T

cell. The T cell can be any type of T cell and can be of any developmental stage, including but not limited to, CD4<sup>+</sup>/CD8<sup>+</sup> double positive T cells, CD4<sup>+</sup> helper T cells, e.g., Th<sub>1</sub> and Th<sub>2</sub> cells, CD4<sup>+</sup> T cells, CD8<sup>+</sup> T cells (e.g., cytotoxic T cells), tumor infiltrating lymphocytes (TILs), memory T cells (e.g., central memory T cells and effector memory T cells), naïve T cells, and the like.

[0075] Also provided by the invention is a population of cells comprising at least one host cell described herein. The population of cells can be a heterogeneous population comprising the host cell comprising any of the recombinant expression vectors described, in addition to at least one other cell, e.g., a host cell (e.g., a T cell), which does not comprise any of the recombinant expression vectors, or a cell other than a T cell, e.g., a B cell, a macrophage, a neutrophil, an erythrocyte, a hepatocyte, an endothelial cell, an epithelial cells, a muscle cell, a brain cell, etc. Alternatively, the population of cells can be a substantially homogeneous population, in which the population comprises mainly of host cells (e.g., consisting essentially of) comprising the recombinant expression vector. The population also can be a clonal population of cells, in which all cells of the population are clones of a single host cell comprising a recombinant expression vector, such that all cells of the population comprise the recombinant expression vector. In one embodiment of the invention, the population of cells is a clonal population comprising host cells comprising a recombinant expression vector as described herein.

[0076] In an embodiment of the invention, the numbers of cells in the population may be rapidly expanded. Expansion of the numbers of T cells can be accomplished by any of a number of methods as are known in the art as described in, for example, U.S. Pat. No. 8,034,334; U.S. Pat. No. 8,383,099; U.S. Patent Application Publication No. 2012/0244133; Dudley et al., *J. Immunother.*, 26:332-42 (2003); and Riddell et al., *J. Immunol. Methods*, 128:189-201 (1990). In an embodiment, expansion of the numbers of T cells is carried out by culturing the T cells with OKT3 antibody, IL-2, and feeder PBMC (e.g., irradiated allogeneic PBMC).

[0077] The invention further provides an antibody, or antigen binding portion thereof, which specifically binds to a functional portion of any of the TCRs described herein. Preferably, the functional portion specifically binds to the cancer antigen, e.g., the functional portion comprising the amino acid sequence SEQ ID NO: 3, 125, 137, or 149 (CDR1 of α chain), SEQ ID NO: 4, 126, 138, or 150 (CDR2 of α chain), SEQ ID NO: 5, 127, 139, 151, or 207 (CDR3 of α chain), SEQ ID NO: 6, 128, 140, or 152 (CDR1 of β chain), SEQ ID NO: 7, 129, 141, or 153 (CDR2 of β chain), SEQ ID NO: 8, 130, 142, or 154 (CDR3 of β chain), SEQ ID NO: 9, 131, 143, 155, or 208 (variable region of α chain), SEQ ID NO: 10, 132, 144, or 156 (variable region of β chain), or a combination thereof, e.g., SEQ ID NOs: 3-5: SEQ ID NOs: 6-8: SEQ ID NOs: 3-8: SEQ ID NO: 9; SEQ ID NO: 10: SEQ ID NOs: 9-10: SEQ ID NOs: 125-127, SEQ ID NOs: 128-130, SEQ ID NOs: 125-130, SEQ ID NOs: 137-139, SEQ ID NOs: 140-142, SEQ ID NOs: 137-142, SEQ ID NOs: 149-151, SEQ ID NOs: 149-150 and 207, SEQ ID NOs: 152-154, SEQ ID NOs: 149-154: SEQ ID NOs: 149-150, 207, and 152-154: SEQ ID NOs: 131-132, SEQ ID NOs: 143-144, SEQ ID NOs: 155-156; SEQ ID NO: 208; or SEQ ID NOs: 208 and 156. More preferably, the functional portion comprises the amino acid sequences of SEQ ID NOs: 3-8, SEQ ID NOs: 9 and 10, SEQ ID NOs:

125-130, SEQ ID NOs: 137-142, SEQ ID NOs: 149-154, SEQ ID NOs: 149-150, 207, and 152-154, SEQ ID NOs: 131-132, SEQ ID NOs: 143-144, SEQ ID NOs: 155-156, or SEQ ID NOs: 208 and 156. In a preferred embodiment, the antibody, or antigen binding portion thereof, binds to an epitope which is formed by all 6 CDRs (CDR1-3 of the α chain and CDR1-3 of the β chain). The antibody can be any type of immunoglobulin that is known in the art. For instance, the antibody can be of any isotype, e.g., IgA, IgD, IgE, IgG, IgM, etc. The antibody can be monoclonal or polyclonal. The antibody can be a naturally-occurring antibody, e.g., an antibody isolated and/or purified from a mammal, e.g., mouse, rabbit, goat, horse, chicken, hamster, human, etc. Alternatively, the antibody can be a genetically-engineered antibody, e.g., a humanized antibody or a chimeric antibody. The antibody can be in monomeric or polymeric form. Also, the antibody can have any level of affinity or avidity for the functional portion of the inventive TCR. Desirably, the antibody is specific for the functional portion of the inventive TCR, such that there is minimal cross-reaction with other peptides or proteins.

[0078] Methods of testing antibodies for the ability to bind to any functional portion or functional variant of the inventive TCR are known in the art and include any antibody-antigen binding assay, such as, for example, radioimmunoassay (RIA), ELISA, Western blot, immunoprecipitation, and competitive inhibition assays.

[0079] Suitable methods of making antibodies are known in the art. For instance, standard hybridoma methods are described in, e.g., C. A. Janeway et al. (eds.). *Immunobiology*, 8<sup>th</sup> Ed., Garland Publishing, New York, NY (2011). Alternatively, other methods, such as EBV-hybridoma methods, methods of producing antibodies in non-human animals, and bacteriophage vector expression systems are known in the art.

[0080] Phage display can also be used to generate the antibody of the invention. In this regard, phage libraries encoding antigen-binding variable (V) domains of antibodies can be generated using standard molecular biology and recombinant DNA techniques (see, e.g., Green and Sambrook et al. (eds.), *Molecular Cloning, A Laboratory Manual*, 4<sup>th</sup> Edition. Cold Spring Harbor Laboratory Press, New York (2012)). Phage encoding a variable region with the desired specificity are selected for specific binding to the desired antigen, and a complete or partial antibody is reconstituted comprising the selected variable domain. Nucleic acid sequences encoding the reconstituted antibody are introduced into a suitable cell line, such as a myeloma cell used for hybridoma production, such that antibodies having the characteristics of monoclonal antibodies are secreted by the cell (see, e.g., Janeway et al., *supra*).

[0081] Methods for generating humanized antibodies are well known in the art. Antibodies can also be produced by transgenic mice that are transgenic for specific heavy and light chain immunoglobulin genes. Such methods are known in the art and described in, for example, Janeway et al., *supra*.

[0082] The invention also provides antigen binding portions of any of the antibodies described herein. The antigen binding portion can be any portion that has at least one antigen binding site, such as Fab, F(ab')<sub>2</sub>, dsFv, sFv, diabodies, and triabodies.

[0083] A single-chain variable region fragment (sFv) antibody fragment, which consists of a truncated Fab fragment

comprising the variable (V) domain of an antibody heavy chain linked to a V domain of a light antibody chain via a synthetic peptide, can be generated using routine recombinant DNA technology techniques (see, e.g., Janeway et al., *supra*). Similarly, disulfide-stabilized variable region fragments (dsFv) can be prepared by recombinant DNA technology. Antibody fragments of the invention, however, are not limited to these exemplary types of antibody fragments.

[0084] Also, the antibody, or antigen binding portion thereof, can be modified to comprise a detectable label, such as, for instance, a radioisotope, a fluorophore (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE)), an enzyme (e.g., alkaline phosphatase, horseradish peroxidase), and element particles (e.g., gold particles).

[0085] The inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells (including populations thereof), and antibodies (including antigen binding portions thereof), can be isolated and/or purified. The term "isolated" as used herein means having been removed from its natural environment. The term "purified" as used herein means having been increased in purity, wherein "purity" is a relative term, and not to be necessarily construed as absolute purity. For example, the purity can be at least about 50%, can be greater than 60%, 70%, 80%, 90%, 95%, or can be 100%.

[0086] The inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells (including populations thereof), and antibodies (including antigen binding portions thereof), all of which are collectively referred to as "inventive TCR materials" hereinafter, can be formulated into a composition, such as a pharmaceutical composition. In this regard, the invention provides a pharmaceutical composition comprising any of the TCRs, polypeptides, proteins, nucleic acids, expression vectors, host cells (including populations thereof), and antibodies (including antigen binding portions thereof) described herein, and a pharmaceutically acceptable carrier. The inventive pharmaceutical compositions containing any of the inventive TCR materials can comprise more than one inventive TCR material, e.g., a polypeptide and a nucleic acid, or two or more different TCRs. Alternatively, the pharmaceutical composition can comprise an inventive TCR material in combination with another pharmaceutically active agent(s) or drug(s), such as a chemotherapeutic agents, e.g., asparaginase, busulfan, carboplatin, cisplatin, daunorubicin, doxorubicin, fluorouracil, gemcitabine, hydroxyurea, methotrexate, paclitaxel, rituximab, vinblastine, vincristine, etc.

[0087] Preferably, the carrier is a pharmaceutically acceptable carrier. With respect to pharmaceutical compositions, the carrier can be any of those conventionally used for the particular inventive TCR material under consideration. Such pharmaceutically acceptable carriers are well-known to those skilled in the art and are readily available to the public. It is preferred that the pharmaceutically acceptable carrier be one which has no detrimental side effects or toxicity under the conditions of use.

[0088] The choice of carrier will be determined in part by the particular inventive TCR material, as well as by the particular method used to administer the inventive TCR material. Accordingly, there are a variety of suitable formulations of the pharmaceutical composition of the invention. Suitable formulations may include any of those for oral, parenteral, subcutaneous, intravenous, intramuscular,

intraarterial, intrathecal, or interperitoneal administration. More than one route can be used to administer the inventive TCR materials, and in certain instances, a particular route can provide a more immediate and more effective response than another route.

[0089] Preferably, the inventive TCR material is administered by injection, e.g., intravenously. When the inventive TCR material is a host cell expressing the inventive TCR (or functional variant thereof), the pharmaceutically acceptable carrier for the cells for injection may include any isotonic carrier such as, for example, normal saline (about 0.90% w/v of NaCl in water, about 300 mOsm/L NaCl in water, or about 9.0 g NaCl per liter of water), NORMOSOL R electrolyte solution (Abbott, Chicago, IL), PLASMA-LYTE A (Baxter, Deerfield, IL), about 5% dextrose in water, or Ringer's lactate. In an embodiment, the pharmaceutically acceptable carrier is supplemented with human serum albumen.

[0090] For purposes of the invention, the amount or dose (e.g., numbers of cells when the inventive TCR material is one or more cells) of the inventive TCR material administered should be sufficient to effect, e.g., a therapeutic or prophylactic response, in the subject or animal over a reasonable time frame. For example, the dose of the inventive TCR material should be sufficient to bind to a cancer antigen (e.g., mutated KRAS), or detect, treat or prevent cancer in a period of from about 2 hours or longer, e.g., 12 to 24 or more hours, from the time of administration. In certain embodiments, the time period could be even longer. The dose will be determined by the efficacy of the particular inventive TCR material and the condition of the animal (e.g., human), as well as the body weight of the animal (e.g., human) to be treated.

[0091] Many assays for determining an administered dose are known in the art. For purposes of the invention, an assay, which comprises comparing the extent to which target cells are lysed or IFN- $\gamma$  is secreted by T cells expressing the inventive TCR, polypeptide, or protein upon administration of a given dose of such T cells to a mammal among a set of mammals of which is each given a different dose of the T cells, could be used to determine a starting dose to be administered to a mammal. The extent to which target cells are lysed or IFN- $\gamma$  is secreted upon administration of a certain dose can be assayed by methods known in the art.

[0092] The dose of the inventive TCR material also will be determined by the existence, nature and extent of any adverse side effects that might accompany the administration of a particular inventive TCR material. Typically, the attending physician will decide the dosage of the inventive TCR material with which to treat each individual patient, taking into consideration a variety of factors, such as age, body weight, general health, diet, sex, inventive TCR material to be administered, route of administration, and the severity of the cancer being treated. In an embodiment in which the inventive TCR material is a population of cells, the number of cells administered per infusion may vary, e.g., from about  $1 \times 10^6$  to about  $1 \times 10^{12}$  cells or more. In certain embodiments, fewer than  $1 \times 10^6$  cells may be administered.

[0093] One of ordinary skill in the art will readily appreciate that the inventive TCR materials of the invention can be modified in any number of ways, such that the therapeutic or prophylactic efficacy of the inventive TCR materials is increased through the modification. For instance, the inventive TCR materials can be conjugated either directly or indirectly through a bridge to a targeting moiety. The prac-

tice of conjugating compounds, e.g., inventive TCR materials, to targeting moieties is known in the art. The term “targeting moiety” as used herein, refers to any molecule or agent that specifically recognizes and binds to a cell-surface receptor, such that the targeting moiety directs the delivery of the inventive TCR materials to a population of cells on which surface the receptor is expressed. Targeting moieties include, but are not limited to, antibodies, or fragments thereof, peptides, hormones, growth factors, cytokines, and any other natural or non-natural ligands, which bind to cell surface receptors (e.g., Epithelial Growth Factor Receptor (EGFR), T cell receptor (TCR), B-cell receptor (BCR), CD28, Platelet-derived Growth Factor Receptor (PDGF), nicotinic acetylcholine receptor (nAChR), etc.). The term “bridge” as used herein, refers to any agent or molecule that links the inventive TCR materials to the targeting moiety. One of ordinary skill in the art recognizes that sites on the inventive TCR materials, which are not necessary for the function of the inventive TCR materials, are ideal sites for attaching a bridge and/or a targeting moiety, provided that the bridge and/or targeting moiety, once attached to the inventive TCR materials, do(es) not interfere with the function of the inventive TCR materials, i.e., the ability to bind to mutated target, e.g., mutated KRAS or to detect, treat, or prevent cancer.

[0094] It is contemplated that the inventive pharmaceutical compositions, TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, or populations of cells can be used in methods of treating or preventing cancer. Without being bound to a particular theory, the inventive TCRs are believed to bind specifically to mutated target, e.g., mutated KRAS, such that the TCR (or related inventive polypeptide or protein), when expressed by a cell, is able to mediate an immune response against a target cell expressing mutated target, e.g., mutated KRAS. In this regard, the invention provides a method of treating or preventing cancer in a mammal, comprising administering to the mammal any of the pharmaceutical compositions. TCRs, polypeptides, or proteins described herein, any nucleic acid or recombinant expression vector comprising a nucleotide sequence encoding any of the TCRs, polypeptides, proteins described herein, or any host cell or population of cells comprising a recombinant vector which encodes any of the TCRs, polypeptides, or proteins described herein, in an amount effective to treat or prevent cancer in the mammal.

[0095] An embodiment of the invention provides any of the pharmaceutical compositions, TCRs, polypeptides, or proteins described herein, any nucleic acid or recombinant expression vector comprising a nucleotide sequence encoding any of the TCRs, polypeptides, proteins described herein, or any host cell or population of cells comprising a recombinant vector which encodes any of the TCRs, polypeptides, or proteins described herein, for use in the treatment or prevention of cancer in a mammal.

[0096] The terms “treat,” and “prevent” as well as words stemming therefrom, as used herein, do not necessarily imply 100% or complete treatment or prevention. Rather, there are varying degrees of treatment or prevention of which one of ordinary skill in the art recognizes as having a potential benefit or therapeutic effect. In this respect, the inventive methods can provide any amount of any level of treatment or prevention of cancer in a mammal. Furthermore, the treatment or prevention provided by the inventive

method can include treatment or prevention of one or more conditions or symptoms of the cancer being treated or prevented. For example, treatment or prevention can include promoting the regression of a tumor. Also, for purposes herein, “prevention” can encompass delaying the onset of the cancer, or a symptom or condition thereof.

[0097] Also provided is a method of detecting the presence of cancer in a mammal. The method comprises (i) contacting a sample comprising one or more cells from the mammal with any of the inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, populations of cells, antibodies, or antigen binding portions thereof, or pharmaceutical compositions described herein, thereby forming a complex, and detecting the complex, wherein detection of the complex is indicative of the presence of cancer in the mammal.

[0098] With respect to the inventive method of detecting cancer in a mammal, the sample of cells can be a sample comprising whole cells, lysates thereof, or a fraction of the whole cell lysates, e.g., a nuclear or cytoplasmic fraction, a whole protein fraction, or a nucleic acid fraction.

[0099] For purposes of the inventive detecting method, the contacting can take place in vitro or in vivo with respect to the mammal. Preferably, the contacting is in vitro.

[0100] Also, detection of the complex can occur through any number of ways known in the art. For instance, the inventive TCRs, polypeptides, proteins, nucleic acids, recombinant expression vectors, host cells, populations of cells, or antibodies, or antigen binding portions thereof, described herein, can be labeled with a detectable label such as, for instance, a radioisotope, a fluorophore (e.g., fluorescein isothiocyanate (FITC), phycoerythrin (PE)), an enzyme (e.g., alkaline phosphatase, horseradish peroxidase), and element particles (e.g., gold particles).

[0101] For purposes of the inventive methods, wherein host cells or populations of cells are administered, the cells can be cells that are allogeneic or autologous to the mammal. Preferably, the cells are autologous to the mammal.

[0102] With respect to the inventive methods, the cancer can be any cancer, including any of acute lymphocytic cancer, acute myeloid leukemia, alveolar rhabdomyosarcoma, bone cancer, brain cancer, breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct, cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vagina, cancer of the vulva, chronic lymphocytic leukemia, chronic myeloid cancer, colon cancer, colorectal cancer, endometrial cancer, esophageal cancer, uterine cervical cancer, gastrointestinal carcinoid tumor, glioma, Hodgkin lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer, lung cancer, malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin lymphoma, cancer of the oropharynx, ovarian cancer, cancer of the penis, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal cancer, skin cancer, small intestine cancer, soft tissue cancer, stomach cancer, testicular cancer, thyroid cancer, cancer of the uterus, ureter cancer, and urinary bladder cancer. A preferred cancer is cancer is pancreatic, colorectal, lung, endometrial, ovarian, or prostate cancer. Preferably, the lung cancer is lung adenocarcinoma, the ovarian cancer is epithelial ovarian cancer, and the pancreatic cancer is pancreatic carcinoma. In another pre-

ferred embodiment, the cancer is a cancer that expresses the mutated amino acid sequence of VVVGADGVGK (SEQ ID NO: 2), VVGADGVGK (SEQ ID NO: 34), VVVGAVGVGK (SEQ ID NO: 33), or VVGAVGVGK (SEQ ID NO: 35), which are present in mutated human KRAS, mutated human NRAS, and mutated human HRAS.

[0103] The mammal referred to in the inventive methods can be any mammal. As used herein, the term "mammal" refers to any mammal, including, but not limited to, mammals of the order Rodentia, such as mice and hamsters, and mammals of the order Logomorpha, such as rabbits. It is preferred that the mammals are from the order Carnivora, including Felines (cats) and Canines (dogs). It is more preferred that the mammals are from the order Artiodactyla, including Bovines (cows) and Swines (pigs) or of the order Perssodactyla, including Equines (horses). It is most preferred that the mammals are of the order Primates, Ceboids, or Simoids (monkeys) or of the order Anthropoids (humans and apes). An especially preferred mammal is the human.

[0104] The following examples further illustrate the invention but, of course, should not be construed as in any way limiting its scope.

#### Example 1

[0105] This example demonstrates the isolation of murine anti-KRAS7-16 G12D 10-mer TCRs.

[0106] A computer algorithm was used to generate candidate HLA-A11\*01 KRAS peptides. For the algorithm, the strong binder threshold was 50 nM, and the weak binder threshold was 500 nM. The candidate peptides are shown in Table 1.

TABLE 1

Description	SEQ ID NO:	Sequence	HLA-A11*01 (nM)
G12D 9-mer	34	VVGADGVGK	194
G12D 10-mer	2	VVVGADGVGK	220
G12V 9-mer	35	VVGAVGVGK	50
G12V 10-mer	33	VVVGAVGVGK	71
G12C 9-mer	36	VVGACGVGK	69
G12C 10-mer	37	VVVGACGVGK	120
G12R 9-mer	38	VVGARGVGK	86
G12R 10-mer	39	VVVGARGVGK	119

[0107] HLA-A11 transgenic mice were immunized with the G12D 10-mer peptide (SEQ ID NO: 2) three times. After the third immunization, the spleen and lymph nodes were removed and cultured in vitro with the G12D 10-mer peptide at various concentrations (1  $\mu$ M, 0.1  $\mu$ M, and 0.01  $\mu$ M) for seven days. T cells isolated from the lymph node (LN) and spleen cultures were tested for reactivity against (i) COS7 cells transduced to express HLA-A11 (COS7/A11) which had been pulsed with (a) no peptide (COS/A11), (b) WT KRAS7-16 peptide (SEQ ID NO: 30) (COS/A11+WT peptide), (c) G12D 10-mer peptide (SEQ ID NO: 2) (COS/A11+G12D peptide), or (d) G12V 10-mer peptide (SEQ ID NO: 33) (COS/A11+G12V peptide); and (ii) COS7/A11 cells transfected with a vector encoding a (a) WT KRAS mini-

gene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT) or (b) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D). Interferon (IFN)- $\gamma$  was measured. The results are shown in Table 2A (pulsed target cells) and Table 2B (transfected target cells). As shown in Tables 2A and 2B, HLA-A11 restricted murine T cells were reactive against KRAS G12D peptide SEQ ID NO: 2.

