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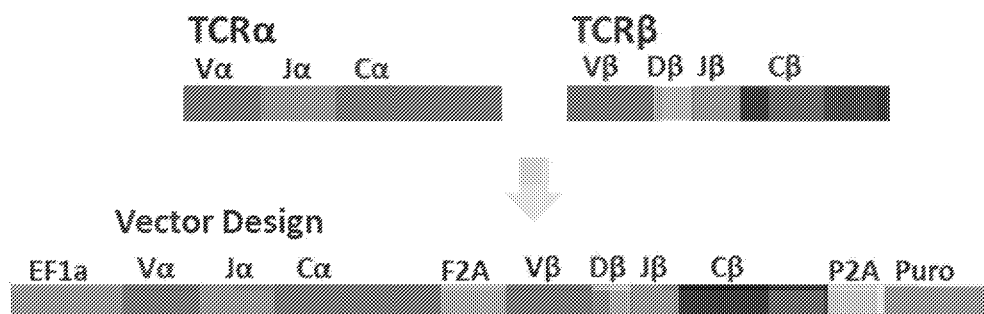


FIG. 3A

(57) **Abstract:** The present disclosure provides T cell receptors (TCRs) against peptide-MHC complexes, isolated nucleic acid molecules encoding TCRs against peptide-MHC complexes, T cells expressing TCRs against peptide-MHC complexes, and pharmaceutical compositions for use in the treatment of diseases.

T CELL RECEPTOR CONSTRUCTS AND USES THEREOF

CROSS REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 62/764,817, filed on August 16, 2018, and U.S. Provisional Application No. 62/810,112, filed on February 25, 2019, both of which are hereby incorporated by reference in their entirety.

BACKGROUND

[0002] T cell receptors (TCRs) are members of the immunoglobulin superfamily and usually consist of two subunits, namely the α - and β -subunits. These possess one N-terminal immunoglobulin (Ig)-variable (V) domain, one Ig-constant (C) domain, a transmembrane/cell membrane-spanning region, and a short cytoplasmic tail at the C-terminal end. The variable domains of both the TCR α -chain and β -chain have three hypervariable or complementarity determining regions (CDRs), whereas the variable region of the β -chain has an additional area of hypervariability (HV4) that does not normally contact antigen and therefore is not considered a CDR.

[0003] CDR3 is the principle CDR responsible for recognizing processed antigen, although CDR1 of the alpha chain has also been shown to interact with the N-terminal part of the antigenic peptide, whereas CDR1 of the β -chain interacts with the C-terminal part of the peptide. CDR2 is thought to recognize the MHC. The constant domain of the TCR domain consists of short connecting sequences in which a cysteine residue forms disulfide bonds, which forms a link between the two chains. The affinity of TCR's for a specific antigen makes them valuable for several therapeutic approaches. For example, cancer patients, such as melanoma patients, can be effectively treated by using adoptive immunotherapy as TCRs are exquisitely sensitive for their antigen and can direct immune responses at tumor cells expressing their cognate antigen. Accordingly, there is a need for TCRs against peptide-MHC complexes for development of new and effective therapeutics.

[0003a] Any reference to any prior art in this specification is not, and should not be taken as an acknowledgement or any form of suggestion that the prior art forms part of the common general knowledge.

SUMMARY

[0003b] The term “comprise” and variants of the term such as “comprises” or “comprising” are used herein to denote the inclusion of a stated integer or stated integers but not to exclude any other integer or any other integers, unless in the context or usage an exclusive interpretation of the term is required.