TABLE 2A

Stimulated with G12D peptide	mIFN- $\gamma$ (pg/ml)			
	COS/A11	COS/A11+WT peptide	COS/A11+G12D peptide	COS/A11+G12V peptide
0.01 $\mu$ M LN-well (W) 1	50	34	>20000	52
LN-W2	52	57	>20000	95
LN-W3	169	92	12849	61
Spleen-W1	32	32	45	33
Spleen-W2	35	50	57	44
Spleen-W3	68	72	94	40
0.1 $\mu$ M LN-W1	38	38	16729	36
LN-W2	62	81	>20000	81
LN-W3	73	116	>20000	129
Spleen-W1	36	43	14423	35
Spleen-W2	33	34	>20000	33
Spleen-W3	44	40	18107	38
1 $\mu$ M LN-W1	101	210	>20000	407
LN-W2	92	248	>20000	577
LN-W3	57	226	>20000	403
Spleen-W1	32	44	>20000	55
Spleen-W2	34	70	>20000	108
Spleen-W3	42	78	>20000	261

TABLE 2B

	mIFN- $\gamma$ (pg/ml)		
	COS/A11	COS/A11/WT	COS/A11/G12D
Spleen-W1	32	32	19184
Spleen-W2	34	36	19545
Spleen-W3	42	45	>20000
LN-W1	101	74	6001
LN-W2	92	147	13589
LN-W3	57	64	11644
Spleen-W1	36	53	12865
Spleen-W2	33	49	12728
Spleen-W3	44	45	12125
LN-W1	38	44	7025
LN-W2	62	54	19384
LN-W3	73	66	17431
Spleen-W1	32	32	52
Spleen-W2	35	35	63
Spleen-W3	68	36	94
LN-W1	50	38	12096
LN-W2	52	56	14098
LN-W3	169	46	6877

[0108] The TCR was isolated from the cells in each positive well using 5' Rapid Amplification of cDNA Ends (RACE). Two dominant alpha chains and four dominant beta chains were identified (Table 3).

TABLE 3

	V Region	D/J Region	CDR3	SEQ ID NO:
Alpha chains	TRAV12N-3*01	39*01	CALRGNAGAKLTF	5
	TRAV16D/DV11*03	52*01	CAMREDTGANTGKLT	40
Beta chains	TRBV4*01 (CB2)	2*01/2-3*01	CASSSRDWSAETLYF	8
	TRBV5*01 (CB2)	2*01/2-1*01	CASSQDSLGRAEQFF	41
	TRBV16*01 (CB2) (LN 0.01)	2*01/2-3*01	CASSSDWGGAETLYF	42
	TRBV16*01 (CB2) (Sp1)	2*01/2-3*01	CASSSGLGSSAETLYF	43

## Example 2

[0109] This example demonstrates that PBL transduced to express a TCR  $\alpha$  chain comprising SEQ ID NO: 11 and a TCR  $\beta$  chain comprising SEQ ID NO: 12 are reactive against HLA-A11+/G12D 10-mer+ targets.

[0110] The two dominant  $\alpha$  chains and four dominant  $\beta$  chains of Table 3 were individually cloned into MSGV1 retroviral vectors. PBL were individually co-transduced to express one of various pairs of an  $\alpha$  and  $\beta$  chain, as shown in Table 4. Transduced PBL were screened for reactivity against (i) HLA-A11-expressing T2/A11+ (Table 4A) or COS7/A11+ (Table 4B) cells pulsed with (a) G12D 10-mer peptide (SEQ ID NO: 2), (b) G12V 10-mer peptide (SEQ ID NO: 33), (c) WT KRAS 10-mer peptide (SEQ ID NO: 30), or (d) no peptide (none); or (ii) COS7/A11 cells transduced with a (a) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V), (c) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT), or (d) no cells (medium only) (Table 4C). IFN- $\gamma$  secretion was measured. The results are shown in Tables 4A-C. In Tables 4A-C, bold IFN- $\gamma$  secretion values indicate those pairs of TCR  $\alpha$  and  $\beta$  chains that demonstrated reactivity, and IFN- $\gamma$  secretion values in bold with underlining indicate the pair of TCR  $\alpha$  and  $\beta$  chains that demonstrated the best reactivity. As shown in Tables 4A-C, PBL co-transduced to express murine TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and murine TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against HLA-A11-expressing COS7 cells pulsed with G12D 10-mer or G12D transfectant target cells.

TABLE 4A

IFN- $\gamma$  (pg/ml) upon co-culture with T2/A11+ target cells

		WT None	10- mer	G12D 10- mer	G12V 10- mer
TRAV12N-3*01	TRBV4*01	108	136	<b>&gt;10000</b>	108
	TRBV5*01	348	138	<u>319</u>	263
	TRBV16*01 (LN)	107	100	93	120
	TRBV16*01 (SP)	234	132	246	132
TRAV16D/DV11*03	TRBV4*01	56	39	<b>595</b>	39
	TRBV5*01	140	146	<b>848</b>	155
	TRBV16*01 (LN)	71	100	135	51
	TRBV16*01 (SP)	228	297	133	144

TABLE 4B

IFN- $\gamma$  (pg/ml) upon co-culture with COS/A11+ targets

		WT None	r10- mer	G12D 10- mer	G12V 10- mer
TRAV12N-3*01	TRBV4*01	123	107	<b>&gt;10000</b>	129
	TRBV5*01	57	71	<u>86</u>	58
	TRBV16*01 (LN)	55	69	70	81
	TRBV16*01 (SP)	98	64	71	78
TRAV16D/DV11*03	TRBV4*01	71	57	<b>246</b>	71
	TRBV5*01	74	66	<b>1228</b>	70
	TRBV16*01 (LN)	74	77	68	85
	TRBV16*01 (SP)	108	121	104	100

TABLE 4C

IFN- $\gamma$  (pg/ml) upon co-culture with target cells

		COS/ A11/WT	COS/ A11/G12D	COS/ A11/G12V	Medium
TRAV12N-3*01	TRBV4*01	130	<b>&gt;10000</b>	126	18
	TRBV5*01	95	<u>106</u>	83	22
	TRBV16*01 (LN)	97	91	98	18
	TRBV16*01 (SP)	129	114	84	23
TRAV16D/DV11*03	TRBV4*01	95	<b>302</b>	89	18
	TRBV5*01	94	92	98	18
	TRBV16*01 (LN)	99	106	114	24
	TRBV16*01 (SP)	176	143	138	26

## Example 3

[0111] This example demonstrates that PBL co-transduced with a TCR  $\alpha$  chain comprising SEQ ID NO: 11 and a TCR  $\beta$  chain comprising SEQ ID NO: 12 are reactive against HLA-A11+/G12D+ pancreatic tumor cell line FA6-2/A11.

[0112] Human PBL were co-transduced with a TCR  $\alpha$  chain comprising SEQ ID NO: 11 and a TCR  $\beta$  chain comprising SEQ ID NO: 12. Co-transduced cells were co-cultured with (i) COS7 cells transfected with (a) HLA-A11 alone (COS7/A11) or HLA-A11 transduced with a (b) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS7/A11/KRAS WT), (c) KRAS G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS7/A11/KRAS G12D), (d) KRAS G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS7/A11/KRAS G12V); (ii) pancreatic tumor cell

lines Mia-Paca2/A11, T3m4/A11, AsPC-1, FA6-2/A11, MDA-Panc-48/A11, PANC-1, PK-45p/A11, SK.PC.3/A11, x135 ml/A11, or (iii) medium alone. IFN- $\gamma$  secretion was measured. The results are shown in Table 5. The KRAS mutations of the tumor cell lines are indicated in parentheses. As shown in Table 5, PBL co-transduced with a TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against HLA-A11+/G12D+ pancreatic tumor cell line FA6-2/A11.

TABLE 5

Target Cell	IFN- $\gamma$ (pg/mL)
COS7/A11	146
COS7/A11/KRAS WT	116
COS7/A11/KRAS (G12D)	18231
COS7/A11/KRAS (G12V)	111
Mia-Paca2/A11 (G12C)*	53
T3m4/A11 (Q61H)*	178
SK.PC.3/A11 (G12V)**	53
x135m1/A11 (G12V)**	105
AsPC-1 (G12D)**	18
FA6-2/A11 (G12D)**	3982
MDA-Panc-48/A11 (G12D)**	56
PANC-1 (A11+, G12D)**	28
PK.45p/A11 (G12D)**	231
Medium (no cells)	26

\*Mutation determined by genotyping.

\*\*Mutation determined by enotypin and mRNA expression (see Tables 13 and 20).

#### Example 4

[0113] This example demonstrates that PBL that were transduced with a retroviral vector encoding a TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against COS7/A11 cells pulsed with KRAS G12D 10-mer peptide (SEQ ID NO: 2).

[0114] Human PBL were transduced with a retroviral vector encoding the TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12). Transduced PBL were co-cultured with COS7/A11 cells that were pulsed with KRAS G12D 10-mer peptide (SEQ ID NO: 2), KRAS G12D 9-mer peptide (SEQ ID NO: 34), KRAS G12D 9-mer peptide SEQ ID NO: 124, KRAS G12V 10-mer peptide (SEQ ID NO: 33), or WT KRAS 10-mer peptide (SEQ ID NO: 30) at various concentrations shown in Table 6. IFN- $\gamma$  secretion was measured. The results are shown in Table 6. As shown in Table 6, human PBL transduced to express a TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against COS7/A11 cells pulsed with KRAS G12D 10-mer peptide (SEQ ID NO: 2).

TABLE 6

Target Cell	IFN- $\gamma$ (pg/mL)
G12D KRAS <sub>7-15</sub> 9-mer	16918
G12V KRAS <sub>8-16</sub> 9-mer	87
WT KRAS 10-mer	97
(VVGADGVG) SEQ ID NO: 124	136
(VVVGADGVGK) SEQ ID NO: 34	78
1 x 10 <sup>-6</sup>	8677
1 x 10 <sup>-7</sup>	91
	83
	95
	88

TABLE 6 -continued

Peptide concentration (M)	IFN- $\gamma$ (pg/mL)				
	G12D KRAS <sub>7-15</sub>		G12D KRAS <sub>8-16</sub>		WT
	G12D mer	9-mer SEQ ID NO: 124	G12V mer	9-mer SEQ ID NO: 34	
1 x 10 <sup>-8</sup>	4220	72	86	99	102
1 x 10 <sup>-9</sup>	775	90	88	90	99
1 x 10 <sup>-10</sup>	115	90	88	85	95
1 x 10 <sup>-11</sup>	98	95	86	85	86
1 x 10 <sup>-12</sup>	111	83	96	94	102
1 x 10 <sup>-13</sup>	80	112	97	115	98

#### Example 5

[0115] This example demonstrates that PBL that were transduced with a retroviral vector encoding a TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against HLA-A11-expressing pancreatic tumor line FA6-2/A11.

[0116] Human PBL were transduced with a retroviral vector encoding the TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12). Untransduced control PBL or transduced PBL were co-cultured with the target cells set forth in Table 7. IFN- $\gamma$  secretion was measured. The results are shown in Table 7. The KRAS mutations of the tumor cell lines are indicated in parentheses. As shown in Table 7, human PBL transduced to express a TCR  $\alpha$  chain TRAV12N-3\*01 (SEQ ID NO: 11) and TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 12) demonstrated reactivity against FA6-2/A11 tumor cell line. Untransduced PBL secreted less than 100 pg/mL IFN- $\gamma$  upon co-culture with each target cell set forth in Table 7.

TABLE 7

Target Cell	IFN- $\gamma$ (pg/mL)
COS7/A11	90
COS7/A11/KRAS WT	71
COS7/A11/KRAS (G12D)	15496
COS7/A11/KRAS (G12V)	58
Barr (A11+, G12R)*	21
BxPC3/A11 (WT)*	18
Mia-Paca2/A11 (G12C)*	57
Paca44/A11 (G12V)**	30
T3m4/A11 (Q61H)*	28
AsPC-1/A11 (G12D)**	60
FA6-2/A11 (G12D)**	753
MDA-Panc-48/A11 (G12D)**	23
PANC-1 (A11+, G12D)**	23
PK.45p/A11 (G12D)**	28
Medium (no cells)	38

\*Mutation (or lack thereof (i.e., "WT")) determined by genotyping.

\*\*Mutation determined by genotyping and mRNA expression (see Tables 13 and 20).

#### Example 6

[0117] This example demonstrates the isolation of murine anti-KRAS7-16 G12V 10-mer TCRs.

[0118] HLA-A11 transgenic mice were immunized with the G12V 10-mer peptide (SEQ ID NO: 33) twice. After the second immunization, the spleen and lymph nodes were removed and cultured in vitro with the G12V 10-mer peptide at various concentrations (1  $\mu$ M, 0.1  $\mu$ M, and 0.01  $\mu$ M) for

seven days. T cells isolated from the lymph node and spleen cultures were tested for reactivity against (i) COS7/A11 cells transfected with a vector encoding (a) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COSA11/G12V); (b) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COSA11/WT); (c) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COSA11/G12D); (ii) HLA-A11-expressing KRAS G12V+ pancreatic tumor cell lines Paca44/A11, SKPC3/A11, or x135 m1/A11; or (iii) no target cells (medium) (Table 8). The results are shown in Table 8. In Table 8, underlined IFN- $\gamma$  secretion values indicate those cells that demonstrated reactivity against transfectants and tumors.

TABLE 8

	mIFN- $\gamma$ (pg/ml)					
	Spleen (1 $\mu$ M)	Spleen (0.1 $\mu$ M)	Spleen (0.01 $\mu$ M)	LN (1 $\mu$ M)	LN (0.1 $\mu$ M)	LN (0.01 $\mu$ M)
Cos7/ A11/WT	34	32	32	38	46	37
Cos7/A11/ G12D	61	32	32	41	41	38
Cos7/A11/ G12V	>20000	12113	58	1685	3126	4765
Paca44/A11	32	32	36	39	44	39
SKPC3/A11	8235	385	41	106	169	164
x135m1/A11	32	36	49	42	40	41
Medium	32	32	50	46	35	42

[0119] Oligoclonal TCRs were isolated from the cells that demonstrated highly specific G12V peptide and transfectant reactivity using 5' RACE. Two dominant alpha chains and three dominant beta chains were identified (Table 9).

TABLE 9

V Region	D/J Region	CDR3	SEQ ID NO:	Frequency
Alpha chains	TRAV19*01	53*01	CAAGDSGGSNYKLTF	139
	TRAV3-3*01	17*01	CAVSGGTNSAGNKLTF	204
Beta chains	TRBV13-1*02 (CB2)	2*01/2-1*01	CASASWGGYAEQFF	205
	TRBV4*01 (CB2)	2*01/2-1*01	CASSRDWGPAEQFF	130
	TRBV1*01 (CB2)	1*01/2-3*01	CTCSADRGAAETLYF	206

## Example 7

[0120] This example demonstrates that PBL transduced to express (i) a TCR  $\alpha$  chain comprising SEQ ID NO: 133 and a TCR  $\beta$  chain comprising SEQ ID NO: 134 or (ii) a TCR  $\alpha$  chain comprising SEQ ID NO: 145 and a TCR  $\beta$  chain comprising SEQ ID NO: 146 are reactive against HLA-A11+/G12V 10-mer+ targets.

[0121] The two dominant  $\alpha$  chains and three dominant  $\beta$  chains of Table 9 were individually cloned into MSGV1 retroviral vectors. Anti-CD3 stimulated PBL were individually co-transduced to express one of various pairs of an  $\alpha$  and  $\beta$  chain, as shown in Tables 10A-10B. Transduced PBL were screened for reactivity against (i) COS7/A11+ cells pulsed with (a) G12D 10-mer peptide (SEQ ID NO: 2), (b) G12V 10-mer peptide (SEQ ID NO: 33), or (c) WT KRAS 10-mer peptide (SEQ ID NO: 30) (Table 10A) or (ii) COS7/A11 cells transduced with a (a) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V), or (c) WT KRAS minigene (encoding 23-mer

SEQ ID NO: 118) (COS/A11/WT) (Table 10B). Untransfected Cos7/A11 cells that were not pulsed with peptide (Cos7/A11) and medium with no cells (medium) served as negative controls. PBL pulsed or transduced with GFP served as a positive control. IFN- $\gamma$  secretion was measured.

[0122] The results are shown in Tables 10A-10B. In Tables 10A-10B, bold IFN- $\gamma$  secretion values indicate those pairs of TCR  $\alpha$  and  $\beta$  chains that demonstrated reactivity. As shown in Tables 10A-10B, PBL co-transduced to express (i) both murine TCR  $\alpha$  chain TRAV19\*01 (SEQ ID NO: 145) and murine TCR  $\beta$  chain TRBV13-1\*02 (SEQ ID NO: 146) or (ii) both murine TCR  $\alpha$  chain TRAV3-3\*01 (SEQ ID NO: 133) and murine TCR  $\beta$  chain TRBV4\*01 (SEQ ID NO: 134) demonstrated reactivity against HLA-A11-expressing COS7 cells pulsed with G12V 10-mer or G12V transfectant target cells, but not control peptides or control transfectants.

TABLE 10A

	(IFN- $\gamma$ (pg/ml))				
	Cos7/ A11	Cos7/A11 + WT 10-mer	Cos7/A11 + G12D 10-mer	Cos7/A11 + G12V 10-mer	Me- dium
GFP	66	50	60	54	17
TRAV19*01 +	105	90	94	<b>14138</b>	29
TRBV13-1*02					
TRAV19*01 +	30	30	30	27	16
TRBV4*01					
TRAV19*01 +	69	37	38	37	16
TRBV1*01					
TRAV3-3*01 +	68	47	49	44	23
TRBV13-1*02					
TRAV3-3*01 +	42	36	39	<b>8374</b>	16
TRBV4*01					

TABLE 10A-continued

	(IFN- $\gamma$ (pg/ml))				
	Cos7/ A11	Cos7/A11 + WT 10-mer	Cos7/A11 + G12D 10-mer	Cos7/A11 + G12V 10-mer	Me- dium
TRAV3-3*01 +	53	41	39	51	16
TRBV1*01					

TABLE 10B

	(IFN- $\gamma$ (pg/ml))				
	Cos7/ A11	Cos7/A11 / WT	Cos7/A11 / G12D	Cos7/A11 / G12V	Me- dium
GFP	66	72	60	55	17
TRAV19*01 +	105	92	81	<b>18058</b>	29
TRBV13-1*02					

TABLE 10B-continued

	(IFN- $\gamma$ (pg/ml))				
	Cos7/ A11	Cos7/A11/ WT	Cos7/A11/ G12D	Cos7/A11/ G12V	Me- dium
TRAV19*01 +	30	32	27	30	16
TRBV4*01					
TRAV19*01 +	69	45	45	44	16
TRBV1*01					
TRAV3-3*01 +	68	51	56	61	23
TRBV13-1*02					
TRAV3-3*01 +	42	41	38	<b>11113</b>	16
TRBV4*01					
TRAV3-3*01 +	53	44	47	45	16
TRBV1*01					

## Example 8

[0123] This example demonstrates that the TRAV3-3\*01/ TRBV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) has a higher affinity for pulsed target peptide as compared to TRAV19\*01/TRBV13-1\*02 murine anti-KRAS G12V TCR (SEQ ID NOS: 145 and 146).

[0124] PBL were transduced with either (i) TRAV3-3\*01/ TRBV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) or (ii) TRAV19\*01/TRBV13-1\*02 murine anti-KRAS G12V TCR (SEQ ID NOS: 145 and 146). Transduced cells were co-cultured with Cos7/A11 cells pulsed with (a) G12D 10-mer peptide (SEQ ID NO: 2), (b) G12V 10-mer peptide (SEQ ID NO: 33), (c) WT KRAS 10-mer peptide (SEQ ID NO: 30), (d) G12D 9-mer peptide (SEQ ID NO: 34), or (e) G12V 9-mer peptide (SEQ ID NO: 35) at the concentrations shown in Tables 11A and 11B. IFN- $\gamma$  secretion was measured.

[0125] The results are shown in Table 11A (TRAV3-3\*01/ TRBV4\*01 (SEQ ID NOS: 133 and 134)) and Table 11B (TRAV19\*01/TRBV13-1\*02 (SEQ ID NOS: 145 and 146)). In Tables 11A-11B, bold IFN- $\gamma$  secretion values indicate those target peptide concentrations at which the TCR demonstrated reactivity. As shown in Tables 11A-11B, T cells transduced with the TRAV3-3\*01/TRBV4\*01 TCR (SEQ ID NOS: 133 and 134) recognized Cos7/All pulsed with both 9-mer and 10-mer peptides and recognized 9-mer at pulsed at a concentration of 0.01 nM. Accordingly, the TRAV3-3\*01/TRBV4\*01 TCR (SEQ ID NOS: 133 and 134) recognized pulsed target peptide with a higher avidity as compared to the TRAV19\*01/TRBV13-1\*02 (SEQ ID NOS: 145 and 146) TCR. The increased reactivity of the TRAV3-3\*01/ TRBV4\*01 (SEQ ID NOS: 145 and 146) TCR against the G12V 9-mer peptide as compared to the 10-mer peptide also suggested that 9-mer peptide is the minimal determinant.