[0003c] In a first aspect, the invention provides a recombinant nucleic acid encoding a T cell receptor (TCR) comprising a TCR beta chain construct comprising a beta chain complementarity determining region 1 (CDR1), a beta chain complementarity determining region 2 (CDR2), and a beta chain complementarity determining

region 3 (CDR3); and a TCR alpha chain construct comprising an alpha chain CDR1, an alpha chain CDR2, and an alpha chain CDR3, wherein

(a) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 50, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 51, the beta chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 52, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 47, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 48, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 49, wherein the TCR specifically binds to a mutated RAS epitope from human RAS in complex with a human MHC encoded by an HLA-A11:01 allele; or

(b) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 66, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 67, the beta chain CDR3 has an amino acid sequence set forth in SEQ ID NO: 68, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 63, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 64, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 65, wherein the TCR specifically binds to the mutated epitope from the human RAS in complex with a human MHC encoded by an HLA-A03:01 allele; or

(c) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 82, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 83, the beta chain CDR3 has an amino acid sequence set forth in SEQ ID NO: 84, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 79, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 80, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 81, wherein the TCR specifically binds to the mutated epitope from the human RAS in complex with the human MHC encoded by the HLA-A03:01 allele;

wherein the mutated epitope from human RAS is characterized by a G12V mutation, wherein the mutated epitope comprises a sequence of VVGAVGVGK or VVGAVGVGK.

[0003d] In a second aspect, the invention provides a T cell comprising the recombinant nucleic acid of the first aspect, capable of expressing the TCR that specifically binds to the mutated epitope of human RAS in complex with a human MHC.

[0003e] In a third aspect, the invention provides a pharmaceutical composition comprising:

(a) the recombinant nucleic acid of the first aspect; or the cell of the second aspect; and,

(b) a pharmaceutically acceptable excipient or diluent.

[0003f] In a fourth aspect, the invention provides a method of treating a subject having a cancer associated with a mutated RAS, comprising administering to the subject the cell of the second aspect or the pharmaceutical composition of the third aspect, wherein the mutated RAS is characterized by a G12V mutation comprising a sequence of VVGAVGVGK or VVGAVGVGK.

[0003g] In a fifth aspect, the invention provides use of the recombinant nucleic acid of the first aspect, or the cell of the second aspect, in the manufacture of a medicament for treating cancer associated with a RAS G12V mutation, wherein the RAS G12V mutation comprises a sequence of VVGAVGVGK or VVGAVGVGK.

[0004] The instant application is based on development of TCRs against peptide-MHC complexes and effective therapeutics comprising the TCRs. Provided herein, isolated nucleic acid molecules encoding TCRs against peptide-MHC complexes, T cells expressing TCRs against peptide-MHC complexes, and pharmaceutical compositions for use in the treatment of diseases.

[0005] Provided herein is a recombinant nucleic acid encoding a T cell receptor (TCR) comprising a TCR beta chain construct comprising a complementarity determining region 3 (CDR3) having an amino acid sequence set forth in SEQ ID NO: 52. In some embodiments, the T cell receptor (TCR) construct further comprises a complementarity determining region 1 (CDR1) and a complementarity determining region 2 (CDR2), wherein the CDR1 has an amino acid sequence set forth in SEQ ID NO: 50; and the CDR2 has an amino acid sequence set forth in SEQ ID NO: 51. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 58. In some embodiments, the TCR beta chain construct comprises a variable region having at least

[Text continues on page 2]

90% sequence identity to an amino acid sequence set forth in SEQ ID NO: 58. In some embodiments, the TCR beta chain construct comprises a variable region having at least 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 58. In some embodiments, the TCR beta chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 58. In some embodiments, the recombinant nucleic acid encoding a T cell receptor (TCR) of any one of the preceding embodiments, further comprises a TCR alpha chain construct having a CDR1, a CDR2, and a CDR3, wherein, the CDR1 has an amino acid sequence set forth in SEQ ID NO: 47; the CDR2 has an amino acid sequence set forth in SEQ ID NO: 48; and, the CDR has an amino acid sequence set forth in SEQ ID NO: 49. In some embodiments, the recombinant nucleic acid of any one of the preceding embodiments, comprises: (a) a sequence having at least 80% sequence identity with SEQ ID NOs: 56 or 57, further comprising a sequence encoding at least SEQ ID NO: 52; and (b) a sequence having at least 80% sequence identity with SEQ ID NOs: 53 or 54, further comprising a sequence encoding at least SEQ ID NO: 49. In some embodiments, the recombinant nucleic acid encoding a T cell receptor (TCR) of any one of the preceding embodiments comprises the TCR alpha chain construct which comprises a variable region having at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 55. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 90% sequence identity to an amino acid sequence set forth in SEQ ID NO: 55. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 55. In some embodiments, the TCR alpha chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 55. In some embodiments, the recombinant nucleic acid encoding a TCR described above comprises: (a) a beta chain having an amino acid sequence set forth in SEQ ID NO: 60, or an amino acid sequence that is at least 80% identical to SEQ ID NO: 60; and (b) an alpha chain having an amino acid sequence set forth in SEQ ID NO: 59, or an amino acid sequence that is at least 80% identical to SEQ ID NO: 59. In some embodiments, the recombinant nucleic acid encoding a TCR of any one of the preceding embodiments, binds to an epitope from human RAS comprising a mutation G12V.