TABLE 11A

Peptide	IFN- $\gamma$ (pg/ml)				
concentration (10 <sup>-8</sup> $\mu$ M)	WT 10-mer	G12D 9-mer	G12D 10-mer	G12V 9-mer	G12V 10-mer
-6	50	47	43	<b>19479</b>	<b>9778</b>
-7	42	48	40	<b>19900</b>	<b>6696</b>
-8	50	49	46	<b>19193</b>	<b>657</b>
-9	50	44	41	<b>9578</b>	<b>104</b>
-10	48	52	53	<b>1877</b>	59

TABLE 11A-continued

Peptide	IFN- $\gamma$ (pg/ml)					
	concentration (10 <sup>-8</sup> $\mu$ M)	WT 10-mer	G12D 9-mer	G12D 10-mer	G12V 9-mer	G12V 10-mer
-11		55	49	43	119	52
-12		47	55	49	56	52
-13		68	52	49	60	52

TABLE 11B

Peptide	IFN- $\gamma$ (pg/ml)					
	concentration (10 <sup>-8</sup> $\mu$ M)	WT 10-mer	G12D 9-mer	G12D 10-mer	G12V 9-mer	G12V 10-mer
-6		57	63	61	112	<b>15184</b>
-7		56	57	50	70	<b>7725</b>
-8		57	48	49	52	<b>2084</b>
-9		49	54	59	55	<b>326</b>
-10		57	62	52	64	61
-11		65	52	64	62	67
-12		67	57	62	66	61
-13		70	70	63	64	71

## Example 9

[0126] This example demonstrates that the TRAV3-3\*01/ TRBV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) recognizes HLA-A11+KRAS G12V+ pancreatic tumor cell lines.

[0127] PBL were transduced with either (i) TRAV3-3\*01/ TRBV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) or (ii) TRAV19\*01/TRBV13-1\*02 murine anti-KRAS G12V TCR (SEQ ID NOS: 145 and 146). Transduced cells were co-cultured with (i) COS7/A11 cells transduced with a (a) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V), or (c) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT); (ii) KRAS G12V negative pancreatic tumor cell lines transduced with HLA-A11; (iii) KRAS G12V+ pancreatic tumor cell lines transduced with HLA-A11; or (iv) parental (untransduced) pancreatic tumor cell lines, as shown in Table 12. IFN- $\gamma$  secretion was measured.

[0128] The results are shown in Table 12. In Table 12, bold IFN- $\gamma$  secretion values indicate those target cells for which the TCR demonstrated reactivity. As shown in Table 12, the TRAV3-3\*01/TRBV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) recognized more HLA-A11+ KRAS G12V+ pancreatic tumor cell lines as compared to the TRAV19\*01/TRBV13-1\*02 murine anti-KRAS G12V TCR (SEQ ID NOS: 145 and 146).

TABLE 12

	IFN- $\gamma$ (pg/ml)	
	TRAV3-3*01/ TRBV4*01	TRAV19*01/ TRBV13-1*02
Transfectants		
Cos/A11	51	55
Cos/A11/G12D	53	44
Cos/A11/WT	52	51
Cos/A11/G12V	<b>24290</b>	<b>11794</b>

TABLE 12-continued

		IFN-γ (pg/ml)	
		TRAV3-3*01/ TRBV4*01	TRAV19*01/ TRBV13-1*02
HLA-A11 transduced, KRAS G12V-	BxPC3/A11 (WT)*	25	32
	MiaPaca2/A11 (G12C)*	16	16
	T3m4/A11 (Q61H)*	26	33
	AsPC-1/A11 (G12D)**	22	26
	FA6-2/A11 (G12D)**	18	18
	MDA-Panc-48/A11 (G12D)**	16	16
	PK.45p/A11 (G12D)**	31	29
	Capan-1/A11 (G12V)**	99	28
	CFPAC-1/A11 (G12V)**	<b>224</b>	28
	Paca44/A11 (G12V)**	<b>577</b>	21
HLA-A11 transduced, KRAS G12V+	SK.PC3/A11 (G12V)**	<b>7947</b>	<b>2658</b>
	x135m1/A11 (G12V)**	<b>1020</b>	90
	BxPC3 (WT)*	16	16
	MiaPaca2 (G12C)*	18	16
	T3m4 (Q61H)*	19	18
	AsPC-1 (G12D)**	16	16
	FA6-2 (G12D)**	23	19
	MDA-Panc-48 (G12D)**	19	21
	PK.45p (G12D)**	16	16
	Capan-1 (G12V)**	22	20
Parental tumor lines	CFPAC-1 (G12V)**	16	16
	Paca44 (G12V)**	16	16
	SK.PC3 (G12V)**	28	19
	x135m1 (G12V)**	27	20
	PANC-1 (HLA-A11+, G12D)**	16	17
	Barr (HLA-A11+, G12R)*	17	22
	Medium	18	16

\*Mutation (or lack thereof, i.e., "WT") determined by genotyping.

\*\*Mutation determined by genotyping and mRNA expression (see Tables 13 and 20).

## Example 10

**[0129]** This example demonstrates the correlation between IFN-γ production and mutated KRAS expression for the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134).

**[0130]** The number of copies of KRAS G12V mRNA expressed by each of the pancreatic tumor cell lines shown in Table 13 was measured and compared to the number of copies of β-actin mRNA expressed by the indicated cell line (Table 13). The amount of IFN-γ secreted by the PBL transduced with the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) upon co-culture with each cell line measured in Example 9 is reproduced in Table 13. The reactivity of the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) (in terms of IFN-γ secretion upon co-culture with target cells) correlated with the number of copies of KRAS G12V mRNA.

TABLE 13

	β-actin (Copy number)	Ref Total KRAS (Copy per 10 <sup>6</sup> β-actin)	G12V (Copy per 10 <sup>6</sup> β-actin)	IFN-γ (pg/ml)
BxPC3/A11	$3.13 \times 10^7$	$6.84 \times 10^3$	2.51	25
MiaPaca2/A11	$2.01 \times 10^7$	$5.87 \times 10^3$	$1.06 \times 10^{-1}$	16
Capan-1/A11	$2.28 \times 10^7$	$5.92 \times 10^3$	$5.42 \times 10^3$	99
CFPAC-1/A11	$1.96 \times 10^7$	$2.09 \times 10^4$	$3.72 \times 10^3$	<b>224</b>
Paca44/A11	$1.80 \times 10^7$	$4.94 \times 10^3$	$3.62 \times 10^3$	<b>577</b>
SK.PC3/A11	$3.28 \times 10^7$	$1.48 \times 10^4$	$1.42 \times 10^4$	<b>7947</b>
x135m1/A11	$8.50 \times 10^6$	$8.75 \times 10^3$	$9.85 \times 10^3$	<b>1020</b>

## Example 11

**[0131]** This example demonstrates that the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) recognizes mutated KRAS either (i) in the presence of CD4 and the absence of CD8 or (ii) in the presence of CD8 and the absence of CD4.

**[0132]** PBL were transduced with a nucleotide sequence encoding the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134). Transduced cells were sorted into the populations shown in Table 14 by flow cytometry. The sorted populations of cells were co-cultured with (i) COS7/All cells transduced with a (a) G12D minigene (encoding 163-mer) (COS/A11/G12D), (b) G12V minigene (encoding 163-mer) (COS/A11/G12V), or (c) WT KRAS minigene (encoding 163-mer) (COS/A11/WT); or (ii) SK.PC3 pancreatic tumor cell line untransduced or transduced with HLA-A11. Medium without cells served as a negative control. IFN-γ secretion was measured.

**[0133]** The results are shown in Table 14. In Table 14, bold IFN-γ secretion values indicate those target cells for which the TCR demonstrated reactivity. As shown in Table 14, the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) recognized target cells either (i) in the presence of CD4 and the absence of CD8 or (ii) in the presence of CD8 and the absence of CD4. Accordingly, the TRAV3-3\*01/BV4\*01 murine anti-KRAS G12V TCR (SEQ ID NOS: 133 and 134) provides highly avid recognition of the target.

TABLE 14

PBL transduced with	IFN-γ (pg/ml)					
TRAV3-3*01/BV4*01	Cos7/A11/WT	Cos7/A11/G12D	Cos7/A11/G12V	SK.PC3	SK.PC3/A11	Medium
Bulk	48	67	<b>8294</b>	41	<b>8944</b>	16
CD8 enriched	49	64	<b>8150</b>	75	<b>8602</b>	16
CD4 enriched	16	16	<b>763</b>	16	<b>458</b>	16
GFP	16	17	16	20	16	16

## Example 12

[0134] This example demonstrates the isolation of murine anti-KRAS7-16 G12D 10-mer TCRs.

[0135] HLA-A11 transgenic mice were immunized with the G12D 10-mer peptide (SEQ ID NO: 2) three times. After the third immunization, the spleen and lymph nodes were removed and cultured in vitro with the G12D 10-mer peptide at various concentrations (1 μM, 0.1 μM, and 0.01 μM) for seven days. T cells isolated from the LN and spleen cultures were tested for reactivity against (i) COS7 cells transduced to express HLA-A11 (COS7/A11) which had been pulsed with (a) no peptide (none), (b) WT KRAS7-16 peptide (SEQ ID NO: 30) (COS/A11+WT peptide), (c) G12D 10-mer peptide (SEQ ID NO: 2) (COS/A11+G12D peptide), (d) G12V 10-mer peptide (SEQ ID NO: 33) (COS/A11+G12V peptide), (e) G12V 9-mer peptide (SEQ ID NO: 35), or (f) G12D 9-mer peptide (SEQ ID NO: 34); and (ii) COS7/A11 cells transfected with a vector encoding a (a) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT), (b) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), or (c) (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V). Interferon (IFN)-γ was measured.

[0136] The results are shown in Table 15A (peptide pulse) and Table 15B (transfectants). In Tables 15A and 15B, bold IFN-γ secretion values indicate those target peptides and target cells for which the TCR demonstrated reactivity. As shown in Tables 15A and 15B, HLA-A11 restricted murine T cells were reactive against KRAS G12D peptide SEQ ID NO: 2.

TABLE 15A

	Stimulated with G12D10-mer	Cos7/A11 pulsed (IFN-γ (pg/ml))					
		WT 10-mer	G12D 9-mer	G12D 10-mer	G12V 9-mer	G12V 10-mer	
Spleen	1 μM	55	49	121	>20000	54	64
	0.1 μM	65	59	120	<b>19521</b>	65	64
	0.01 μM	82	61	87	<b>1060</b>	66	66
LN	1 μM	57	98	807	>20000	68	95
	0.1 μM	80	86	375	>20000	108	89
	0.01 μM	349	339	435	>20000	296	325

TABLE 15B

	(IFN-γ (pg/ml))		
	Cos7/A11/WT	Cos7/A11/G12D	Cos7/A11/G12V
Spleen	50	>20000	49
	53	>20000	59
	80	<b>847</b>	81
LN	71	>20000	75
	235	>20000	102
	440	>20000	328

[0137] T cells isolated from the LN and spleen cultures were also stimulated in vitro with various concentrations of G12D peptides for 6-7 days and were then co-cultured with the HLA-A11-expressing, KRAS G12D+ pancreatic cell lines shown in Table 16. IFN-γ was measured.

[0138] The results are shown in Table 16. In Table 16, bold IFN-γ secretion values indicate those target cells for which the TCR demonstrated reactivity. As shown in Table 16, T cells isolated from the LN and spleen cultures were reactive with HLA-A11-expressing, KRAS G12D+ pancreatic cell lines.

TABLE 16

	stimulated with G12D10-mer	IFN-γ (pg/ml)					
		Medium	FA6-2/A11	MDA-Panc48/A11	Panc-1	PK.45p/A11	
Spleen	1 μM	47	<b>2134</b>	<b>1322</b>	48	46	
	0.1 μM	46	<b>1588</b>	<b>665</b>	54	54	
	0.01 μM	59	116	<b>443</b>	54	59	
LN	1 μM	55	<b>4614</b>	<b>202</b>	61	57	
	0.1 μM	121	<b>4512</b>	<b>211</b>	68	74	
	0.01 μM	279	<b>3019</b>	<b>559</b>	96	249	

[0139] The TCR was isolated from the reactive cells using 5' RACE. Two dominant alpha chains and one dominant beta chain were identified (Table 17).

TABLE 17

	V Region	D/J Region	CDR3	SEQ ID NO:	Frequency
Alpha chains	TRAV4-4/DV10*01(1)	49*01	CAADSSNTGYQNFYF	151	30%
	TRAV4-4/DV10*01(2)	49*01	CAALNTGYQNFYF	161	10%
Beta chains	TRBV12-2*01	1*01/1-2*01	CASSLTDPLDSDYTF	154	18%

## Example 13

[0140] This example demonstrates that PBL transduced to express a TCR  $\alpha$  chain comprising SEQ ID NO: 157 and a TCR  $\beta$  chain comprising SEQ ID NO: 158 are reactive against HLA-A11+/G12D 10-mer+ targets.

[0141] The two dominant  $\alpha$  chains and the  $\beta$  chains of Table 17 were individually cloned into MSGV1 retroviral vectors. PBL were individually co-transduced to express one of the two pairs of the  $\alpha$  and  $\beta$  chain, as shown in Table 18. Transduced PBL were screened for reactivity against (i) COS7/A11 cells transduced with a (a) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V), (c) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT), or (d) no cells (medium only) (Table 18). IFN- $\gamma$  secretion was measured.

[0142] The results are shown in Table 18. As shown in Table 18, PBL co-transduced to express murine TCR  $\alpha$  chain TRAV4-4\*01 (1) (SEQ ID NO: 157) and murine TCR  $\beta$  chain TRBV12-2\*01 (SEQ ID NO: 158) demonstrated reactivity against HLA-A11-expressing G12D transfectant target cells.

TABLE 18

	IFN- $\gamma$ (pg/ml)			
	Cos/A11/ WT	Cos/A11/ G12D	Cos/A11/ G12V	Medium
TRAV4-4*01(1)/ TRBV12-2*01	31	34440	32	32
TRAV4-4*01(2)/ TRBV12-2*01	48	79	36	40

[0143] PBL were transduced to express the TCR TRAV4-4\*01 (1)/TRBV12-2\*01 (SEQ ID NOS: 157 and 158) and screened for reactivity against COS7/A11 cells transduced with a (a) G12D minigene (encoding 23-mer SEQ ID NO: 119) (COS/A11/G12D), (b) G12V minigene (encoding 23-mer SEQ ID NO: 120) (COS/A11/G12V), (c) WT KRAS minigene (encoding 23-mer SEQ ID NO: 118) (COS/A11/WT), (d) the pancreatic tumor lines shown in Table 19 that were untransduced or transduced to express HLA-A11 and the indicated KRAS mutation. In Table 19, the KRAS mutation expressed by each pancreatic tumor cell line is indicated. IFN- $\gamma$  secretion was measured.

[0144] The results are shown in Table 19. As shown in Table 19, PBL transduced with the TCR TRAV4-4\*01 (1)/TRBV12-2\*01 (SEQ ID NOS: 157 and 158) recognized HLA-A11+/G12D+ pancreatic tumor lines.

TABLE 19

	IFN- $\gamma$ (pg/ml) TRAV4-4/DV*01/TRBV12-2*01
Cos/A11/WT	96
Cos/A11/G12D	45214
Cos/A11/G12V	99
BxPC3/A11 (WT)*	22
MiaPaca2/A11 (G12C)*	16
SK.PC.3/A11 (G12V)**	22
T3m4/A11 (Q61H)*	42
Barr (A11+, G12R)*	17

TABLE 19-continued

	IFN- $\gamma$ (pg/ml) TRAV4-4/DV*01/TRBV12-2*01
AsPC-1/A11 (G12D)**	7321
FA6-2/A11 (G12D)**	11287
MDA-Panc-48/A11 (G12D)**	238
PANC-1 (A11+, G12D)**	114
PK.45p/A11 (G12D)**	70
BxPC3	16
MiaPaca2	16
SK.PC.3	17
T3m4	38
AsPC-1	16
FA6-2	16
MDA-Panc-48	16
PK.45p	16
Medium	16

\*Mutation (or lack thereof, i.e., "WT") determined by genotyping.

\*\*Mutation determined by genotyping and mRNA expression (see Tables 13 and 20).

## Example 14

[0145] This example demonstrates the correlation between IFN- $\gamma$  production and mutated KRAS expression for the TRAV4-4\*01 (1)/TRBV12-2\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158).

[0146] The number of copies of KRAS G12D mRNA expressed by each of the pancreatic tumor cell lines shown in Table 20 was measured and compared to the number of copies of  $\beta$ -actin mRNA expressed by each cell line (Table 20). The amount of IFN- $\gamma$  secreted by the PBL transduced with the TRAV4-4\*01 (1)/TRBV12-2\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) upon co-culture with each cell line is shown in Table 13. The reactivity of the TRAV4-4\*01 (1)/TRBV12-2\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) (in terms of IFN- $\gamma$  secretion upon co-culture with target cells) was correlated with the number of copies of KRAS G12D mRNA.

TABLE 20

	$\beta$ -actin (Copy number)	Ref Total KRAS (Copy per $10^6$ $\beta$ -actin)	G12D (Copy per $10^6$ $\beta$ -actin)	IFN- $\gamma$ (pg/ml)
BxPC3/A11	$3.13 \times 10^7$	$6.22 \times 10^3$	$2.91 \times 10^1$	26
Barr	$1.88 \times 10^7$	$7.98 \times 10^3$	$2.41 \times 10^{-1}$	43
T3m4/A11	$3.40 \times 10^7$	$1.56 \times 10^4$	$5.26 \times 10^{-1}$	49
ASPC-1/A11	$2.69 \times 10^7$	$1.40 \times 10^4$	$5.99 \times 10^3$	<b>7320</b>
FA6-2/A11	$3.01 \times 10^7$	$1.1 \times 10^5$	$3.99 \times 10^4$	<b>31688</b>
MDA-Panc- 48/A11	$4.56 \times 10^7$	$4.01 \times 10^3$	$1.90 \times 10^3$	<b>433</b>
PANC-1	$3.48 \times 10^7$	$1.39 \times 10^4$	$4.28 \times 10^3$	17
PK.45p/A11	$4.04 \times 10^7$	$1.66 \times 10^4$	$2.80 \times 10^2$	52

## Example 15

[0147] This example demonstrates that the TRAV4-4/DV10\*01/BV12-2\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) has a higher affinity for pulsed target peptide as compared to the TRAV12N-3\*01/BV4\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 11 and 12).

[0148] PBL were transduced with either (i) T TRAV4-4/DV10\*01/BV12-2\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) or (ii) TRAV12N-3\*01/BV4\*01

murine anti-KRAS G12D TCR (SEQ ID NOS: 11 and 12). Transduced cells were co-cultured with Cos7/All cells pulsed with (a) G12D 10-mer peptide (SEQ ID NO: 2), (b) WT KRAS 10-mer peptide (SEQ ID NO: 30), (c) G12D 9-mer peptide (SEQ ID NO: 34), or (d) WT KRAS 9-mer peptide (SEQ ID NO: 31) at the concentrations shown in Tables 21A and 21B. IFN- $\gamma$  secretion was measured.

[0149] The results are shown in Table 21A (TRAV4-4/DV10\*01/BV12-2\*0 (SEQ ID NOS: 157 and 158)) and Table 21B (TRAV12N-3\*01/BV4\*01 (SEQ ID NOS: 11 and 12)). As shown in Tables 21A-21B, T cells transduced with the TRAV4-4/DV10\*01/BV12-2\*0 (SEQ ID NOS: 157 and 158) recognized 10-mer at pulsed at a concentration of  $1 \times 10^{-9}$  M. Accordingly, the TRAV4-4/DV10\*01/BV12-2\*0 (SEQ ID NOS: 157 and 158) recognized pulsed target peptide with a higher avidity as compared to the TRAV12N-3\*01/BV4\*01 (SEQ ID NOS: 11 and 12) TCR.

TABLE 21A

Peptide	IFN- $\gamma$ (pg/ml)				
	concentration ( $10^{-9}$ M)	WT 9-mer	WT 10-mer	G12D 9-mer	G12D 10-mer
-6	54	56	131	27407	
-7	53	57	60	29508	
-8	59	51	47	6131	
-9	54	51	53	2075	
-10	51	54	53	402	
-11	48	50	52	63	
-12	52	44	58	50	
-13	51	54	51	51	

TABLE 21B

Peptide	IFN- $\gamma$ (pg/ml)				
	concentration ( $10^{-9}$ M)	WT 9-mer	WT 10-mer	G12D 9-mer	G12D 10-mer
-6	90	82	125	18948	
-7	96	77	86	11623	
-8	95	85	90	3852	
-9	88	102	92	108	
-10	95	88	95	212	
-11	84	81	88	103	
-12	105	76	91	93	
-13	103	92	84	93	

## Example 16

[0150] This example demonstrates that the TRAV4-4/DV10\*01/BV12-2\*0 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) has a higher affinity for G12D+ pancreatic tumor cell lines as compared to TRAV12N-3\*01/BV4\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 11 and 12).

[0151] PBL were transduced with either (i) TRAV4-4/DV10\*01/BV12-2\*0 murine anti-KRAS G12D TCR (SEQ ID NOS: 157 and 158) or (ii) TRAV12N-3\*01/BV4\*01 murine anti-KRAS G12D TCR (SEQ ID NOS: 11 and 12). Transduced cells were co-cultured with pancreatic cell lines that were untransduced or transduced with HLA-A11 and mutated KRAS as shown in Table 22. IFN- $\gamma$  secretion was measured.