[0006] Provided herein is a recombinant nucleic acid encoding a TCR comprising a TCR beta chain construct and a TCR alpha chain construct, the TCR beta chain construct comprising a complementarity determining region 3 (CDR3) having an amino acid sequence selected from SEQ ID NO: 537 and 563. In some embodiments, the TCR beta chain construct comprises a CDR3 having an amino acid sequence of SEQ ID NO: 537. In some embodiments, the TCR beta chain construct comprising a CDR3 having an amino acid sequence of SEQ ID NO: 537, comprises a variable region having at least 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to an amino acid sequence set forth in SEQ ID NO: 541. In some embodiments, the TCR beta chain construct has an amino acid sequence identity set forth in SEQ ID NO: 541. In some embodiments, the TCR comprising a TCR beta chain CDR3 having an amino acid sequence of SEQ ID NO: 537, further comprises a TCR alpha chain construct that comprises a variable region having at least 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to an amino acid sequence set forth in SEQ ID NO: 539 or SEQ ID NO: 552.

In some embodiments, the TCR alpha chain construct has an amino acid sequence identity set forth in SEQ ID NO: 539. In some embodiments, the TCR alpha chain construct has an amino acid sequence identity set forth in SEQ ID NO: 552. In some embodiments, the recombinant nucleic acid described above encodes a TCR comprising a beta chain having an amino acid sequence set forth in SEQ ID NO: 543, or a sequence that has at least 80% sequence identity to SEQ ID NO: 543; and an alpha chain having an amino acid sequence set forth in SEQ ID NO: 542, or a sequence that has at least 80% sequence identity to SEQ ID NO: 542. In some embodiments, the recombinant nucleic acid described above encodes a TCR comprising a beta chain having an amino acid sequence set forth in SEQ ID NO: 543, or a sequence that has at least 80% sequence identity to SEQ ID NO: 543; and an alpha chain having an amino acid sequence set forth in SEQ ID NO: 555, or a sequence that has at least 80% sequence identity to SEQ ID NO: 555. In some embodiments, the recombinant nucleic acid described above encodes a TCR comprising a beta chain variable domain having an amino acid sequence set forth in SEQ ID NO: 541, or a sequence that has at least 80% sequence identity to SEQ ID NO: 541; and an alpha chain variable domain having an amino acid sequence set forth in SEQ ID NO: 539, or a sequence that has at least 80% sequence identity to SEQ ID NO: 539. In some embodiments, the recombinant nucleic acid described above encodes a TCR comprising a beta chain variable domain having an amino acid sequence set forth in SEQ ID NO: 541, or a sequence that has at least 80% sequence identity to SEQ ID NO: 541; and an alpha chain variable domain having an amino acid sequence set forth in SEQ ID NO: 552, or a sequence that has at least 80% sequence identity to SEQ ID NO: 552.

[0007] In some embodiments, the recombinant nucleic acid encoding a TCR comprising a TCR beta chain construct and a TCR alpha chain construct, the TCR beta chain construct comprises a CDR3 having an amino acid sequence of SEQ ID NO: 563. In some embodiments the TCR beta chain construct comprises a variable region having at least 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to an amino acid sequence set forth in SEQ ID NO: 567. In some embodiments the TCR alpha chain construct comprises a variable region having at least 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to an amino acid sequence set forth in SEQ ID NO: 565. In some embodiments, the recombinant nucleic acid described above encodes a TCR comprising a beta chain having an amino acid sequence set forth in SEQ ID NO: 569, or a sequence that has at least 80% sequence identity to SEQ ID NO: 569; and an alpha chain variable domain having an amino acid sequence set forth in SEQ ID NO: 568, or a sequence that has at least 80% sequence identity to SEQ ID NO: 568. Disclosed herein is a vector comprising the recombinant nucleic acid of any one of the embodiments described above. Also disclosed herein is a cell comprising the recombinant nucleic acid of any one of the embodiments described above or the vector of as described above.

[0008] Provided herein is a recombinant nucleic acid encoding a TCR construct comprising: (a) a TCR beta chain construct, and (b) a TCR alpha chain construct; wherein the TCR recognizes and binds to an epitope from human RAS comprising a point mutation G12V or G12C, the epitope being in a human MHC-protein complex, wherein the human MHC-protein is an HLA antigen encoded by the HLA A03:01 allele. In some embodiments, the TCR beta chain construct comprises a CDR3 having an amino acid sequence set forth in SEQ ID NO: 68.

In some embodiments, the TCR beta chain construct further comprises a complementarity determining region 1 (CDR1) and a complementarity determining region 2 (CDR2), wherein the CDR1 has an amino acid sequence set forth in SEQ ID NO: 66; and the CDR2 has an amino acid sequence set forth in SEQ ID NO: 67. In some embodiments, the recombinant nucleic acid encoding a T cell receptor (TCR) described in this paragraph, further comprising a TCR alpha chain construct having a CDR1, a CDR2, and a CDR3, wherein, the CDR1 has an amino acid sequence set forth in SEQ ID NO: 63; the CDR2 has an amino acid sequence set forth in SEQ ID NO: 64; and, the CDR3 has an amino acid sequence set forth in SEQ ID NO: 65. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 74. In some embodiments, the TCR beta chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 74. In some embodiments, T cell receptor (TCR) comprises a TCR alpha chain construct, wherein the TCR alpha chain construct comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 71. In some embodiments, the TCR alpha chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 71. In some embodiment, the TCR comprises a beta chain construct having an amino acid sequence set forth in SEQ ID NO: 76, or a sequence having at least 80% sequence identity to SEQ ID NO: 76; and an alpha chain construct having an amino acid sequence set forth in SEQ ID NO: 75, or a sequence having at least 80% sequence identity to SEQ ID NO: 75. Provided herein is a vector comprising a recombinant nucleic acid of any one of the embodiments described in this paragraph. Also provided herein is a cell comprising any one of the recombinant nucleic acid of any one of the embodiments described in this paragraph or the vector described in this paragraph.

[0009] In some embodiments, the TCR that recognizes and binds to an epitope from human RAS comprising a point mutation G12V in complex with an HLA antigen encoded by the HLA A03:01 allele, comprises a TCR beta chain construct comprising a CDR3 having an amino acid sequence set forth in SEQ ID NO: 84. In some embodiments, the TCR beta chain construct further comprises a complementarity determining region 1 (CDR1) and a complementarity determining region 2 (CDR2), wherein the CDR1 has an amino acid sequence set forth in SEQ ID NO: 82; and the CDR2 has an amino acid sequence set forth in SEQ ID NO: 83. In some embodiments, the TCR further comprises a TCR alpha construct having a CDR1, a CDR2, and a CDR3, wherein, the CDR1 has an amino acid sequence set forth in SEQ ID NO: 79; the CDR2 has an amino acid sequence set forth in SEQ ID NO: 80; and, the CDR3 has an amino acid sequence set forth in SEQ ID NO: 81. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 90. In some embodiments, the TCR beta chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 90. In some embodiments, the TCR described above further comprises a TCR alpha chain construct that comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 87. In some embodiments, the TCR

alpha chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 71. In some embodiments, the TCR comprises a beta chain construct having an amino acid sequence of SEQ ID NO: 92, or a sequence that has at least 80% sequence identity to SEQ ID NO: 92; and an alpha chain construct having an amino acid sequence of SEQ ID NO: 91, or a sequence that has at least 80% sequence identity to SEQ ID NO: 91. Provided herein is a vector comprising the recombinant nucleic acid of any one of the embodiments described in this paragraph and a cell comprising any one of the recombinant nucleic acid of any one of the embodiments described herein.