[0152] The results are shown in Table 22. As shown in Table 22, T cells transduced with the TRAV4-4/DV10\*01/

BV12-2\*0 (SEQ ID NOS: 157 and 158) recognized G12D+ pancreatic tumor cell lines with a higher avidity as compared to the TRAV12N-3\*01/BV4\*01 (SEQ ID NOS: 11 and 12) TCR.

TABLE 22

	IFN- $\gamma$ (pg/ml)	
	TRAV4-4/DV10*01/ BV12-2*01	TRAV12N-3*01/ BV4*01
BxPC3/A11 (WT)*	28	37
MiaPaca2/A11 (G12C)*	27	57
SK.PC.3/A11 (G12V)**	41	44
T3m4/A11 (Q61H)*	42	135
Barr (A11+, G12R)*	31	21
AsPC-1/A11 (G12D)**	7478	980
FA6-2/A11 (G12D)**	8027	1494
MDA-Panc-48/A11 (G12D)**	362	66
PANC-1 (A11+, G12D)**	148	34
PK.45p/A11 (G12D)**	52	113
AsPC-1	24	16
FA6-2	41	26
MDA-Panc-48	43	134
PK.45p	31	35
Medium	28	20

\*Mutation (or lack thereof, i.e., "WT") determined by genotyping.

\*\*Mutation determined by genotyping and mRNA expression (see Tables 13 and 20).

## Example 17

[0153] This example demonstrates a Phase I/II study administering PBL transduced with a vector encoding the murine TCR recognizing mutated KRAS to patients with mutated KRAS-expressing cancer.

[0154] To be eligible for inclusion in the study, patients meet the normal criteria for adoptive cell therapy (ACT)/IL-2 and have the following:

[0155] an HLA-A11+, mutated KRAS-expressing tumor (as measured by immunohistochemistry);

[0156] radioiodine-refractory cancer; and

[0157] a positron emission tomography (PET) avid tumor or demonstrate tumor progression within the last 6 months.

[0158] Autologous PBL are retrovirally transduced with a vector encoding the alpha and beta chains of the murine anti-mutated KRAS TCR (SEQ ID NOS: 11 and 12). The patient is treated with preparative, non-myeloablative, high-dose cyclophosphamide (Cy) and fludarabine (Flu). The patient is treated with high-dose, IL-2 every eight hours until tolerance. In Phase I, the patient is treated with a starting dose of  $1 \times 10^8$  retrovirally transduced cells. The dose is increased by half-logs, with one patient per cohort up to a dose of  $1 \times 10^{10}$  cells, followed by three patients per cohort. Phase II has a two-stage design with a targeted response rate of 20%.

## Example 18

[0159] This example demonstrates the frequency of KRAS mutations in human cancers.

[0160] The frequency (%) of KRAS mutations in various human cancers is set forth in Table 23. Table 23 also shows the frequency (%) of specific KRAS mutations among all KRAS mutations.

TABLE 23

Tumor	Frequency of KRAS mutation	% of all KRAS mutations						
		G12A	G12D	G12R	G12C	G12S	G12V	G13D
Pancreatic carcinoma	70%	2	51	12	3	2	30	1
Colorectal	36%	7	34	1	9	5	24	19
Lung adenocarcinoma	20%	7	17	2	42	5	20	2
Endometrial	18%	11	36	0	9	2	24	15
Epithelial ovarian cancer	14%	4	41	2	5	0	37	5
Prostate	7%	2	22	1	10	3	35	23

## Example 19

[0161] This example demonstrates that a substitution of the glycine residue in the CDR3 $\alpha$  region of the TRAV4-4/DV10\*01/BV12-2\*01 TCR provides enhanced anti-KRAS reactivity as compared to the wild-type TRAV4-4/DV10\*01/BV12-2\*01 TCR.

[0162] The glycine residue in the CDR3 $\alpha$  region of the TRAV4-4/DV10\*01/BV12-2\*01 TCR was replaced with an alanine residue to provide a substituted TRAV4-4/DV10\*01/BV12-2\*01 TCR (CDR3alpha G112A). PBL were transduced with either (i) wild-type TRAV4-4/DV10\*01/BV12-2\*01 TCR (SEQ ID NOS: 157 and 158) or (ii) substituted TRAV4-4/DV10\*01/BV12-2\*01 TCR (SEQ ID NOS: 209 and 158). Transduced cells were co-cultured with Cos cells transduced with HLA-A11 and WT KRAS (Cos/A11/WT), Cos cells transduced with HLA-A11 and G12D KRAS (Cos/A11/G12D), pancreatic tumor cell line FA6-2 transduced with HLA-A11 (FA6-2/A11), or pancreatic tumor cell line Panc-1. Transduced cells cultured alone (medium) served as control. IFN- $\gamma$  secretion (pg/ml) was measured. The results are shown in Table 24.

TABLE 24

WT TRAV4-4/ DV10*01/BV12-2*01 (SEQ ID NOS: 157 and 158)	Substituted TRAV4-4/ DV10*01/BV12-2*01 (CDR3alpha G112A) (SEQ ID NOS: 209 and 158)
Cos/A11/WT	51
Cos/A11/G12D	465
FA6-2/A11	2628
Panc-1	37
Medium	48

[0163] As shown in Table 24, a substitution of the glycine residue in the CDR3 $\alpha$  region of the TRAV4-4/DV10\*01/BV12-2\*01 TCR provided enhanced anti-KRAS reactivity as compared to the wild-type TRAV4-4/DV10\*01/BV12-2\*01 TCR.

[0164] All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

[0165] The use of the terms “a” and “an” and “the” and “at least one” and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The use of the term “at least one” followed by a list of one or more items (for example, “at least one of A and B”) is to be construed to mean one item selected from the listed items (A or B) or any combination of two or more of the listed items (A and B), unless otherwise indicated herein or clearly contradicted by context. The terms “comprising,” “having,” “including,” and “containing” are to be construed as open-ended terms (i.e., meaning “including, but not limited to,”) unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., “such as”) provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

[0166] Preferred embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Variations of those preferred embodiments may become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventors expect skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

## SEQUENCE LISTING

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tcagcgcagc tgcacatcc tgcctgtac tactgtgtc tgagggggaa tgcagggtgcc 360
aagctcacat tccggaggggg aacaagggtt acggcagac ccgacatcca gaaccggaaa 420
cctgctgtgt accaggtaaa agatctctcg ttcaggaca gcacccctcg cctgttcaacc 480
gactttgact cccaaatcaaat tggccggaaa accatggaaat ctggaaacgtt catactgac 540
aaaactgtgc tggacatggaa agtcatggaa tccaagagca atggggccat tgcctggagc 600
aaccagacaa gtttccatcg ccaagatata ttcaagagca ccaacgcac ctaccccaatg 660
tcagacgttc cctgtgtatgc cacgttact gagaaaaagct ttgaaacaga tatgaaccta 720
aactttcaaa acctgtcactg tttggggactt cgaatccctcc tgctgaaatg agccggattt 780
aacctgtctca tgacgctgag gctgtgtcc agttga
SEQ ID NO: 18      moltype = DNA length = 921
FEATURE          Location/Qualifiers
misc_feature     1..921
                  note = Synthetic
source           1..921
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 18
atggggctgta ggctcctaag ctgtgtggcc ttctgcctct tggaaatagg ccctttggag 60
acggctgttt tccagactcc aaactatcat gtcacacagg tggaaatga agtgtcttc 120
aattgtaaagc aaactctggg ccacgatact atgtatttggt acaagcaaga ctctaagaaa 180
ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagtctca 240
aggcgcttcc cacctcagtc ttcaaaaaa gtcatttga atcttcgaat caagtctgta 300
gagccggagg actctgtgt gtatctgtt gccagcagct cccggactg gagtgcagaa 360
acgctgtatt ttggctcagg aaccagactg actgttctcg aggatctgag aaatgtgact 420
ccacccaaagg ttccttctt tgagccatca aaacggagca atggggccat tgcctggagc 480
accctctgtt gttggccag gggtttcc cctgaccacg tggagctgag ctgggggttg 540
aatggcaagg aggtccacag tgggttcagc acggacccctc aggctacaaa ggagagcaat 600
tatagctact gcttgcacag ccgcgttccat cttctgtcc caatcttcga 660
aaccacttcc gtcgtcaatg cagttccat gggcttccat aggaggacaa gtggccagag 720
ggctcaccca aacatgtcac acagaacatc agtgcagagg cctggggccg agcagactgt 780
ggaatcaactt cagcatccat tcatcagggg gttctgttgc caaccatctt ctatgagatc 840
ctactggggaa aggccacccctt atatgtgtt ctggctcagg gcttgggtgt gatggccatg 900
gtcaagaaaaaaa atttcctca
SEQ ID NO: 19      moltype = DNA length = 413
FEATURE          Location/Qualifiers
misc_feature     1..413
                  note = Synthetic
source           1..413
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 19
acatccagaaa cccagaaccc tgcgtgttacc agttaaaaga tcctcggtct caggacagca 60
ccctctgtctt gtttccatcg ttttgcactccaa atatcaatgt gccgaaatccc atggaaatctg 120
gaacgttcat cactgacaaa actgtgttccat gatgaaatccat ttttgcactccaa aagagcaatg 180
ggccatccatc ctggggccac cagacaagct tcacacttccaa agatatcttc aaagagacca 240
acgcccacccat ccccaatgttca gacgttccat gtttgcactccaa gtttgcactccaa aagagcaatg 300
aaacacatgat gacatccatc ttccaaatccat gggactccat atcccttc

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tggaaatgtgc cggatttaac ctgctcatga cgctgaggct gtggtccagt tga          413
SEQ ID NO: 20      moltype = DNA  length = 521
FEATURE           Location/Qualifiers
misc_feature      1..521
note = Synthetic
source            1..521
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 20
aggatcttag aatgtgact ccacccaagg ttccttggt tgagccatca aaaggagaga  60
ttgcaaaca aaaaaaggct accctcggt gcttggccag gggcttctc cctgaccacg 120
tggagcttag ctgggtgggt aatggcaagg aggtccacag tggggtcagc acggacctc 180
aggcctacaa ggagagcaat tatactact gcttgacccgg cccgctgggg gtctctgtca 240
ccttctggca caatctcgaa aaccacttc gctgccaaggt gcaatccat gggcttccag 300
aggaggacaa gtggccagag ggctcacca aacctgtcac agacaatc agtgcagagg 360
cctggggccg agcagactgt ggaatcaatt cagcatctta tcattcagggg gttctgtcg 420
caaccatct ctatgagatc ctactgggg aggccaccct atatgtgtc ctggtagtgc 480
gccttagtgc gatggccatg gtcaagaaaa aaaattcctg a                      521

SEQ ID NO: 21      moltype = DNA  length = 1815
FEATURE           Location/Qualifiers
misc_feature      1..1815
note = Synthetic
source            1..1815
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 21
atcgctctg tcacctgtc agttttgtc ctctccatca tgctcaggag gagcaatggc 60
gatggagact cggtgaccca gacagaaggc ctggtcactc tcacagaagg gttgccttgt 120
atgtgtgaatc gcacccatca gactttatc tcaaatcctt tctttctg gtatgtccaa 180
catctcaatg aatcccctcg gctactctg aagagctca cagacaacaa gaggaccgag 240
caccagggt tccacqccac tctccataag agcagcagct cttccatct gcagaatgtcc 300
tcagcgcagc tgcagactc tgccctgtac tactgtgctc tgagggggaa tgcagggtcc 360
aagctcacat tccggggggg aacaagggtt acggcagatcc cccgacatcca gaaccaggaa 420
cctgctgtgtt accaggtaaa agatcctcg ttcctggcaga gcacccctcg cctgttccacc 480
gactttgact cccaaatcaa ttgtccggaaa accatggaaat ctggaaacgtt catcaactgac 540
aaaaactgtgc tggacatgaa agctatggat tccaaaggaga atggggccat tgcctggagc 600
aaccacgaaa gttcacctt ccaagatato ttcaaaaggaga ccaacgcac ctaccccaatg 660
tcagacgttc cctgtgtac gagaatgtt gagaatggggaa ttgaaacaga tatgaactca 720
aacttccaa acctgtcact tttggactc cgaatccctc tgctgaaatg agccgattt 780
aacctgtctca tgacgtcgag gctgtgtcc agtgcggccca agcgggtccgg atccggagcc 840
accaacttca gctgtgtgaa gcaggccggc gacgtggagg aqaaaccccg ccccatgggc 900
tggtaggtcc taagctgtgtt ggccttgcgat tttttggaa taggccttggggatggacggct 960
gtttccaga ctccaaacta tcatgtcaca caggtggggaa atgaaatgtc ttcaattgt 1020
aagcaaaactc tggggccacga taactatgtat ttgtacaagg aagactctaa gaaattgtcg 1080
aagattatgt ttagtccatca taataaggca ctcatgttca acggaaacagt tccaaaggcc 1140
tttcacccctc agtcttcaga tttaaacttca ttgaatcttca gaatcaatc tgtagagccg 1200
gaggacttgc ctgtgttatct ctgtgccago agtccccggg actggagtgc agaaaacgtc 1260
tattttggct caggaaccag actgactgtt ctgcaggatc tgagaaatgt gactccaccc 1320
aagggtctct tttttggatc atcaaaaggca gagattggca acaaacaaaa ggctaccctc 1380
gtgtgtttgg ccagggttctt ccgttttgcac cagtggtggc tgagttgggg ggtgaatggc 1440
aaggaggatcc acagtggggcgtt cagcaggccat ccccttggcc acaggagag caattatagc 1500
tactgcgtga gcaggccctt gagggtctct gtcacccctt ggcacaatcc tcgaaaccac 1560
ttccgcgtcc aagtgcgtt ccatggggctt tcagaggagg acaagttggcc agagggctca 1620
cccaaaccatc tccacacggaa catcaatgtca gaggccctgggg gecgagcaga ctgtggaaatc 1680
acttcacatc cttatcatca ggggttctg ttgtcaacca ttcttcatca gatctactg 1740
gggaaggccca cccttatatgc ttgtgtggtc agtggccctgg tgctgtatggc catgtcaag 1800
aaaaaaaaattt cctga                                         1815

SEQ ID NO: 22      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic
source            1..21
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 22
actatattact caaatccctt c                                         21

SEQ ID NO: 23      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic
source            1..21
mol_type = other DNA

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SEQUENCE: 23	organism = synthetic construct	
agcttcacag acaacaagag g		21
SEQ ID NO: 24	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
misc_feature	1..33	
note = Synthetic		
source	1..33	
mol_type = other DNA		
organism = synthetic construct		
SEQUENCE: 24		
gctctgaggg ggaatgcagg tgccaagtc aca		33
SEQ ID NO: 25	moltype = DNA length = 15	
FEATURE	Location/Qualifiers	
misc_feature	1..15	
note = Synthetic		
source	1..15	
mol_type = other DNA		
organism = synthetic construct		
SEQUENCE: 25		
ctgggccacg atact		15
SEQ ID NO: 26	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
note = Synthetic		
source	1..18	
mol_type = other DNA		
organism = synthetic construct		
SEQUENCE: 26		
tacaataata agcaactc		18
SEQ ID NO: 27	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
misc_feature	1..39	
note = Synthetic		
source	1..39	
mol_type = other DNA		
organism = synthetic construct		
SEQUENCE: 27		
gccagcagct cccgggactg gagtgtcagaa acgtgttat		39
SEQ ID NO: 28	moltype = AA length = 27	
FEATURE	Location/Qualifiers	
REGION	1..27	
note = Synthetic		
source	1..27	
mol_type = protein		
organism = synthetic construct		
SEQUENCE: 28		
RAKRSGSGAT NFSLLKQAGD VEENPGP		27
SEQ ID NO: 29	moltype = AA length = 189	
FEATURE	Location/Qualifiers	
source	1..189	
mol_type = protein		
organism = Homo sapiens		
SEQUENCE: 29		
MTBYKLVVG AGGVGKSLT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG	60	
QEELYSAMRDQ YMRTGEGLC VFAINNTKSF EDIHHYREQI KRVKDSEDPV MVLVGNKCDL	120	
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ RVEDAFYTLV REIRQYRLKK ISKEEKTPGC	180	
VKIKKCIIM	189	
SEQ ID NO: 30	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
mol_type = protein		
organism = Homo sapiens		
SEQUENCE: 30		
VVVGAGGVGK		10
SEQ ID NO: 31	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	

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	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 31	
VVGAGGVGK	9
SEQ ID NO: 32	moltype = AA length = 189
FEATURE	Location/Qualifiers
source	1..189
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 32	
MTEYKLVVG AVGVGKSAIT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG 60	
QEEYSAMRDQ YMRTGEGLC VFAINNTKSF EDIHHYREQI KRVKDSEDP MVLVGNKCDL 120	
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ RVEDAFYTLV REIRQYRLKK ISKEEKTPGC 180	
VKIKKCIIM	189
SEQ ID NO: 33	moltype = AA length = 10
FEATURE	Location/Qualifiers
source	1..10
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 33	
VVVGAVGVGK	10
SEQ ID NO: 34	moltype = AA length = 9
FEATURE	Location/Qualifiers
source	1..9
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 34	
VVGADGVGK	9
SEQ ID NO: 35	moltype = AA length = 9
FEATURE	Location/Qualifiers
source	1..9
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 35	
VVGAVGVGK	9
SEQ ID NO: 36	moltype = AA length = 9
FEATURE	Location/Qualifiers
source	1..9
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 36	
VVGACGVGK	9
SEQ ID NO: 37	moltype = AA length = 10
FEATURE	Location/Qualifiers
source	1..10
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 37	
VVVGACGVGK	10
SEQ ID NO: 38	moltype = AA length = 9
FEATURE	Location/Qualifiers
source	1..9
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 38	
VVGARGVGK	9
SEQ ID NO: 39	moltype = AA length = 10
FEATURE	Location/Qualifiers
source	1..10
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 39	
VVVGARGVGK	10
SEQ ID NO: 40	moltype = AA length = 16
FEATURE	Location/Qualifiers
source	1..16
	mol_type = protein

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SEQUENCE: 40 CAMREDTGAN TGKLTF	organism = Mus musculus	
		16
SEQ ID NO: 41 FEATURE source	moltype = AA length = 15 Location/Qualifiers 1..15 mol_type = protein organism = Mus musculus	
SEQUENCE: 41 CASSQDSLGR AEQFF		15
SEQ ID NO: 42 FEATURE source	moltype = AA length = 15 Location/Qualifiers 1..15 mol_type = protein organism = Mus musculus	
SEQUENCE: 42 CASSSDWGGA ETLYF		15
SEQ ID NO: 43 FEATURE source	moltype = AA length = 16 Location/Qualifiers 1..16 mol_type = protein organism = Mus musculus	
SEQUENCE: 43 CASSSGLGSS AETLYF		16
SEQ ID NO: 44 FEATURE misc_feature source	moltype = DNA length = 81 Location/Qualifiers 1..81 note = Synthetic 1..81 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 44 cgggccaaac ggtccggatc cgagccacc aacttcaggc tgctgaagca ggccggcgac gtggaggaga accccggccc c		60 81
SEQ ID NO: 45 FEATURE REGION source	moltype = AA length = 604 Location/Qualifiers 1..604 note = Synthetic 1..604 mol_type = protein organism = synthetic construct	
SEQUENCE: 45 MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTII SNPFLFWYVQ HILNESPRLLL KSFTDNKRTH HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA KLTFGGGTRLR TVRPDIQNPE PAVYQLKDPR SQDSTLCCLFT DFDSQINVPK TMESGTFITD KTVLDDMKAMD SKSNGAIAWS NQTSFTCQDI FKBTNATYPS SDVPCDATLT EKSFETDMNL NFQNLSVMGL RILLLKVAGF NLLMLTLLRLLWS SRAKRSGSGA DVEENPGPMG 300 CRLLSCVAFC LLGIGPLETA VFQTPNYHVT QVGNEVSFNC KOTLGHDHTM WYKQDSKLL 360 KIMFSYNNKQ LIVNETVPRR FSPQSSDKAH LNLRIKSVEP EDSAVYLCAS SSRDWSAETL 420 YFGSGTRLTV LEDLRNVTTP KVSLFEPSKA EIANKQKATL VCLARGFPD HVELSWWVNG 480 KEVHSGVSTD PQAYKESNSY YCLSSRLRVS ATFWHNPRNH FRCQVQFHGL SEEDKWPEG PKPVTQNISA EAWGRADCIGI TSASYHQGV SATILYEILL GKATLYAVLV SGLVLMAMVK KKNS	60 120 180 240 300 360 420 480 540 600 604	
SEQ ID NO: 46 FEATURE REGION VARIANT source	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic 2 note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 46 CXLRGNAGAK LTF		13
SEQ ID NO: 47 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic	

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VARIANT          3
source           note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 47
CAXRGNAGAK LTF                                         13

SEQ ID NO: 48
FEATURE
REGION
1..13
note = Synthetic
VARIANT          4
note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 48
CALXGNAGAK LTF                                         13

SEQ ID NO: 49
FEATURE
REGION
1..13
note = Synthetic
VARIANT          5
note = X Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu,
                 Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 49
CALRXNAGAK LTF                                         13

SEQ ID NO: 50
FEATURE
REGION
1..13
note = Synthetic
VARIANT          6
note = X is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 50
CALRGXAGAK LTF                                         13

SEQ ID NO: 51
FEATURE
REGION
1..13
note = Synthetic
VARIANT          7
note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 51
CALRGNXGAK LTF                                         13

SEQ ID NO: 52
FEATURE
REGION
1..13
note = Synthetic
VARIANT          8
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..13
mol_type = protein
organism = synthetic construct

SEQUENCE: 52
CALRGNAXAK LTF                                         13

SEQ ID NO: 53
FEATURE
Location/Qualifiers

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REGION          1..13
VARIANT        note = Synthetic
               9
               note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
               Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source          1..13
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 53
CALRGNAGXK LTF                                     13

SEQ ID NO: 54          moltype = AA length = 13
FEATURE          Location/Qualifiers
REGION           1..13
VARIANT          note = Synthetic
               10
               note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
               Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source          1..13
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 54
CALRGNAGAX LTF                                     13

SEQ ID NO: 55          moltype = AA length = 13
FEATURE          Location/Qualifiers
REGION           1..13
VARIANT          note = Synthetic
               11
               note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
               Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source          1..13
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 55
CALRGNAGAK XTF                                     13

SEQ ID NO: 56          moltype = AA length = 13
FEATURE          Location/Qualifiers
REGION           1..13
VARIANT          note = Synthetic
               12
               note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
               Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.
source          1..13
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 56
CALRGNAGAK LXF                                     13

SEQ ID NO: 57          moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
               2
               note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
               Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source          1..15
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 57
CXSSSRDWSA ETLYF                                     15

SEQ ID NO: 58          moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
               3
               note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
               Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source          1..15
               mol_type = protein
               organism = synthetic construct

SEQUENCE: 58
CAXSSRDWSA ETLYF                                     15

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SEQ ID NO: 59      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 4
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
source           Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 59
CAXSRDWSA ETLYF                                         15

SEQ ID NO: 60      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 5
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
source           Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 60
CASSXRDWSA ETLYF                                         15

SEQ ID NO: 61      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 6
                 note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
source           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 61
CASSSXDWFA ETLYF                                         15

SEQ ID NO: 62      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 7
                 note = X is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile,
source           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 62
CASSSRXWFA ETLYF                                         15

SEQ ID NO: 63      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 8
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
source           Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 63
CASSSRDXSA ETLYF                                         15

SEQ ID NO: 64      moltype = AA length = 15
FEATURE          Location/Qualifiers
REGION           1..15
VARIANT          note = Synthetic
                 9
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
source           Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
                 1..15
                 mol_type = protein
                 organism = synthetic construct
SEQUENCE: 64

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CASSSRDWXA ETLYF	15
SEQ ID NO: 65	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
VARIANT	note = Synthetic
	10
	note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
	Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..15
	mol_type = protein
SEQUENCE: 65	organism = synthetic construct
CASSSRDWSX ETLYF	15
SEQ ID NO: 66	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
VARIANT	note = Synthetic
	11
	note = X is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile,
	Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..15
	mol_type = protein
SEQUENCE: 66	organism = synthetic construct
CASSSRDWSA XTLYF	15
SEQ ID NO: 67	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
VARIANT	note = Synthetic
	12
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
	Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.
source	1..15
	mol_type = protein
SEQUENCE: 67	organism = synthetic construct
CASSSRDWSA EXLYF	15
SEQ ID NO: 68	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
VARIANT	note = Synthetic
	13
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
	Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..15
	mol_type = protein
SEQUENCE: 68	organism = synthetic construct
CASSSRDWSA ETXYF	15
SEQ ID NO: 69	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
VARIANT	note = Synthetic
	14
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
	Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..15
	mol_type = protein
SEQUENCE: 69	organism = synthetic construct
CASSSRDWSA ETLXF	15
SEQ ID NO: 70	moltype = AA length = 135
FEATURE	Location/Qualifiers
REGION	1..135
VARIANT	note = Synthetic
	113
	note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
	Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..135
	mol_type = protein

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SEQUENCE: 70
organism = synthetic construct
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCXLGNAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 71      moltype = AA length = 135
FEATURE          Location/Qualifiers
REGION           1..135
VARIANT          note = Synthetic
                 114
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                           Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 71
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCAXRGNAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 72      moltype = AA length = 135
FEATURE          Location/Qualifiers
REGION           1..135
VARIANT          note = Synthetic
                 115
                 note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 72
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALXGNAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 73      moltype = AA length = 135
FEATURE          Location/Qualifiers
REGION           1..135
VARIANT          note = Synthetic
                 116
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile,
                           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 73
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRXNAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 74      moltype = AA length = 135
FEATURE          Location/Qualifiers
REGION           1..135
VARIANT          note = Synthetic
                 117
                 note = X is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile,
                           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 74
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGXAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 75      moltype = AA length = 135
FEATURE          Location/Qualifiers
REGION           1..135
VARIANT          note = Synthetic
                 118
                 note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                           Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
                 mol_type = protein
                 organism = synthetic construct

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SEQUENCE: 75
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNXGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 76      moltype = AA length = 135
FEATURE           Location/Qualifiers
REGION            1..135
VARIANT           note = Synthetic
119
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
mol_type = protein
organism = synthetic construct

SEQUENCE: 76
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAXA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 77      moltype = AA length = 135
FEATURE           Location/Qualifiers
REGION            1..135
VARIANT           note = Synthetic
120
note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
mol_type = protein
organism = synthetic construct

SEQUENCE: 77
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGX 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 78      moltype = AA length = 135
FEATURE           Location/Qualifiers
REGION            1..135
VARIANT           note = Synthetic
121
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
mol_type = protein
organism = synthetic construct

SEQUENCE: 78
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA 120
KLTFGGGTRL TVRPD 135

SEQ ID NO: 79      moltype = AA length = 135
FEATURE           Location/Qualifiers
REGION            1..135
VARIANT           note = Synthetic
122
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..135
mol_type = protein
organism = synthetic construct

SEQUENCE: 79
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA 120
KXTFGGGTRL TVRPD 135

SEQ ID NO: 80      moltype = AA length = 135
FEATURE           Location/Qualifiers
REGION            1..135
VARIANT           note = Synthetic
123
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.
source            1..135
mol_type = protein
organism = synthetic construct

SEQUENCE: 80

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MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HINESPRLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA 120
KLXFGGGTRL TVRPD 135

SEQ ID NO: 81      moltype = AA length = 134
FEATURE
REGION
1..134
note = Synthetic
VARIANT
111
note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source
1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 81
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC XSSSRDWSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 82      moltype = AA length = 134
FEATURE
REGION
1..134
note = Synthetic
VARIANT
112
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source
1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 82
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC AXSSRDWSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 83      moltype = AA length = 134
FEATURE
REGION
1..134
note = Synthetic
VARIANT
113
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source
1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 83
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASXSRDWSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 84      moltype = AA length = 134
FEATURE
REGION
1..134
note = Synthetic
VARIANT
114
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source
1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 84
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSXRDWSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 85      moltype = AA length = 134
FEATURE
REGION
1..134
note = Synthetic
VARIANT
115
note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source
1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 85
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK 60

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LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSXDWASAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 86 moltype = AA length = 134
FEATURE Location/Qualifiers
REGION 1..134
VARIANT note = Synthetic
116
note = X is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source 1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 86
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDXSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 87 moltype = AA length = 134
FEATURE Location/Qualifiers
REGION 1..134
VARIANT note = Synthetic
117
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.
source 1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 87
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDXSAE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 88 moltype = AA length = 134
FEATURE Location/Qualifiers
REGION 1..134
VARIANT note = Synthetic
118
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source 1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 88
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDXAEE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 89 moltype = AA length = 134
FEATURE Location/Qualifiers
REGION 1..134
VARIANT note = Synthetic
119
note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source 1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 89
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDXSXE 120
TLYFGSGTRL TVLE 134

SEQ ID NO: 90 moltype = AA length = 134
FEATURE Location/Qualifiers
REGION 1..134
VARIANT note = Synthetic
120
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source 1..134
mol_type = protein
organism = synthetic construct

SEQUENCE: 90
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDXSAX 120

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TLYFGSGTRL TVLE	134
SEQ ID NO: 91	moltype = AA length = 134
FEATURE	Location/Qualifiers
REGION	1..134
VARIANT	note = Synthetic
	121
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.
source	1..134
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 91	
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK	60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDWSAE	120
TXYFGSGTRL TVLE	134
SEQ ID NO: 92	moltype = AA length = 134
FEATURE	Location/Qualifiers
REGION	1..134
VARIANT	note = Synthetic
	122
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..134
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 92	
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK	60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDWSAE	120
TXYFGSGTRL TVLE	134
SEQ ID NO: 93	moltype = AA length = 134
FEATURE	Location/Qualifiers
REGION	1..134
VARIANT	note = 'Synthetic
	123
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val.
source	1..134
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 93	
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK	60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSSRDWSAE	120
TXYFGSGTRL TVLE	134
SEQ ID NO: 94	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic
	113
	note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 94	
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIIY SNPFLFWYVQ	60
HILNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCXLRGNAGA	120
KLTFGGGTRL TVRPDIQNPE PAVYOLKDPR SQDSTLCLFT FDFSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGIAIWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLSVMGL RILLLKVAGF NLLMTLRLWS S	271
SEQ ID NO: 95	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic
	114
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 95	
MRPVTCVSLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIIY SNPFLFWYVQ	60

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HLNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCAXRGNAGA	120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDRP SQDSTLCLFT DFDSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLNSVMGL RILLLKVAGF NLLMTRLRLWS S	271

SEQ ID NO: 96	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic 115
	note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 96	
MRPVTCVLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ	60
HLNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALXGNAGA	120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDRP SQDSTLCLFT DFDSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLNSVMGL RILLLKVAGF NLLMTRLRLWS S	271

SEQ ID NO: 97	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic 116
	note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 97	
MRPVTCVLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ	60
HLNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRXNAGA	120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDRP SQDSTLCLFT DFDSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLNSVMGL RILLLKVAGF NLLMTRLRLWS S	271

SEQ ID NO: 98	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic 117
	note = X is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 98	
MRPVTCVLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ	60
HLNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGXAGA	120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDRP SQDSTLCLFT DFDSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLNSVMGL RILLLKVAGF NLLMTRLRLWS S	271

SEQ ID NO: 99	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271
VARIANT	note = Synthetic 118
	note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source	1..271
	mol_type = protein
	organism = synthetic construct

SEQUENCE: 99	
MRPVTCVLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ	60
HLNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNXGA	120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDRP SQDSTLCLFT DFDSQINVPK TMESGTFITD	180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL	240
NFQNLNSVMGL RILLLKVAGF NLLMTRLRLWS S	271

SEQ ID NO: 100	moltype = AA length = 271
FEATURE	Location/Qualifiers
REGION	1..271

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VARIANT          note = Synthetic
                 119
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..271
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 100
MRPVTCsvLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HlNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAXA 120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDPR SQDSTLCCLFT DFDSQINVPK TMESGTFITD 180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL 240
NFQNLSVMGL RILLLKVAGF NLLMTLRLWS S 271

SEQ ID NO: 101      moltype = AA length = 271
FEATURE          Location/Qualifiers
REGION           1..271
VARIANT          note = Synthetic
                 120
                 note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..271
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 101
MRPVTCsvLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HlNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGX 120
KLTFGGGTRL TVRPDIQNPE PAVYQLKDPR SQDSTLCCLFT DFDSQINVPK TMESGTFITD 180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL 240
NFQNLSVMGL RILLLKVAGF NLLMTLRLWS S 271

SEQ ID NO: 102      moltype = AA length = 271
FEATURE          Location/Qualifiers
REGION           1..271
VARIANT          note = Synthetic
                 121
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..271
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 102
MRPVTCsvLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HlNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA 120
XLTFGGGTRL TVRPDIQNPE PAVYQLKDPR SQDSTLCCLFT DFDSQINVPK TMESGTFITD 180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL 240
NFQNLSVMGL RILLLKVAGF NLLMTLRLWS S 271

SEQ ID NO: 103      moltype = AA length = 271
FEATURE          Location/Qualifiers
REGION           1..271
VARIANT          note = Synthetic
                 122
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..271
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 103
MRPVTCsvLV LLLMLRRSNG DGDSVTQTEG LVTLTEGLPV MLNCTYQTIY SNPFLFWYVQ 60
HlNESPRLLL KSFTDNKRTE HQGFHATLHK SSSSFHLQKS SAQLSDSALY YCALRGNAGA 120
KXTFGGGTRL TVRPDIQNPE PAVYQLKDPR SQDSTLCCLFT DFDSQINVPK TMESGTFITD 180
KTVLDMKAMD SKSNGAIAWS NQTSFTCQDI FKETNATYPS SDVPCDATLT EKSFETDMNL 240
NFQNLSVMGL RILLLKVAGF NLLMTLRLWS S 271

SEQ ID NO: 104      moltype = AA length = 271
FEATURE          Location/Qualifiers
REGION           1..271
VARIANT          note = Synthetic
                 123
                 note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..271
                 mol_type = protein
                 organism = synthetic construct

SEQUENCE: 104

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MRPVTCVSLV	LLMLRRSNG	DGDSVTQTEG	LVTLTEGLPV	MNCTYQTIY	SNPFLFWYQ	60
HINESPRLL	KSFTDNKRTH	HQGFHATLHK	SSSFHLQKS	SAQLSDSALY	YCALRGNAGA	120
KLXFGGGTRL	TVRPDIQNPE	PAVYQLKDPR	SQDSTLCLFT	DFDSQINVPK	TMESGTFITD	180
KTVLDMKAMD	SKSNGAIAWS	NQTSFTCQDI	FKBTNATYPS	SDVPCDATLT	EKSFETDMNL	240
NFQNLSVMGL	RILLKVAGF	NLLMTLRLWS	S			271

```
SEQ ID NO: 105      moltype = AA  length = 306
FEATURE          Location/Qualifiers
REGION           1..306
VARIANT          note = Synthetic
                  111
                  note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                         Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source            1..306
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 105
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSQSSDK AHLNLRIKSV EPEDSAVYLC XSSSRDWSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMAM 300
VKKKNS                                     306
```

```
SEQ ID NO: 106      moltype = AA  length = 306
FEATURE          Location/Qualifiers
REGION           1..306
VARIANT          note = Synthetic
                  112
                  note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                         Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source            1..306
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 106
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSQSSDK AHLNLRIKSV EPEDSAVYLC AXSSRDWSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMAM 300
VKKKNS                                     306
```

```
SEQ ID NO: 107      moltype = AA  length = 306
FEATURE          Location/Qualifiers
REGION           1..306
VARIANT          note = Synthetic
                  113
                  note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                         Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source            1..306
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 107
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSQSSDK AHLNLRIKSV EPEDSAVYLC ASXSRDWSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMAM 300
VKKKNS                                     306
```

```
SEQ ID NO: 108      moltype = AA  length = 306
FEATURE          Location/Qualifiers
REGION           1..306
VARIANT          note = Synthetic
                  114
                  note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                         Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source            1..306
                  mol_type = protein
                  organism = synthetic construct
```

```
SEQUENCE: 108
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSQSSDK AHLNLRIKSV EPEDSAVYLC ASSXRDWSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMAM 300
```

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VKKKNS

306

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SEQ ID NO: 109      moltype = AA length = 306
FEATURE
REGION          Location/Qualifiers
1..306
note = Synthetic
VARIANT          115
note = X is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 109
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSXDWSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 110      moltype = AA length = 306
FEATURE
REGION          Location/Qualifiers
1..306
note = Synthetic
VARIANT          116
note = X is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile,
                 Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 110
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDXSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 111      moltype = AA length = 306
FEATURE
REGION          Location/Qualifiers
1..306
note = Synthetic
VARIANT          117
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 111
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDXSAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 112      moltype = AA length = 306
FEATURE
REGION          Location/Qualifiers
1..306
note = Synthetic
VARIANT          118
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
                 Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 112
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDXWAE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF PDHVELSWWV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 113      moltype = AA length = 306
FEATURE

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REGION          1..306
note = Synthetic
VARIANT         119
note = X is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile,
               Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source          1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 113
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDWSXE 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWNV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 114      moltype = AA length = 306
FEATURE          Location/Qualifiers
REGION           1..306
note = Synthetic
VARIANT          120
note = X is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile,
               Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 114
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDWSAX 120
TLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWNV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 115      moltype = AA length = 306
FEATURE          Location/Qualifiers
REGION           1..306
note = Synthetic
VARIANT          121
note = X is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile,
               Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 115
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDWSAE 120
XLYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWNV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 116      moltype = AA length = 306
FEATURE          Location/Qualifiers
REGION           1..306
note = Synthetic
VARIANT          122
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,
               Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.
source           1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 116
MGCRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYL ASSSRDWSAE 120
TXYFGSGTRL TVLEDLRNVT PPKVSLFEPS KABIANQKA TLVCLARGFF PDHVELSWNV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASAYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKKNS          306

SEQ ID NO: 117      moltype = AA length = 306
FEATURE          Location/Qualifiers
REGION           1..306
note = Synthetic
VARIANT          123
note = X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His,

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source          Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val.
               1..306
mol_type = protein
organism = synthetic construct

SEQUENCE: 117
MGRRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 60
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHNLNLRIKSV EPEDSAVYLC ASSSRDWSAE 120
TLXFGSGTRL TVLEDLRNVF PPKVSLFEPS KABIANQKKA TLVCLARGFF PDHVELSWNV 180
NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH GLSEEDKWPE 240
GSPKPVTQNI SAEAWGRADC GITASASYHQG VLSATILYEI LLGKATLYAV LVSGLVLMM 300
VKKNS                      306

SEQ ID NO: 118      moltype = AA length = 23
FEATURE           Location/Qualifiers
source            1..23
mol_type = protein
organism = Homo sapiens

SEQUENCE: 118
MTEYKLVVVG AGGVGKSAALT IQL                         23

SEQ ID NO: 119      moltype = AA length = 23
FEATURE           Location/Qualifiers
source            1..23
mol_type = protein
organism = Homo sapiens

SEQUENCE: 119
MTEYKLVVVG ADGVGKSAALT IQL                         23

SEQ ID NO: 120      moltype = AA length = 23
FEATURE           Location/Qualifiers
source            1..23
mol_type = protein
organism = Homo sapiens

SEQUENCE: 120
MTEYKLVVVG AVGVGKSAALT IQL                         23

SEQ ID NO: 121      moltype = AA length = 188
FEATURE           Location/Qualifiers
source            1..188
mol_type = protein
organism = Homo sapiens

SEQUENCE: 121
MTEYKLVVVG AGGVGKSAALT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG 60
QEELYSAMRDQ YMRTGEGLC VFIAINNTKSF EDIHHYREQI KRVKDSEDVPM MVLVGNKCDL 120
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ GVDDAFYTLV REIRKHKEKM SKDGKKKKK 180
SKTKCVIM                      188

SEQ ID NO: 122      moltype = AA length = 188
FEATURE           Location/Qualifiers
source            1..188
mol_type = protein
organism = Homo sapiens

SEQUENCE: 122
MTEYKLVVVG ADGVGKSAALT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG 60
QEELYSAMRDQ YMRTGEGLC VFIAINNTKSF EDIHHYREQI KRVKDSEDVPM MVLVGNKCDL 120
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ GVDDAFYTLV REIRKHKEKM SKDGKKKKK 180
SKTKCVIM                      188

SEQ ID NO: 123      moltype = AA length = 188
FEATURE           Location/Qualifiers
source            1..188
mol_type = protein
organism = Homo sapiens

SEQUENCE: 123
MTEYKLVVVG AVGVGKSAALT IQLIQNHFVD EYDPTIEDSY RKQVVIDGET CLLDILDTAG 60
QEELYSAMRDQ YMRTGEGLC VFIAINNTKSF EDIHHYREQI KRVKDSEDVPM MVLVGNKCDL 120
PSRTVDTKQA QDLARSYGIP FIETSAKTRQ GVDDAFYTLV REIRKHKEKM SKDGKKKKK 180
SKTKCVIM                      188

SEQ ID NO: 124      moltype = AA length = 9
FEATURE           Location/Qualifiers
source            1..9
mol_type = protein
organism = Homo sapiens

SEQUENCE: 124
VVVGADGVG

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SEQ ID NO: 125	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
source	1..6	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 125		
DPNSYY		6
SEQ ID NO: 126	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
source	1..7	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 126		
VFSSTEI		7
SEQ ID NO: 127	moltype = AA length = 16	
FEATURE	Location/Qualifiers	
source	1..16	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 127		
CAVSGGTNSA GNKLTF		16
SEQ ID NO: 128	moltype = AA length = 5	
FEATURE	Location/Qualifiers	
source	1..5	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 128		
LGHDT		5
SEQ ID NO: 129	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
source	1..6	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 129		
YNNKQL		6
SEQ ID NO: 130	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
source	1..14	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 130		
CASSRDWGPA EQFF		14
SEQ ID NO: 131	moltype = AA length = 137	
FEATURE	Location/Qualifiers	
source	1..137	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 131		
MKTVTGPLFL CFWLQLNCVS RGEQVEQRPP HLSVREGDSA VITCTYTDNP SYYFFWYKQE	60	
PGASLQLLMK VFSSTEINEG QGFTVLLNKK DKRLSLNLTA AHPGDSAAVF CAVSGGTNSA	120	
GNKLTFGIGT RVLVRPD	137	
SEQ ID NO: 132	moltype = AA length = 133	
FEATURE	Location/Qualifiers	
source	1..133	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 132		
MGRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWYKQDSKK	60	
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYLC ASSRDWGPAE	120	
QFFGPGTRLT VLE	133	
SEQ ID NO: 133	moltype = AA length = 273	
FEATURE	Location/Qualifiers	
source	1..273	
	mol_type = protein	
	organism = Mus musculus	
SEQUENCE: 133		
MKTVTGPLFL CFWLQLNCVS RGEQVEQRPP HLSVREGDSA VITCTYTDNP SYYFFWYKQE	60	