[0010] In some embodiments, the recombinant nucleic acid of embodiment described in the preceding paragraph, the TCR that recognizes and binds to an epitope from human RAS comprising a point mutation G12V or G12C in complex with an HLA antigen encoded by the HLA A03:01 allele, comprises a TCR beta chain construct comprises a CDR3 having an amino acid sequence set forth in SEQ ID NO: 388. In some embodiments, the TCR beta chain construct further comprises a complementarity determining region 1 (CDR1) and a complementarity determining region 2 (CDR2), wherein the CDR1 has an amino acid sequence set forth in SEQ ID NO: 386; and the CDR2 has an amino acid sequence set forth in SEQ ID NO: 387. In some embodiments, the TCR further comprises a TCR alpha construct having a CDR1, a CDR2, and a CDR3, wherein, the CDR1 has an amino acid sequence set forth in SEQ ID NO: 383; the CDR2 has an amino acid sequence set forth in SEQ ID NO: 384; and, the CDR3 has an amino acid sequence set forth in SEQ ID NO: 385. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 394. In some embodiments, the TCR beta chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 394. In some embodiments, the TCR described above further comprises a TCR alpha chain construct that comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 391. In some embodiments, the TCR alpha chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 391. In some embodiments, the TCR comprises a beta chain construct having an amino acid sequence of SEQ ID NO: 396, or a sequence that has at least 80% sequence identity to SEQ ID NO: 396; and an alpha chain construct having an amino acid sequence of SEQ ID NO: 395, or a sequence that has at least 80% sequence identity to SEQ ID NO: 395. Provided herein is a vector comprising the recombinant nucleic acid of any one of the embodiments described in this paragraph and a cell comprising any one of the recombinant nucleic acid of any one of the embodiments described herein.

[0011] In some embodiments, the recombinant nucleic acid of embodiment described in the preceding paragraph, the TCR that recognizes and binds to an epitope from human RAS comprising a point mutation G12C in complex with an HLA antigen encoded by the HLA A03:01 allele, comprises a TCR beta chain construct comprises a CDR3 having an amino acid sequence set forth in SEQ ID NO: 100. In some embodiments, the TCR beta chain construct further comprises a complementarity determining region 1 (CDR1) and a complementarity determining region 2 (CDR2), wherein the CDR1 has an amino acid sequence set forth

in SEQ ID NO: 98; and the CDR2 has an amino acid sequence set forth in SEQ ID NO: 99. In some embodiments, the TCR further comprises a TCR alpha construct having a CDR1, a CDR2, and a CDR3, wherein, the CDR1 has an amino acid sequence set forth in SEQ ID NO: 95; the CDR2 has an amino acid sequence set forth in SEQ ID NO: 96; and, the CDR3 has an amino acid sequence set forth in SEQ ID NO: 97. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 106. In some embodiments, the TCR beta chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 106. In some embodiments, the TCR described above further comprises a TCR alpha chain construct that comprises a variable region having at least 80%, or at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to an amino acid sequence set forth in SEQ ID NO: 103. In some embodiments, the TCR alpha chain construct comprises a variable region having an amino acid sequence set forth in SEQ ID NO: 103. In some embodiments, the TCR comprises a beta chain construct having an amino acid sequence of SEQ ID NO: 108, or a sequence that has at least 80% sequence identity to SEQ ID NO: 108; and an alpha chain construct having an amino acid sequence of SEQ ID NO: 107, or a sequence that has at least 80% sequence identity to SEQ ID NO: 107. Provided herein is a vector comprising the recombinant nucleic acid of any one of the embodiments described in this paragraph and a cell comprising any one of the recombinant nucleic acid of any one of the embodiments described herein.