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PGASLQLLMK VFSSTEINEG QGFTVLLNK DKRLSLNLTA AHPGDSAAVF CAVSGGTNSA	120
GNKLTFGIGT RVLVRPDION PEPAVYQLKD PRSQDSTLCL FTDFDSQINV PKTMESGTFI	180
TDKTVLDMKA MDSKSNGAIA WSNQTSFTCQ DIFKETNATY PSSDVPCDAT LTEKSFETDM	240
NLNFQNLSVW GFLRILLLKVA GFNLLMTLRL WSS	273
SEQ ID NO: 134 moltype = AA length = 305	
FEATURE Location/Qualifiers	
source 1..305	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 134	
MGRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVFS NCKQTLGHDT MYWKQDSKK	60
LLKIMFSYNN KQLIVNETVP RRFSPQSSDK AHLNLRIKSV EPEDSAVYL ASSRDWGPAAE	120
QFFGPGTRLT VLEDLRNVTPKVSLFEPSK AEIANKQKAT LVCLARGFFP DHVELSWWN	180
GKEVHSGVST DPQAYKESNY SYCLSSRLRV SATFWHNPRN HFRCQVQFHG LSEEDKWPEG	240
SPKPVTONIS AEAAGRADC G ITSASYHQGV LSATILYBIL LGKATLYAVL VSGLVLMAMV	300
KKKNS	305
SEQ ID NO: 135 moltype = AA length = 136	
FEATURE Location/Qualifiers	
source 1..136	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 135	
IQNPEPAVYQ LKDPRSQDST LCLFTDFDSQ INVPKTMESG TFITDKTVLD MKAMDSKNG	60
AIAWSNQTSF TCQDIFKETN ATYPSSDVP DATLTEKSFE TDMNLNFQNL SVMGLRILL	120
KVAGFNLLMT LRLWSS	136
SEQ ID NO: 136 moltype = AA length = 172	
FEATURE Location/Qualifiers	
source 1..172	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 136	
DLRNVTPPKV SLFEPSKAEI ANKQKATLVC LARGFFPDHV ELSWWVNGKE VHSGVSTDPO	60
AYKESNYSYC LSSRLRVSAT FWHPNPRNHFR CQVQFHGLSE EDKWPESPK PVTQNISAEA	120
WGRADCITS ASYHQGVLSA TILYEILLGK ATLYAVLVSG LVLMAMVKKK NS	172
SEQ ID NO: 137 moltype = AA length = 6	
FEATURE Location/Qualifiers	
source 1..6	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 137	
NDMFDY	6
SEQ ID NO: 138 moltype = AA length = 7	
FEATURE Location/Qualifiers	
source 1..7	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 138	
VRSNVDK	7
SEQ ID NO: 139 moltype = AA length = 15	
FEATURE Location/Qualifiers	
source 1..15	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 139	
CAAGDGGSN YKLTF	15
SEQ ID NO: 140 moltype = AA length = 5	
FEATURE Location/Qualifiers	
source 1..5	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 140	
NSHNY	5
SEQ ID NO: 141 moltype = AA length = 6	
FEATURE Location/Qualifiers	
source 1..6	
mol_type = protein	
organism = Mus musculus	
SEQUENCE: 141	

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SYGAGN

6

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SEQ ID NO: 142      moltype = AA length = 14
FEATURE
source
1..14
mol_type = protein
organism = Mus musculus

SEQUENCE: 142
CASASWGGYA EQFF

SEQ ID NO: 143      moltype = AA length = 141
FEATURE
source
1..141
mol_type = protein
organism = Mus musculus

SEQUENCE: 143
MTGFLKALLL VLCLRPEWIK SQQKTTGGQQV KQSSPSLTVO EGGILILNCD YENDMFDYFA 60
WYKKYPDNSP TLLISVRNSV DKREDGRFTV FLNKGSKHFS LHITASQPED TAVYLCAAGD 120
SGGSNYKLTG GKGTLLTVTP N 141

SEQ ID NO: 144      moltype = AA length = 131
FEATURE
source
1..131
mol_type = protein
organism = Mus musculus

SEQUENCE: 144
MGSRLFLVLS LLCTKHMEAA VTQSPRNKV VTGGNVTLSC RQTNSHNMY WYRQDTGHGL 60
RLIHYSYGAG NLQIGDVPDG YKATRTTQED FFLLLELASP SQTSLYFCAS ASWGGYAEQF 120
FGPGTRLTVL E 131

SEQ ID NO: 145      moltype = AA length = 277
FEATURE
source
1..277
mol_type = protein
organism = Mus musculus

SEQUENCE: 145
MTGFLKALLL VLCLRPEWIK SQQKTTGGQQV KQSSPSLTVO EGGILILNCD YENDMFDYFA 60
WYKKYPDNSP TLLISVRNSV DKREDGRFTV FLNKGSKHFS LHITASQPED TAVYLCAAGD 120
SGGSNYKLTG GKGTLLTVTP NIQNPEPavy QLKDPRSQDS TLCLFTDFDS QINVPKTMES 180
GTFITDKTVL DMKAMDSKSN GAIAWSNQTSF FTCQDIFKET NATYPSSDVP CDATLTEKSF 240
ETDMNLNFQNL SVMGLRILL LKVAGFNLLM TLRLWSS 277

SEQ ID NO: 146      moltype = AA length = 303
FEATURE
source
1..303
mol_type = protein
organism = Mus musculus

SEQUENCE: 146
MGSRLFLVLS LLCTKHMEAA VTQSPRNKV VTGGNVTLSC RQTNSHNMY WYRQDTGHGL 60
RLIHYSYGAG NLQIGDVPDG YKATRTTQED FFLLLELASP SQTSLYFCAS ASWGGYAEQF 120
FGPGTRLTVL EDLRNVTTPK VSLFEPSKAE IANKQKATLV CLARGFPDH VELSWWVNNGK 180
EVHSGVSTDQ QAYKESNYSY CLSSRLRVSA TFWHNPRNHF RCQVQFHGLS EEDKWPEGSP 240
KPVQTQNSAEE AWGRADCQITS ASYHQGVLSL ATLYEILLGK KATLYAVLVS GLVLMAMVKK 300
KNS 303

SEQ ID NO: 147      moltype = AA length = 136
FEATURE
source
1..136
mol_type = protein
organism = Mus musculus

SEQUENCE: 147
IQNPEPavy Q LKDPRSQDST LCLFTDFDSQ INVPKTMESG TFITDKTVLD MKAMDSKSN 60
AIAWSNQTSF TCQDIFKETN ATYPSSDVP C DATLTEKSFE TDMNLNFQNL SVMGLRILL 120
KVAGFNLLMT LRLWSS 136

SEQ ID NO: 148      moltype = AA length = 172
FEATURE
source
1..172
mol_type = protein
organism = Mus musculus

SEQUENCE: 148
DLRNVTTPKV SLFEPSKAEI ANKQKATLVC LARGFPDHV ELSWWVNGKE VHSGVSTDQ 60
AYKESNYSY CLSSRLRVSA TFWHNPRNHF CQVQFHGLSE EDKWPPEGSPK PVTQNISAEA 120
WGRADCQITS ASYHQGVLSA TILYEILLGK ATLYAVLVSG LVLMAMVKK NS 172

SEQ ID NO: 149      moltype = AA length = 5

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FEATURE	Location/Qualifiers
source	1..5
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 149	
TTMRS	5
SEQ ID NO: 150	moltype = AA length = 5
FEATURE	Location/Qualifiers
source	1..5
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 150	
LASGT	5
SEQ ID NO: 151	moltype = AA length = 15
FEATURE	Location/Qualifiers
source	1..15
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 151	
CAADSSNTGY QNFYFF	15
SEQ ID NO: 152	moltype = AA length = 5
FEATURE	Location/Qualifiers
source	1..5
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 152	
SGHLS	5
SEQ ID NO: 153	moltype = AA length = 6
FEATURE	Location/Qualifiers
source	1..6
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 153	
HYDKME	6
SEQ ID NO: 154	moltype = AA length = 15
FEATURE	Location/Qualifiers
source	1..15
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 154	
CASSLTDPLD SDYTF	15
SEQ ID NO: 155	moltype = AA length = 133
FEATURE	Location/Qualifiers
source	1..133
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 155	
MQRNLGAVLG ILWVQICWVR GDQVEQSPSA LSLHEGTDSA LRCNFTTMR SVQWFRQNSR 60 GSLISLFLYA SGTKENGRLK SAFDSKERRY STLHIRDAQL EDSGTYFCAA DSSNTGYQNF 120 YFGKGTSLTV IPN 133	
SEQ ID NO: 156	moltype = AA length = 143
FEATURE	Location/Qualifiers
source	1..143
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 156	
MSNTAFTPDA WNTTLLSWVA LFLLGTTSAN SGVVQSPRYI IKGKGERSIL KCIPISGHL 60 WAVYQQTQGQ ELKFFIQHYD KMERDKGNLP SRFSVQQFDD YHSEMNMSAL ELEDSAVYFC 120 ASSLTDPPLD DYTFGSGTRL LVI 143	
SEQ ID NO: 157	moltype = AA length = 269
FEATURE	Location/Qualifiers
source	1..269
	mol_type = protein
	organism = Mus musculus
SEQUENCE: 157	
MQRNLGAVLG ILWVQICWVR GDQVEQSPSA LSLHEGTDSA LRCNFTTMR SVQWFRQNSR 60 GSLISLFLYA SGTKENGRLK SAFDSKERRY STLHIRDAQL EDSGTYFCAA DSSNTGYQNF 120 YFGKGTSLTV IPNIQNPEPA VYQLKDPRSQ DSTLCLFDTF DSQINVPKTM ESGTFITDKT 180	

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VLDMKAMDSK SNGAIAWSNQ TSFTCQDIFK ETNATYPSSD VPCDATLKEK SFETDMNLNF	240
QNLSVVMGLRI LLLKVAGFNL LMTLRLWSS	269
SEQ ID NO: 158 moltype = AA length = 316	
FEATURE Location/Qualifiers	
source 1..316	
mol_type = protein	
organism = Mus musculus	
 SEQUENCE: 158	
MSNTAFTPDA WNTTLLSWVA LFLLGTSSAN SGVVQSPRYI IKGKGERSIL KCIPISGHLS	60
VAWYQQTQGQ ELKFFIQHYD KMERDKGNLP SRFSVQQFDD YHSEMNMSAL ELEDSAVYFC	120
ASSLTDPPLDS DYTFGSGTRL LVIEDLRNVT PPKVSLFEPS KAEIANKQKA TLVCLARGFF	180
PDHVVELSWV NGKEVHSGVS TDPQAYKESN YSYCLSSRLR VSATFWHNPR NHFRCQVQFH	240
GLSEEDKGPE GSPKPVTQNI SAEAWGRADC GITSAFYQQG VLSATILYEI LLGKATLYAV	300
LVSTLVVMAM VKRKNS	316
 SEQ ID NO: 159 moltype = AA length = 136	
FEATURE Location/Qualifiers	
source 1..136	
mol_type = protein	
organism = Mus musculus	
 SEQUENCE: 159	
IQNPEPAPVYQ LKDPRSQDST LCLFTDFDSQ INVPKTMESG TFITDKTVLD MKAMDSKSNG	60
AIAWSNQTSF TCQDIFKETN ATYPSSDVPC DATLTEKSFE TDMNLFQNL SVMGLRILL	120
KVAGFNLLMT LRLWSS	136
 SEQ ID NO: 160 moltype = AA length = 173	
FEATURE Location/Qualifiers	
source 1..173	
mol_type = protein	
organism = Mus musculus	
 SEQUENCE: 160	
EDLRNVTTPK VSLFEPSKAE IANKQKATLV CLARGFFPDH VELSWWWNGK EVHSGVSTD	60
QAYKESNSY CLSSRLRVSA TFWHNPRNHF RCQVQFHGLS EEDKWPEGSP KPVTQNISAE	120
AWGRADCGIT SASYQQGVLS ATILYEILLG KATLYAVLVS TLVVMAMVKR KNS	173
 SEQ ID NO: 161 moltype = AA length = 13	
FEATURE Location/Qualifiers	
source 1..13	
mol_type = protein	
organism = Mus musculus	
 SEQUENCE: 161 CAALNTGYQN FYF	13
 SEQ ID NO: 162 moltype = AA length = 612	
FEATURE Location/Qualifiers	
REGION 1..612	
note = Synthetic	
source 1..612	
mol_type = protein	
organism = synthetic construct	
 SEQUENCE: 162	
MQRNLGAVLG ILWVQICWVR GDQVEQSPSA LSLHEGTDSA LRCNFDTTMR SVQWPRQNSR	60
GSLISLFLYA SGTKENGRWK SAFDSKERRY STLHIRDAQL EDGTYFCAA DSSNTGYQNF	120
YFGKGTSLTV IPNIQNPPEPA VYQLKDPRSQ DSTLCDFDF DSQINVPKTM ESGTFITDKT	180
VLDMKAMDSK SNGAIAWSNQ TSFTCQDIFK ETNATYPSSD VPCDATLKEK SFETDMNLNF	240
QNLSVVMGLRI LLLKVAGFNL LMTLRLWSSR AKRGSGATN FSLLKQAGDV EENPGPMNT	300
AFPDPAWNTT LLSWVALFLL GTSSANSVV QSPRYIIKGK GERSILKCIP ISGHLSSAWY	360
QQTQGQELKF FIQHYDKMER DKGNLPSRFS VQQFDDYHSE MNMSALELED SAVYPCASSL	420
TDPLDSDYTF GSGTRLLVIE DLRNVTTPKV SLFEPSKAEI ANKQKATLVC LARGFFPDHV	480
EISLWWVNGKE VHSGVSTDQY AKYESNSYCL LSSRLRVSAT FWHNPRNHFR CQVQPHGLSE	540
EDKWPEGSPK PVTQNISAEA WGRADCGITS ASYQQGVLSA TILYEILLGK ATLYAVLVST	600
LVVMAMVKR NS	612
 SEQ ID NO: 163 moltype = DNA length = 1839	
FEATURE Location/Qualifiers	
misc_feature 1..1839	
note = Synthetic	
source 1..1839	
mol_type = other DNA	
organism = synthetic construct	
 SEQUENCE: 163	
atgcagagga acctggggacg tgtgtgggg attctgtggg tgcagatttgc ctgggtgaga	60
ggggatcagg tggagcagag tccttcagcc ctgagcctcc acgagggaaac cgattctgc	120
ctgagatcga atttacgac caccatgagg agtgtgcagt ggttccgaca gaattccagg	180
ggcagcctca tcagttgtt ctacttggct tcaggaacaa aggagaatgg gaggttaaag	240

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tcagcattg attctaagga gggcgcgtac agcacccgc acatcaggga tgcccagctg 300
gaggactcag gcaacttactt ctgtctgtc gactcttcga acacgggta ccagaacctc 360
tattttggaa aaggaacaag ttgactgtc attccaaaca tccagaaccc agaacatgtc 420
gtgtaccagt taaaagatcc tcggtctcg gacagcacc tctgcctgtt caccgactt 480
gactcccaa tcaatgtgcc gaaaaccatg gaatctggaa cggtcatcac tgacaaaact 540
gtgctggaca tgaaaagctat ggatccaag agcaatgggg ccattgcctg gagcaaccag 600
acaagctca ctgcacaaga tatctccaa gagaccaacg ccacctacc cagttcagac 660
gttccctgtg atgccccgtt gaccgagaaa agcttggaa catatgtaa cctgaacctt 720
caaaacctgt cagttatggg actccgaatc ctctgtcga aagttagcggg atttaacctg 780
ctcatgacgc tgaggctgtg gtccagtcgg gccaagecggt ccggatccgg agccaccaac 840
ttcagcgtgc tgaaggcaggc cgccgacgtg gaggagaaccc cggccccat gtctaaact 900
gcctccctg accccgcctg gaacaccacc ctgtctatctt ggggtgtct cttdtcctg 960
ggaacaagg t cagcaattc tgggggtgtc cagtcctcaaa gatacataat caaaggaaag 1020
ggagagatgg ccattcttaaa atgttattccc atctctggac atctctctgt ggcctggat 1080
caacagactc aggggcaggaa actaaaggttt ttcattcage attatgataa aatggagaga 1140
gataaaggaa acctgcccacg cagatctca gtccaaacagt ttgtatgacta tcactctcg 1200
atgaacatga gtgccttggaa gctagaggac tctgcctgtt acttctgtgc cagctcttc 1260
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gatctggaaa atgtgactcc acccaagggtc tccttggatgg agccatcaaa agcagagatt 1380
gcaacaaac aaaaggctac cctctgtgc ttggccagggg gtttctccc tgaccacgtg 1440
gagctgagct ggtgggtgaa ttggcaaggag gtccacacgtt ggggtcagcac ggaccctcg 1500
gcctacaagg agagaattt tagctactgc ctgagcagcc gcctgagggt ctctgttacc 1560
ttctggcaca atccctgcaaa ccacttcggc tgccaaatgtgc agttccatgg gtttcaagag 1620
gaggacaatgtt ggcccgagggtt ctcacccaaa cctgtcacaac agaacatcag tgccaggccc 1680
ttggggcccgag cagactgtgg gattacctca gcatcttatac aacaagggtt ctgtctgc 1740
accatctct atgagatccct gctaggaaa gcaaccctgt atgtgtgtc tgcgttaca 1800
ctggctgtga tggctatggt caaaagaaaat tttcatga 1839

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SEQ ID NO: 164      moltype = DNA length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic
source            1..15
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 164
accaccaatgaa ggagt                                         15

SEQ ID NO: 165      moltype = DNA length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic
source            1..15
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 165
ttggcttcgtt gaaac                                         15

SEQ ID NO: 166      moltype = DNA length = 39
FEATURE           Location/Qualifiers
misc_feature      1..39
note = Synthetic
source            1..39
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 166
gctgctgact cttcgaacac gggttaccag aacttcttat                                         39

SEQ ID NO: 167      moltype = DNA length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic
source            1..15
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 167
tctggacatc tctct                                         15

SEQ ID NO: 168      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
note = Synthetic
source            1..18
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 168

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cattatgata aaatggag	18
SEQ ID NO: 169 moltype = DNA length = 39	
FEATURE Location/Qualifiers	
misc_feature 1..39	
note = Synthetic	
source 1..39	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 169	
ggcagcttc tcacagatcc gctagactcc gactacacc	39
SEQ ID NO: 170 moltype = DNA length = 399	
FEATURE Location/Qualifiers	
misc_feature 1..399	
note = Synthetic	
source 1..399	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 170	
atgcagagga acctggggc tgcagattt ctgggtgaga 60	
ggggatcagg tggagcacag tccttcagcc ctgagctcc acgaggaaac cgattctgt 120	
cttgatcga attttacgac caccatggg agtgtgcagt ggttccgaca gaattccagg 180	
ggcagctca tcagttgtt ctacttggc tcaggaacaa aggagaatgg gaggttaaag 240	
ttagttttt attctaaggc gcccgcgtac agcaccctgc acatcaggga tgccagctg 300	
gaggactcg gacttactt ctgtgtctgt gactcttcga acacgggtta ccagaacctc 360	
tatccatggaa aaggaaacaaat ttgtactgtc attccaaac 399	
SEQ ID NO: 171 moltype = DNA length = 429	
FEATURE Location/Qualifiers	
misc_feature 1..429	
note = Synthetic	
source 1..429	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 171	
atgtctaaca ctgccttccc tgacccgcc tggAACACCA ccctgtatc ttgggttgc 60	
ctttttcc tcggaaacaag ttccagaaat tctgggttgc tccagttccc aagatacata 120	
atcaaaggaa agggagaaag gtccatttc aaatgttattt ccatcttgg acatctct 180	
gtggccttgc atcaacacag tcaggccgcg gaactaaatg tccatttcgc gcattatgt 240	
aaaatggaga gagataaagg aaacctgccc agcagatttc cagtcacaca gtttgatgac 300	
tatcactctg agatgaacat gatgtccctt gagcttagagg actctgcgt gtacttctgt 360	
gcccgcgttc tcacagatcc gctagactcc gactacacct tcggctcagg gaccaggctt 420	
ttggtaataa 429	
SEQ ID NO: 172 moltype = DNA length = 807	
FEATURE Location/Qualifiers	
misc_feature 1..807	
note = Synthetic	
source 1..807	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 172	
atgcagagga acctggggc tgcagattt ctgggtgaga 60	
ggggatcagg tggagcacag tccttcagcc ctgagctcc acgaggaaac cgattctgt 120	
cttgatcga attttacgac caccatggg agtgtgcagt ggttccgaca gaattccagg 180	
ggcagctca tcagttgtt ctacttggc tcaggaacaa aggagaatgg gaggttaaag 240	
ttagttttt attctaaggc gcccgcgtac agcaccctgc acatcaggga tgccagctg 300	
gaggactcg gacttactt ctgtgtctgt gactcttcga acacgggtta ccagaacctc 360	
tatccatggaa aaggaaacaaat ttgtactgtc attccaaac 420	
gtgttaccatc taaaatgtcc tcggctcagg gacagacccc tctgcctttt caccgactt 480	
gactcccaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcatcac tgacaaaact 540	
gtgtctggaca tgaaagctat ggatccaag agcaatgggg ccattgcctg gagcaaccag 600	
acaagcttca ctcggcaaga tatccatcaa gagaccaacg ccacccatccc cagttcagac 660	
gttccctgtc atgcccacgtt gaccggaaaa agctttgaaa cagatgtaaa cctgaaacctt 720	
caaaacctgtt cttttatggg actccaaatc ctcctgtca aagtagcggg atttaacctg 780	
ctcatgacgc tgaggctgtc gtccatgtc 807	
SEQ ID NO: 173 moltype = DNA length = 951	
FEATURE Location/Qualifiers	
misc_feature 1..951	
note = Synthetic	
source 1..951	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 173	

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atgtctaaca ctgcctccc tgaccccgcc tggAACACCA ccctgtatc ttgggttgc 60
cttttccctc tgggaacaag ttcaGAAAT tcTGGGTTG tccAGTCCTC aAGATACTA 120
atcaaaggaa agggagaaag gtccATTCTA aaATGTATTC cCATCTCTGG acATCTCT 180
gtggcctggt atcaacagac tcAGGGCAG gaACTAAAGT tCTTCATCTA gcATTATGAT 240
aaaatggaga gagataaagg aaACCTGCCD agcAGATTCT cAGTCCAACA gTTGTATGAC 300
tatcaCTCG agatGAACAT gagTGCCCTG gagCTAGAGG acTCTGCGT gtACTTCGT 360
gccAGCTCTC tcACAGATCC gCTAGACTCC gACTACACCT cTGGCTCAAGG gACCAGGCT 420
ttggtaatAG aggATCTGAG aaATGTACT ccACCCAAAGG tCTCCTGTT tgAGCCATCA 480
aaAGCAGAGA ttGCAACAA aCAAAGGCT acCCTGTGT gTTGGCCAG gGGCTCTC 540
cCTGACCCAGC tggAGCTGAG ctggTGGGTG aATGGCAAGG agGTCCACAG tggGGTCAAG 600
acggACCCCTC aggCCCTAGG ggAGAGAAAT tATAGTACT GCTGTAGAGC cCGCTGAGG 660
gttCTGCTGA cTTCTGGCA caATCCTCGO aACCACTCC GCTGCAAGT GCAgTCCAT 720
gggCTTCAG aggAGGACAA gtggCCAGAG ggCTCACCCA aACCTGTCAc ACAGAACATC 780
agtGCAAGGG CTCGGGGCCG agCAAGACTGT gggATTACCT cAGCATCTA tcaACAAAGG 840
gttCTGCTG cACCATCTC CTATGAGATC CTGCTAGGG AAGCCACCT GTATGCTGT 900
cttGCTAGTA cACTGCTGTG gATGCTATG gTCAAAGAGA AGAATTCTATG A 951

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SEQ ID NO: 174 moltype = DNA length = 408
FEATURE Location/Qualifiers
misc_feature 1..408
note = Synthetic
source 1..408
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 174
atccagaacc cagaacCTGC tGTGTACCG taaaaAGATC cTCGGTCTCA ggACAGCACC 60
cttgcctgt tcaCCGCTGT tgactCCAA atcaATGTGT CGAAAAACCAT ggaATCTGGA 120
acgttcatca tcgacAAACAC tGTGTGGAC atgAAAGCTA tgGATTCAA gAGCAATGGG 180
gccattgcct ggAGCAACCA gacaAGCTC acCTGCCAAG atATCTCAA agAGACCAAC 240
gccacCCtAC CCAGTTCAGA cgttCCCTGT gatGCCACGT tgACCGAGAA aAGCTTGAA 300
acagatATGA acCTAAACCT tcaAAACCTC tcaGTTATGG gACTCCGAAT CCTCTGCTG 360
aaAGTAGCGG gATTTAACCT gCTCATGACG ctGAGGCTGT gGTCCAGT 408

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SEQ ID NO: 175 moltype = DNA length = 522
FEATURE Location/Qualifiers
misc_feature 1..522
note = Synthetic
source 1..522
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 175
gaggatGTGA gaaATGTGAC tCCACCCAAg gtCTCCTGTG ttGAGCCATC AAAAGCAGAG 60
attGCAACAA aACAAAGGAC tacCCCTCGTG tgCTTGGACCG ggggCTCTT CCCTGACAC 120
gtggAGGTGA gGTGGGGGTG gaATGGCAAG gAGGTCCACCA gTGGGGTCAg cACGGACCT 180
caggCCtACCA aggAGGACAA ttATAGCTAC tgCTGAGACCA gCCGCTCTGAG gGTCTCTGT 240
acCTTCTGGC aCAATCCTCG caACCACCTC CGCTGCCAAG tgCAGTTCA tgGGCTTCA 300
gaggAGGAGA atGGGGCAGA gggCTCACCC AACACCTGTCA cacAGAACAT cAGTGCAGAG 360
gcCTGGGGCC gAGCAGACTG tgGGGATTACO tcaGCTACCTC atcaACAAAGG gGTCTTGT 420
gcACCCATCC tCTATGAGAT CTCGCTAGGG AAAGCCACCC tGTATGCTGT gTTGTCAgT 480
acactGGTGG tgATGGCTAT gGTCAAAGAGA aAGAATTCTATG A 522

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SEQ ID NO: 176 moltype = DNA length = 1818
FEATURE Location/Qualifiers
misc_feature 1..1818
note = Synthetic
source 1..1818
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 176
atgaAGACGG tgACTGGACC ttGTTCTCTG tgCTTCTGGC tgCAGCTGAA ctGTGTGAGC 60
agAGGCGAGC agGTGGAGCA gCGCCCTCT cacCTGAGTG tCCGGGAGGG agACAGTGCC 120
gttATCACCT GCACTTACAC agACCTAAC agTTATTACT tCTTCTGGTA caAGCAAGAG 180
ccggggggAA gTCTTCAgTT gCTTATGAAG gTTTCTCAA gTACGGAAAT AAACGAAGGA 240
caaggGATCA ctGTGCTACT gaACAAAGAAA gACAAACGAC tCTCTCTGAA CCTCACAGGT 300
gcccACATCTG gggACTCAGC cCGCTACTTG tgCGCAGTCA tgGGGGGAGC TAACAGTGCA 360
ggGAACAAAGC taACTTTGGG aTTGGAAACC agGGGTGTG TGAGGCCAGA CATCCAGAAC 420
ccAGAACCTG CTGTGTACCA gTTAAAGAT CCTCGGTCTC AGGACAGCAC CCTCTGCTG 480
ttcAccGACT ttGACTCCCA aATCAATGTG CGAAACACCA TGGAACTGG AACGTTCTAC 540
actGACAAA ctGTGTGAGC catGAAAGCT atGGATTCGA AGAGCAATGG ggCCATTGCC 600
tggAGCAACC agACAGACTT cacCTGCCAA gATATCTCA aAGAGACAA CGCCACCTAC 660
cccAGTCTAG acGTTCTCTG tgATGCCACG ttGACCGAGA AAAGCTTGA AACAGATAG 720
aacCTAAACT ttCAAACCTC GTCAGTTATG GGACTCCGAA tCTCTCTGT gAAAGTAGCG 780
ggATTTAACC tgCTCATGAC gCTGAGGCTG tgGTCCAGTC gggCCAAGCG gTCCGGATCC 840
ggAGGCAACCA actTCAGCTC GCTGAAGCAG gCCGGCAGAC tgGAGGAGAA CCCGGCCCC 900
atGGGCTGTA ggCTCTAAG ctGTGTGGCC tCTGCTCTC tgGGAATAGG CCCTTGGAG 960
acggCTGTT tCCAGACTCC AAACATCTATC GTCACACAGG TGGAAATGA AGTGTCTTC 1020

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aattgtaaagc aaactctggg ccacgatact atgtattggg acaaggaaa ctctaagaaa 1080
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aggcgcttct cacctcagtc ttcaaaaa gtcatttga atcttcgaat caagtctgt 1200
gagccggagg actctgtgt gtatctctgt gccagcagtc gggactgggg gcctgctgag 1260
cagttcttcg gaccaggac acgactcacc gtcctagagg atctgaaaaa tgtgactcca 1320
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ctcgctgtgt tggccagggg cttttcctt gaccacgtgg agctgagctg gtgggtgaat 1440
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agctactgc tgagcagccg cttgggggtc tctgtactt tctggcacaac tcctcgaac 1560
cacttccgtt gccaatgtca gttccatggg ctttcagagg aggacaatgg gccaaggggc 1620
tcacccaaatc otgtcacaca gaacatcgtt gcaaggccctt gggggcggc agactgtgg 1680
atcaacttcg catcttcatca tcagggggtt ctgtctcaaa ccattctta tgagatctta 1740
ctggggaaagg ccaccctata tgctgtgtgt gtcagtgccc ttgtgtgtat ggccatggtc 1800
aagaaaaaaaaa attcctga 1818

SEQ_ID NO: 177      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
note = Synthetic
source            1..18
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 177
gaccctaaca gttattac 18

SEQ_ID NO: 178      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic
source            1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 178
gttttctcaa gtacggaaat a 21

SEQ_ID NO: 179      moltype = DNA length = 48
FEATURE           Location/Qualifiers
misc_feature      1..48
note = Synthetic
source            1..48
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 179
tgcgcaagtca gtggaggggac taacagtgc gggacaacaac taactttt 48

SEQ_ID NO: 180      moltype = DNA length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic
source            1..15
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 180
ctggggccacg atact 15

SEQ_ID NO: 181      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
note = Synthetic
source            1..18
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 181
tacaataata agcaactc 18

SEQ_ID NO: 182      moltype = DNA length = 42
FEATURE           Location/Qualifiers
misc_feature      1..42
note = Synthetic
source            1..42
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 182
tgtgccagca gtcggggactg ggggcctgt gaggcgttct tc 42

SEQ_ID NO: 183      moltype = DNA length = 411

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FEATURE          Location/Qualifiers
misc_feature    1..411
                  note = Synthetic
source          1..411
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 183
atgaagacgg tgactggacc tttgttcctg tgcttctggc tgcagctgaa ctgtgtgagc 60
agaggcgagc aggtggagca ggcgcctct cacctgagtg tccgggaggg agacagtgcc 120
gttataccct gcacctacac agaccctaa acgttattact tttctggta caagcaagag 180
ccggggccaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga 240
caaggattca ctgtctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct 300
gcgcattctg gggactcagc cgctacttc tgcgactcgtca gtggaggggac taacagtgc 360
gggaacaacg taacttttg aatttggacc agggtgtctgg tcaggccaga c 411

SEQ_ID NO: 184      moltype = DNA length = 399
FEATURE          Location/Qualifiers
misc_feature    1..399
                  note = Synthetic
source          1..399
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 184
atgggctgtaa ggctcctaag ctgtgtggcc ttctgcctct tggaaatagg ccctttggag 60
acggctgttt tccagactcc aaactatcat gtcacacagg tggaaatga agtgtcttc 120
aatttgaacg aaactctggg ccacgatact atgttattgtt acaagcaaga ctctaagaaa 180
ttgctgaaga ttatgttag ctacaataat aagcaactca ttgtaaacga aacagtccca 240
aggcgcttcc caccctcgtc ttcaaaaaa gtcatttga atcttcgaat caagtctgt 300
gagccggagg actctgtctgt gtatctctgt gccagcgtc gggactgggg gcctgctgag 360
cagttcttcg gaccaggac acgactcacc gtccttagag 399

SEQ_ID NO: 185      moltype = DNA length = 819
FEATURE          Location/Qualifiers
misc_feature    1..819
                  note = Synthetic
source          1..819
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 185
atgaagacgg tgactggacc tttgttcctg tgcttctggc tgcagctgaa ctgtgtgagc 60
agaggcgagc aggtggagca ggcgcctct cacctgagtg tccgggaggg agacagtgcc 120
gttataccct gcacctacac agaccctaa acgttattact tttctggta caagcaagag 180
ccggggccaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga 240
caaggattca ctgtctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct 300
gcgcattctg gggactcagc cgctacttc tgcgactcgtca gtggaggggac taacagtgc 360
gggaacaacg taacttttg aatttggacc agggtgtctgg tcaggccaga catccagaac 420
ccagaaacctt ctgtgtacca gttaaaaatg ctctcggttcc aggacacac cctctgcctg 480
ttcaccactt tgacttccca aatcaatgtg cgaaaaaccca tggaaatctgg aacgttcatc 540
actgacaaaa ctgtgtgg aatcaatgtg atggatttca agagcaatgg ggccatttgc 600
tggagcaacc agacaagctt cacctgcca gatatcttca aagagaccaa cgccacctac 660
cccaagttcag acgttccctg tgatggccacg ttgaccgaga aagctttga aacagatatg 720
aacctaaact ttcaaaacct gtcagttatg ggactccac tctctctgt gaaagttagcg 780
ggattnaacc tgctcatgac gctggggctg tggccagt 819

SEQ_ID NO: 186      moltype = DNA length = 918
FEATURE          Location/Qualifiers
misc_feature    1..918
                  note = Synthetic
source          1..918
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 186
atgggctgtaa ggctcctaag ctgtgtggcc ttctgcctct tggaaatagg ccctttggag 60
acggctgttt tccagactcc aaactatcat gtcacacagg tggaaatga agtgtcttc 120
aatttgaacg aaactctggg ccacgatact atgttattgtt acaagcaaga ctctaagaaa 180
ttgctgaaga ttatgttag ctacaataat aagcaactca ttgtaaacga aacagtccca 240
aggcgcttcc caccctcgtc ttcaaaaaa gtcatttga atcttcgaat caagtctgt 300
gagccggagg actctgtctgt gtatctctgt gccagcgtc gggactgggg gcctgctgag 360
cagttcttcg gaccaggac acgactcacc gtccttagag atctgagaaa tggactcca 420
cccaaggtct ctttggat gccatcaaaa gcaagatgg caaacaacaa aaaggctacc 480
ctctgtgtct tggccagggg ctcttcctt gaccacgtgg agctgagctg gtgggttcaat 540
ggcaaggagg tccacacgtgg ggtcagacgac gaccctcagg ctatcaagga gagcaattat 600
agctactgca tgacgacggc cctgagggtc tctgtctact tctggcacaac tcctcgaaac 660
cacttccgct gccaagtgc gttccatggg ctttcagagg aggacaaatg gccagaggcc 720
tcacccaaac ctgtcacaca gaacatcgt gcaaggccat gggccgagc agactgtgg 780
atcaacttcacatcata tcagggggtt ctgtctgcaaa ccacatctca tgagatctca 840

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ctgggaaagg ccaccata tgcgtgctg gtcagtgcc tggtgctgat ggccatggc 900
aagaaaaaaa attcctga                                         918

SEQ ID NO: 187      moltype = DNA  length = 408
FEATURE           Location/Qualifiers
misc_feature      1..408
                   note = Synthetic
source            1..408
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 187
atccagaac cagaacctgc tgtgttaccag taaaagatc ctgggtctca ggacagcacc 60
ctctgcgtgt tcacccactt tgactccaa atcaatgtgc cgaaaaccat ggaatctgga 120
acgttcatca ctgacaaaac ttgtgtggac atgaaagctc tggatccaa gagcaatggg 180
gccattgcctt gggacaacca gacaagttc acctgccaag atatcttcaa agagccaac 240
gccacccatcc ccagttcaga cgttccctgt gatgccactg tgaccgagaa aagcttgaa 300
acagatatga acctaaacctt tcaaaccctg tcagttatgg gactccgaat cctcctgctg 360
aaagttagcg gatttaaacct gctcatgacg ctgaggctgt ggtccactg 408

SEQ ID NO: 188      moltype = DNA  length = 519
FEATURE           Location/Qualifiers
misc_feature      1..519
                   note = Synthetic
source            1..519
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 188
gatctgagaa atgtgactcc acccaaggtc tccttgtttt agccatcaaa agcagagatt 60
gcaaacaac aaaaggctac cctctgtgc ttggccaggg gcttcttccc tgaccacgtg 120
gagctgagct ggtgggtgaa tggcaaggag gtccacagtgg gggtcagcac ggaccctcag 180
gccttacaaagg agagcaattt tagetactgc ctgagcagcc gcctgaggg ctctgttacc 240
tttctggcaca atccctcgaaa ccacttccgc tgccaaatgc agttccatgg gctttcagag 300
gaggacaagt ggcacagaggc ctacccaaa cctgtcacac agaacatcag tgcaagggcc 360
tggggcccgag cagactgtgg aatcaattca gcatcctatc atcagggggt tctgtctgca 420
accatctct atgagatctt actggggaaag gccacccat atgctgtgt ggtcagtggc 480
ctgggtgtga tggccatggt caagaaaaaa aattcctgtg 519

SEQ ID NO: 189      moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
                   note = Synthetic
source            1..18
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 189
aatgatatgt ttgactat                                         18

SEQ ID NO: 190      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
                   note = Synthetic
source            1..21
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 190
gtacgctcaa atgtggataa g                                         21

SEQ ID NO: 191      moltype = DNA  length = 45
FEATURE           Location/Qualifiers
misc_feature      1..45
                   note = Synthetic
source            1..45
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 191
tgcgcgacg gttgacagtgg aggcaaat tacaactga cattt                                         45

SEQ ID NO: 192      moltype = DNA  length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
                   note = Synthetic
source            1..15
                   mol_type = other DNA
                   organism = synthetic construct
SEQUENCE: 192
aatacgccaca actac                                         15

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SEQ ID NO: 193      moltype = DNA  length = 18
FEATURE          Location/Qualifiers
misc_feature      1..18
source            note = Synthetic
                  1..18
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 193
tcatatggtg ctggcaac                                         18

SEQ ID NO: 194      moltype = DNA  length = 42
FEATURE          Location/Qualifiers
misc_feature      1..42
source            note = Synthetic
                  1..42
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 194
tgtgccagcg cgagctgggg gggctatgtc gagcagtct tc                                         42

SEQ ID NO: 195      moltype = DNA  length = 423
FEATURE          Location/Qualifiers
misc_feature      1..423
source            note = Synthetic
                  1..423
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 195
atgactggct tcctgaaggc cttgtgttg gttctgtgcc tgccggccaga atggataaaag 60
agtcaacaga agactggtg ccagcaagtt aaacaaaagct ctccatcgct gactgttcaa 120
ggggggggg tattgtatcc gaattgtat tacgagaatg atatgttta ctatggcc 180
tggtacaaaa aataccctga caacagcccc acactctgtatccgtacg ctcaaatgtg 240
gataagaggg aagacggaaag attcacagtt ttcttgaaca aaagcggcaa acacttc 300
ctgcacatca cagccccc gcctgaagac acagcagtgt acctctgcgc agcagggtac 360
agtggggcca gcaattacaa actgacattt gggaaaggaa ctctttaac tgtgacttca 420
aac                                         423

SEQ ID NO: 196      moltype = DNA  length = 393
FEATURE          Location/Qualifiers
misc_feature      1..393
source            note = Synthetic
                  1..393
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 196
atggggctcca ggctctttct ggttttggc ctccctgtgtca caaaacacat ggaggctgca 60
gtcacccaaa gccttagaaa caagggtgaca gtaacaggaa gaaacgtgac attgagctgt 120
cgccagacta atagccacaa ctatgtac tggtgcggc aggacactgg gcatggctg 180
aggctgtatcc attactcata tggtgcggc aaccttcaaa taggagatgt ccctgtatgg 240
tacaaggccca ccagaacaac gcaagaagac ttcttctcc tgctggaaatt ggcttctcc 300
tctcagacat ctttgtatcc ctgtgcggc gcgagctggg gggctatgc tgagcgttca 360
ttccggccagg ggacacgact caccgttca gag                                         393

SEQ ID NO: 197      moltype = DNA  length = 831
FEATURE          Location/Qualifiers
misc_feature      1..831
source            note = Synthetic
                  1..831
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 197
atgactggct tcctgaaggc cttgtgttg gttctgtgcc tgccggccaga atggataaaag 60
agtcaacaga agactggtg ccagcaagtt aaacaaaagct ctccatcgct gactgttcaa 120
ggggggggg tattgtatcc gaattgtat tacgagaatg atatgttta ctatggcc 180
tggtacaaaa aataccctga caacagcccc acactctgtatccgtacg ctcaaatgtg 240
gataagaggg aagacggaaag attcacagtt ttcttgaaca aaagcggcaa acacttc 300
ctgcacatca cagccccc gcctgaagac acagcagtgt acctctgcgc agcagggtac 360
agtggggcca gcaattacaa actgacattt gggaaaggaa ctctttaac tgtgacttca 420
aacatccaga acccagaacc tgctgtgtac cagttaaaatg atccctcggtc tcaggacagc 480
accctctgcg tggcacccga ctttgactcc caaatcaatg tgccgaaaac catggatct 540
ggaacgttca tcaactgacaa aactgtgtg gacatgaaag ctatggattc caagggaaat 600
ggggccattt gctggagca ccagacaago ttccacgttcc aagatatctt caaagggacc 660
aacggccacct accccagttc agacgttccc tggtatgcca cgttgaccga gaaaagctt 720
gaaacagata tgaacctaaa ctttcaaaac ctgtcagttt tgggactcgg aatcctctg 780
ctgaaagttag cgggatttaa cctgtctatg acgctggc tggtggccatg t                                         831

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SEQ ID NO: 198      moltype = DNA length = 912
FEATURE           Location/Qualifiers
misc_feature      1..912
source            note = Synthetic
                  1..912
mol_type          mol_type = other DNA
organism          organism = synthetic construct