[0012] In some embodiments, the epitope has a length of from 8-25 amino acids. In some embodiments the epitope comprises a mutation that differs from the wild type epitope by at least one amino acid. In some embodiments, the epitope binds to the human MHC with a greater affinity than a corresponding wild-type epitope. In some embodiments, the epitope binds to the human MHC with a K_D or an IC_{50} less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM. In some embodiments, the mutation is not present in non-cancer cells of a subject. In some embodiments, the TCR binds to an MHC-peptide complex with a K_D or an IC_{50} of less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM. In some embodiments, the nucleic acid is operably linked to a promoter. In some embodiments, the cell is a $CD4^+$ T cell. In some embodiments, the cell is a $CD8^+$ T cell. In some embodiments, the cell is isolated from a subject having a RAS mutation.

[0013] Provided herein is a pharmaceutical composition comprising: (a) the nucleic acid of any one of embodiments described above; or, the vector of any one of embodiments described above; or, the cell of any one of embodiments above; and, (b) a pharmaceutically acceptable excipient or diluent. In some embodiments, the pharmaceutical composition further comprising an immunomodulatory agent or an adjuvant. In some embodiments, the adjuvant is poly I:C. In some embodiments, the pharmaceutical composition of any one of embodiments described above is for use in treating an immune disease or cancer.

[0014] Provided herein is method of treating a subject having a disease or condition, comprising administering to the subject the pharmaceutical composition of any one of embodiments described above. In some embodiments, the method of treating a subject with cancer comprises administering to the subject the pharmaceutical composition of any one of embodiments described above.

[0015] Also provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising determining the subject as a subject that expresses a protein encoded by an HLA-A03:01 allele or an HLA-A11:01 allele, wherein the therapeutic is the pharmaceutical composition selected from any one of embodiments described above.

[0016] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3, 18, 33, 49, 65, 81, 97, 113, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 401, 417, and 433 and/or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6, 21, 36, 52, 68, 84, 100, 116, 244, 260, 276, 292, 308, 324, 340, 356, 372, 388, 404, 420, and 436.

[0017] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the epitope from RAS comprises a region having at least 70% sequence identity to an amino acid sequence selected from SEQ ID NOs: 15, 30, 45, 46, 61, 62, 77, 78, 93, 94, 109, 110, 125, 126, 219-222, 253, 254, 269, 270, 285, 286, 301, 302, 317, 318, 333, 334, 349, 350, 365, 366, 381, 382, 397, 398, 413, 414, 429, 430, 445 and 446.

[0018] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele. In some embodiments, the alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 71, 87, 103, 295, 311, 327, 343, 359 and 391, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 74, 90, 106, 298, 314, 330, 346, 362 and 394, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele.

[0019] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 63, 79, 95, 287, 303, 319, 335, 351 and 383. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 66, 82, 98, 290, 306, 322, 338, 354 and 386. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 64, 80, 96, 288, 304, 320, 336, 352 and 384. In some embodiments, the TCR beta chain construct comprises a complementarity

determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 67, 83, 99, 291, 307, 323, 339, 355 and 387. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 65, 81, 97, 289, 305, 321, 337, 353 and 385. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 68, 84, 100, 292, 308, 324, 340, 356 and 388.

[0020] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele. In some embodiments, the alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 9 and 24 wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 12 and 27, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele.

[0021] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 1 and 16. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 4 and 19. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 2 and 17. In some embodiments TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 5 and 20. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3 and 18. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6 and 21.

[0022] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 39, 55, 122, 247, 263, 279, 375, 407, and 423, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele. In some embodiments, the TCR beta chain

construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 42, 58, 125, 250, 266, 282, 378, 413, and 426, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele.