SEQUENCE: 198
atggggctcaa ggcttttctt ggttttgcg ctccctgtgt caaaacacat ggaggctgca 60
gtcacccaaa gcccataaaa caaggtgaca gtaacaggaa gaaacgtgac attgagctgt 120
cgccagacta atagccacaa ctatcatgtac tggatccggc aggacactgg gcatggctg 180
aggctgtatcc attactcata tggatccggc aaccttcaaa taggagatgt ccctgtatggg 240
tacaaggcoca ccagaacaac gcaagaagac ttcttcctcc tgctggaaatt ggcttctccc 300
tctcagacat ctttgtactt ctgttgccggc gcgagctggg ggggctatgc tgagcaggte 360
ttccggaccac ggacacgact caccgttca gaggatgtga gaaatgtgac tccacccaag 420
gtctccttgc ttgagccatc aaaaggcagag attgcaaaaca aacaaaaggc taccctcg 480
tgcttgcaca ggggttctt ccctggccatc gtggagctga gctgggtggt gaatggcaag 540
gagggtccaca tggggtttagc cacggaccatc cagggccatc aggagagcaa ttatagctac 600
tgccctgtggc gcccgttgcgatc ggttctgtc accttctggc aacatcttcg aaaccatcc 660
cgctgccaag tgcagttca tgggtttca gaggaggaca agtggccaga gggctcaccc 720
aaacctgtca cacagaacatc caglgcagag gcttggggcc gaggcagactg tggaaatcact 780
tcagcattctt atcatcaggg ggttctgtct gcaaccatcctt cttatgagat cctactggg 840
aaggccaccc tataatgtgt gctgttgc ggcctgttgc tgatggccat ggtcaagaaa 900
aaaaattctt ga 912

SEQ ID NO: 199      moltype = DNA length = 408
FEATURE           Location/Qualifiers
misc_feature      1..408
source            note = Synthetic
                  1..408
mol_type          mol_type = other DNA
organism          organism = synthetic construct

SEQUENCE: 199
atcccagaacc cagaacactgc tttgttaccat taaaagatc ctcggtctca ggacagcacc 60
ctctgcctgt tcaccgttgc tttactccaa atcaatgtc cgaaaaccat ggaatctgg 120
acgttcatca ctgacaaaac tttgtgtggac atgaaagcttca tggattccaa gagaaatggg 180
ggcattgttgcgatc gggcaacca gacaagcttc acctggcaag atatcttcaaa agagaccaac 240
ggccacccatcc ccagttcaga ctttttttttgcgatc gtttttttttgcgatc aagtttttggaa 300
acagatgttca accttttttttgcgatc ttttttttttgcgatc gtttttttttgcgatc 360
aaatgttgcgatc gtttttttttgcgatc gtttttttttgcgatc 408

SEQ ID NO: 200      moltype = DNA length = 519
FEATURE           Location/Qualifiers
misc_feature      1..519
source            note = Synthetic
                  1..519
mol_type          mol_type = other DNA
organism          organism = synthetic construct

SEQUENCE: 200
gttctgtggaaatcgttactcc accaaagggtc ttcttgggtttt agccatcaaa agcagagatt 60
gcaaaacaaac aaaaggctac cctctgtgtc ttggccaggag gtttcttccc tgaccacgtg 120
gagctgtggact ggttgggtgaa tggcaaggag qttccacatq gggtaacgac gggccctcag 180
gcttacaagg agagcaattt tagtactgc ctgagcggc gcttgggggt ctctgttacc 240
tttctggcaca atccctcgaaa ccacttccgc tgccaaatgtc agttccatgg gctttcagag 300
gaggacaatgttccacccaa ctttttttttgcgatc gtttttttttgcgatc ttttttttttgcgatc 360
ttggggccggcagactgtgg aatacttca gtttttttttgcgatc atcagggggt ttttttttttgcgatc 420
accatcttctt atgagatctt actggggaaag gtttttttttgcgatc atgctgtgt ggttgcgatc 480
ctgggtgttgcgatc ttttttttttgcgatc caaaaaaaaaa aatcccttgcgatc 519

SEQ ID NO: 201      moltype = AA length = 605
FEATURE           Location/Qualifiers
REGION            1..605
source            note = Synthetic
                  1..605
mol_type          mol_type = protein
organism          organism = synthetic construct

SEQUENCE: 201
MKTVTGPLFL CFWLQLNCSV RGEQVEQRPP HLSVREGDSA VITCTYTDPN SYYFFWYKQE 60
PGASLQLLMK VFSSSTEINEG QGFTVLLNNK DKRLSLNLTA AHPGDSAAVF CAVSGGTNSA 120
GNKLTFGIGT RVLVRPDIQN PEPAVYQLKD PRSQDSTLCL FTDFDSQINV PKTMESGTFI 180
TDKTVLDMKA MDSKSNGAIA WSNQTSFTCQ DIFKETNATY PSSDVPCDAT LTEKSFETDM 240
NLNFQNLNSVM GLRILLLKVA GFNLLMLTRL WSSRAKRSGS GATNFSSLKQ AGDVEENPGP 300
MCGRLLSCVA FCLLGIGPLE TAVFQTPNYH VTQVGNEVSF NCKQTLGHDT MYWYKQDSKK 360
LLKIMFSYNN KQLIVNETVP RRFSPOSSDK AHLNLRIKSV EPEDSAVYLC ASSRDWGPAAE 420
QFFGPGTRLTL VLEDLRNVTP PKVSLFEPSK AEIANKQKAT LVCLARGFFP DHVELSWWN 480

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GKEVHSGVST DPQAYKESNY SYCLSSRLRV SATFWHNPRN HFRCQVQFHG LSEEDKWPEG SPKPVTQNIS AEAWGRADCG ITSASYHQGV LSATILYIEL LGKATLYAVL VSGLVLMAMV KKKNS	540 600 605
 SEQ ID NO: 202                    moltype = DNA length = 1824	
FEATURE                        Location/Qualifiers	
misc_feature                1..1824	
note = Synthetic	
source                        1..1824	
mol_type = other DNA	
organism = synthetic construct	
 SEQUENCE: 202	
atgactggct tcctgaaggc cttgtgttg gttctgtgcc tgccggccaga atggataaag 60	
agtcaacaga agactggctt ccacaaaggctt aaacaaaggctt ctccatcgactgttcaa 120	
gaggggaggat tattgtatc gaattgtatc tacgagaatg atatgttgcatccttgc 180	
tggtacaaaa aataccctga caacaccccc acacttcgttatccgtacg ctcaaatgt 240	
gataagaggaa aagacggaaat attcacagtt ttcttgcaca aagacggccaa acacccatca 300	
ctgcacatca cagccatccc gcctgaaagc acacggatgtt acctctgcgc acggatgt 360	
agtggaggaa gcaatttacaa actgacattt gggaaaggat ccctcttaac tttttttttt 420	
aacatccaga accccagaacc tggctgtatc cttccatccgc tcaggacacg 480	
accctctgc ttgttccaccgc ctttgcacttccaaatcaatg tgccggaaaac catggatct 540	
gaaacgcgttca tcaactgttca aactgtgtgcg gatcatgaaatg ctatggatcc caagacaaat 600	
ggggccatttgcg cttggggatcc ccacacaatgcg ttcacctgcg aatggatctt caaaggagacc 660	
aacggccacccatccggatcc acacgttccgc acatggatccgc tttttttttt 720	
gaaacacata tgaacctaaa ctttccaaatc ctgtcgtatc tggggactccg aatctctcg 780	
ctgaaatgttgcgggatccatccgc acgctgtatc acggatgttgcg tttttttttt 840	
cgggtccggatccggggatccacaaatccgc acatggatccgc acggatgttgcg tttttttttt 900	
aaccccccggccatccggatccacaaatccgc acatggatccgc acggatgttgcg tttttttttt 960	
atggaggcttgc acgttccatccgc aacaaaggatgc acatggatccgc acggatgttgcg tttttttttt 1020	
acattgtatcgttgc acatggatccgc aacaaaggatgc acatggatccgc acggatgttgcg tttttttttt 1080	
ggggcatggccatccggatccatccgc acatggatccgc acggatgttgcg tttttttttt 1140	
gtccctgtatcgttgc acatggatccgc acggatgttgcg tttttttttt 1200	
tttgcttccttccttcagac atctttgtatc ttttgcgcgacggccggccgcgatggatccgc 1260	
gctgagatgttgc acatggatccgc acggatgttgcg tttttttttt 1320	
actcccccacatggatccgc acatggatccgc acggatgttgcg tttttttttt 1380	
gctaccctcgatccatccgc acatggatccgc acggatgttgcg tttttttttt 1440	
gtgaatggatccatccgc acatggatccgc acggatgttgcg tttttttttt 1500	
aattatgtatcgttgc acatggatccgc acggatgttgcg tttttttttt 1560	
cggaaacacttccatccgc acatggatccgc acggatgttgcg tttttttttt 1620	
gagggatccatccgc acatggatccgc acggatgttgcg tttttttttt 1680	
tgttgcatccatccgc acatggatccgc acggatgttgcg tttttttttt 1740	
atccctacttgcg ggaaggccac cttatatgcgttgc acatggatccgc acggatgttgcg tttttttttt 1800	
atggatccatccgc acatggatccgc acggatgttgcg tttttttttt 1824	
 SEQ ID NO: 203                    moltype = AA length = 607	
FEATURE                        Location/Qualifiers	
REGION                        1..607	
note = Synthetic	
source                        1..607	
mol_type = protein	
organism = synthetic construct	
 SEQUENCE: 203	
MTGFLKALLVLCLRPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFA 60	
WYKKYPDNSPTLLISVRNSNDKREDGRFTVFLNKSGKHFSLHITASQPEDTAVYLCAAGD 120	
SGGSNNYKLTFGKGTLTTVTPNIQNPPEPAVYQLKDPRSODSTLCCLFTDFDSQINVPKTMES 180	
GTFITDKTVELDMKAMDSKSN GAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSF 240	
ETDMMLNLFQNL SVMGLRILLMLKAVGFNLLMLRLWSSRAK RSGSGATNFSLLKQAGDVEE 300	
NPGPMGSRLF LVLSLLCTKHMEAATQSPRNKVTVTGGNVTLSCRQTNSHNYMYWYRQDT 360	
GHGLRLLIHYSYGAGNLQIGDVPDGKATRTTQEDFFLILLELASPSQTSLYFCASASWGGY 420	
AEGFFGPGTRLTVLEDLRNVTPPKVSLFEPSKAEIANKQKATLVCLARGFPFDHVELSWW 480	
VNGKEVHSVGIVSTDPAQYKESNYSYCLSSRLRVSATFWHNPTRNHFRQVQFHGLSEEDKWP 540	
EGSPKPVTQNISAEAWGRACCGITSASYYHQGVLSATILYIEILLGKATLYA VLVSGLVLMA 600	
MVKKNS                        607	
 SEQ ID NO: 204                    moltype = AA length = 16	
FEATURE                        Location/Qualifiers	
source                        1..16	
mol_type = protein	
organism = Mus musculus	
 SEQUENCE: 204	
CAVSGGTNSA GNKLTF	16
 SEQ ID NO: 205                    moltype = AA length = 14	
FEATURE                        Location/Qualifiers	
source                        1..14	
mol_type = protein	

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SEQUENCE: 205          organism = Mus musculus
CASASWGGYA EQFF

SEQ ID NO: 206          moltype = AA length = 14
FEATURE
source
1..14
mol_type = protein
organism = Mus musculus

SEQUENCE: 206          moltype = AA length = 14
CTCSADRGAE TLYF

SEQ ID NO: 207          moltype = AA length = 15
FEATURE
VARIANT
9
note = Wherein X is alanine, arginine, asparagine,
aspartic acid, cysteine, glutamic acid, glutamine,
histidine, isoleucine, leucine, lysine, methionine,
phenylalanine, proline, serine, threonine, tryptophan,
tyrosine, or valine
source
1..15
mol_type = protein
organism = Mus musculus

SEQUENCE: 207          moltype = AA length = 15
CAADSSNTXY QNFYF

SEQ ID NO: 208          moltype = AA length = 133
FEATURE
source
1..133
mol_type = protein
organism = Mus musculus

VARIANT
116
note = Wherein X is alanine, arginine, asparagine,
aspartic acid, cysteine, glutamic acid, glutamine,
histidine, isoleucine, leucine, lysine, methionine,
phenylalanine, proline, serine, threonine, tryptophan,
tyrosine, or valine

SEQUENCE: 208
MQRNILGAVLG ILWVQICWVR GDQVEQSPSA LSLHEGTDSA LRCNFETTMR SVQWFRQNSR 60
GSLISLFLYLA SGTKENGRLK SAFDSKERRY STLHIRDAQL EDSGTYFCAA DSSNTXYQNF 120
YFGKGTSLTV IPN 133

SEQ ID NO: 209          moltype = AA length = 269
FEATURE
VARIANT
116
note = Wherein X is alanine, arginine, asparagine,
aspartic acid, cysteine, glutamic acid, glutamine,
histidine, isoleucine, leucine, lysine, methionine,
phenylalanine, proline, serine, threonine, tryptophan,
tyrosine, or valine
source
1..269
mol_type = protein
organism = Mus musculus

SEQUENCE: 209
MQRNILGAVLG ILWVQICWVR GDQVEQSPSA LSLHEGTDSA LRCNFETTMR SVQWFRQNSR 60
GSLISLFLYLA SGTKENGRLK SAFDSKERRY STLHIRDAQL EDSGTYFCAA DSSNTXYQNF 120
YFGKGTSLTV IPN 180
VLDMKAMDSK SNGAIAWSNQ TSFTCQDIFK ETNATYPSSD VPCDATLTEK SFETDMNLNF 240
QNL SVMGLRI LLLKVAGFNL LMTLRLWSS 269

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1. A method of producing a human cell, or population of human cells, expressing a TCR, the method comprising:

introducing a recombinant expression vector to a human cell, or a population of human cells, wherein the recombinant expression vector comprises a nucleotide sequence encoding a T cell receptor (TCR),

wherein the TCR has antigenic specificity for a mutated epitope presented by an HLA-A11 molecule, wherein the mutated epitope (a) comprises VVVGADGVGK (SEQ ID NO: 2) or (b) consists of VVVGAVGVGK (SEQ ID NO: 33) or VVGAVGVGK (SEQ ID NO: 35), and wherein the TCR comprises:

- (a) an  $\alpha$  chain complementarity determining region (CDR) 1 comprising the amino acid sequence of SEQ ID NO: 3, an  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 4, an  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 5, a  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 6, a  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 7, and a  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 8;
- (b) an  $\alpha$  chain CDR 1 comprising the amino acid sequence of SEQ ID NO: 125, an  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 126, an  $\alpha$  chain CDR3 comprising the amino acid

- sequence of SEQ ID NO: 127, a  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 128, a  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 129, and a  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 130;
- (c) an  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 137, an  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 138, an  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 139, a  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 140, a  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 141, and a  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 142;
  - (d) an  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 149, an  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 150, an  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 151, a  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 152, a  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 153, and a  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 154; or
  - (e) an  $\alpha$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 149, an  $\alpha$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 150, an  $\alpha$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 207, a  $\beta$  chain CDR1 comprising the amino acid sequence of SEQ ID NO: 152, a  $\beta$  chain CDR2 comprising the amino acid sequence of SEQ ID NO: 153, and a  $\beta$  chain CDR3 comprising the amino acid sequence of SEQ ID NO: 154.
- 2.** The method of claim 1, wherein the TCR comprises:
- (a) an  $\alpha$  chain variable region comprising the amino acid sequence of SEQ ID NO: 9 and a  $\beta$  chain variable region comprising the amino acid sequence of SEQ ID NO: 10;
  - (b) an  $\alpha$  chain variable region comprising the amino acid sequence of SEQ ID NO: 131 and a  $\beta$  chain variable region comprising the amino acid sequence of SEQ ID NO: 132;
  - (c) an  $\alpha$  chain variable region comprising the amino acid sequence of SEQ ID NO: 143 and a  $\beta$  chain variable region comprising the amino acid sequence of SEQ ID NO: 144;
  - (d) an  $\alpha$  chain variable region comprising the amino acid sequence of SEQ ID NO: 155 and a  $\beta$  chain variable region comprising the amino acid sequence of SEQ ID NO: 156; or
  - (e) an  $\alpha$  chain variable region comprising the amino acid sequence of SEQ ID NO: 208 and a  $\beta$  chain variable region comprising the amino acid sequence of SEQ ID NO: 156.
- 3.** The method of claim 1, wherein the TCR further comprises:
- (a) an  $\alpha$  chain constant region comprising the amino acid sequence of SEQ ID NO: 13 and a  $\beta$  chain constant region comprising the amino acid sequence of SEQ ID NO: 14;
  - (b) an  $\alpha$  chain constant region comprising the amino acid sequence of SEQ ID NO: 135 and a  $\beta$  chain constant region comprising the amino acid sequence of SEQ ID NO: 136;
  - (c) an  $\alpha$  chain constant region comprising the amino acid sequence of SEQ ID NO: 147 and a  $\beta$  chain constant region comprising the amino acid sequence of SEQ ID NO: 148; or
  - (d) an  $\alpha$  chain constant region comprising the amino acid sequence of SEQ ID NO: 159 and a  $\beta$  chain constant region comprising the amino acid sequence of SEQ ID NO: 160.
- 4.** The method of claim 1, wherein the TCR comprises:
- (a) an  $\alpha$  chain comprising the amino acid sequence of SEQ ID NO: 11 and a  $\beta$  chain comprising the amino acid sequence of SEQ ID NO: 12;
  - (b) an  $\alpha$  chain comprising the amino acid sequence of SEQ ID NO: 133 and a  $\beta$  chain comprising the amino acid sequence of SEQ ID NO: 134;
  - (c) an  $\alpha$  chain comprising the amino acid sequence of SEQ ID NO: 145 and a  $\beta$  chain comprising the amino acid sequence of SEQ ID NO: 146;
  - (d) an  $\alpha$  chain comprising the amino acid sequence of SEQ ID NO: 157 and a  $\beta$  chain comprising the amino acid sequence of SEQ ID NO: 158; or
  - (e) an  $\alpha$  chain comprising the amino acid sequence of SEQ ID NO: 209 and a  $\beta$  chain comprising the amino acid sequence of SEQ ID NO: 158.
- 5.** The method of claim 1, wherein the TCR has antigenic specificity for the mutated epitope comprising VVVGAD-GVKG (SEQ ID NO: 2).
- 6.** The method of claim 1, wherein the TCR has antigenic specificity for the mutated epitope consisting of VVVGAVGVGK (SEQ ID NO: 33) or VVGAvgVGK (SEQ ID NO: 35).
- 7.** A method of producing a human cell expressing a polypeptide, or a population of human cells expressing the polypeptide, the method comprising:
- introducing a recombinant expression vector to an isolated human cell, or an isolated population of human cells,
  - wherein the recombinant expression vector comprises a nucleotide sequence encoding the polypeptide,
  - wherein the polypeptide comprises a functional portion of a TCR, and wherein the functional portion comprises:
  - (i) the amino acid sequences of SEQ ID NOs: 3-8;
  - (ii) the amino acid sequences of SEQ ID NOs: 125-130;
  - (iii) the amino acid sequences of SEQ ID NOs: 137-142;
  - (iv) the amino acid sequences of SEQ ID NOs: 149-154; or
  - (v) the amino acid sequences of SEQ ID NOs: 149-150, 207, and 152-154.
- 8.** The method of claim 7, wherein the functional portion comprises:
- (i) the amino acid sequence of both SEQ ID NOs: 9 and 10;
  - (ii) the amino acid sequence of both SEQ ID NOs: 131 and 132;
  - (iii) the amino acid sequence of both SEQ ID NOs: 143 and 144;
  - (iv) the amino acid sequence of both SEQ ID NOs: 155 and 156; or
  - (v) the amino acid sequence of both SEQ ID NOs: 208 and 156.

**9.** The method of claim **7**, wherein the functional portion comprises:

- (i) the amino acid sequence of both SEQ ID NOs: 11 and 12;
- (ii) the amino acid sequence of both SEQ ID NOs: 133 and 134;
- (iii) the amino acid sequence of both SEQ ID NOs: 145 and 146;
- (iv) the amino acid sequence of both SEQ ID NOs: 157 and 158; or
- (v) the amino acid sequence of both SEQ ID NOs: 209 and 158.

**10.** A method of producing a human cell expressing a protein, or a population of human cells expressing the protein, the method comprising:

introducing a recombinant expression vector to an isolated human cell, or an isolated population of human cells,

wherein the recombinant expression vector comprises a nucleotide sequence encoding the protein, and wherein the protein comprises:

- (a) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 3-5 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 6-8;
- (b) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 125-127 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 128-130;
- (c) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 137-139 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 140-142;
- (d) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 149-151 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 152-154; or
- (e) a first polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 149, 150, and 207 and a second polypeptide chain comprising the amino acid sequences of SEQ ID NOs: 152-154.

**11.** The method according to claim **10**, wherein:

- (a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 9 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 10;
- (b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 131 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 132;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 143 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 144;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 155 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 156; or

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 208 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 156.

**12.** The method of claim **10**, wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 11 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 12;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 133 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 134;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 145 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 146;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 157 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 158; or

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO: 209 and the second polypeptide chain comprises the amino acid sequence of SEQ ID NO: 158.

**13.** The method of claim **1**, wherein the recombinant expression vector is a viral vector.

**14.** The method of claim **7**, wherein the recombinant expression vector is a viral vector.

**15.** The method of claim **10**, wherein the recombinant expression vector is a viral vector.

**16.** The method of claim **1**, wherein the population of human cells is a population of human peripheral blood mononuclear cells.

**17.** The method of claim **7**, wherein the population of human cells is a population of human peripheral blood mononuclear cells.

**18.** The method of claim **10**, wherein the population of human cells is a population of human peripheral blood mononuclear cells.

**19.** The method of claim **1**, wherein the recombinant expression vector is a retroviral vector.

**20.** The method of claim **7**, wherein the recombinant expression vector is a retroviral vector.

\* \* \* \* \*