[0023] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 31, 47, 111, 239, 255, 271, 367, 399, and 415. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 34, 50, 114, 242, 258, 274, 370, 402, and 418. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 32, 48, 112, 240, 256, 272, 368, 400, and 416. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 35, 51, 115, 243, 259, 275, 371, 403, and 419. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 33, 49, 113, 241, 257, 273, 369, 401, 417, and 433. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 36, 52, 116, 244, 260, 276, 372, 404, and 420. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 9; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 12. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 1, a CDR2 of SEQ ID NO: 2, and a CDR3 of SEQ ID NO: 3; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 4, a CDR2 of SEQ ID NO: 5, and a CDR3 of SEQ ID NO: 6. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 13, or a sequence that has at least 80% identity to SEQ ID NO: 13. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 14 or a sequence that has at least 80% identity to SEQ ID NO: 14. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 24; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 27. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 16, a CDR2 of SEQ ID NO: 17, and a CDR3 of SEQ ID NO: 18; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 19, a CDR2 of SEQ ID NO: 20, and a CDR3 of SEQ ID NO: 21. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 28, or a sequence that has at least 80% identity to SEQ ID NO: 28. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 29 or a sequence that has at least 80% identity to SEQ ID NO: 29. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 39; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 42. In some embodiments, the TCR alpha chain construct

comprises a CDR1 of SEQ ID NO: 31, a CDR2 of SEQ ID NO: 32, and a CDR3 of SEQ ID NO: 33; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 34, a CDR2 of SEQ ID NO: 35, and a CDR3 of SEQ ID NO: 36. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 43, or a sequence that has at least 80% identity to SEQ ID NO: 43. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 44 or a sequence that has at least 80% identity to SEQ ID NO: 44. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 55; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 58. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 47, a CDR2 of SEQ ID NO: 48, and a CDR3 of SEQ ID NO: 49; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 50, a CDR2 of SEQ ID NO: 51, and a CDR3 of SEQ ID NO: 52. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 71; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 74. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 63, a CDR2 of SEQ ID NO: 64, and a CDR3 of SEQ ID NO: 65; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 66, a CDR2 of SEQ ID NO: 67, and a CDR3 of SEQ ID NO: 68. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 75, or a sequence that has at least 80% identity to SEQ ID NO: 75. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 76 or a sequence that has at least 80% identity to SEQ ID NO: 76. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 87; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 90. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 79, a CDR2 of SEQ ID NO: 80, and a CDR3 of SEQ ID NO: 81; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 82, a CDR2 of SEQ ID NO: 83, and a CDR3 of SEQ ID NO: 84. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 91, or a sequence that has at least 80% identity to SEQ ID NO: 91. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 92 or a sequence that has at least 80% identity to SEQ ID NO: 92. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 103; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 106. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 95, a CDR2 of SEQ ID NO: 96, and a CDR3 of SEQ ID NO: 97; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 98, a CDR2 of SEQ ID NO: 99, and a CDR3 of SEQ ID NO: 100. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 107, or a sequence that has at least 80% identity to SEQ ID NO: 107. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 108 or a sequence that has at least 80% identity to SEQ ID NO: 108. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 119; and the TCR beta chain construct comprises a variable region having at least 80% sequence

identity to SEQ ID NO: 122. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 111, a CDR2 of SEQ ID NO: 112, and a CDR3 of SEQ ID NO: 113; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 114, a CDR2 of SEQ ID NO: 115, and a CDR3 of SEQ ID NO: 116. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 123, or a sequence that has at least 80% identity to SEQ ID NO: 123. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 124 or a sequence that has at least 80% identity to SEQ ID NO: 124. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 247; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 250. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 239, a CDR2 of SEQ ID NO: 240, and a CDR3 of SEQ ID NO: 241; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 242, a CDR2 of SEQ ID NO: 243, and a CDR3 of SEQ ID NO: 244. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 251, or a sequence that has at least 80% identity to SEQ ID NO: 251. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 252 or a sequence that has at least 80% identity to SEQ ID NO: 252. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 263; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 266. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 255, a CDR2 of SEQ ID NO: 256, and a CDR3 of SEQ ID NO: 257; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 258, a CDR2 of SEQ ID NO: 259, and a CDR3 of SEQ ID NO: 260. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 267, or a sequence that has at least 80% identity to SEQ ID NO: 267. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 268 or a sequence that has at least 80% identity to SEQ ID NO: 268. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 279; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 282. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 271, a CDR2 of SEQ ID NO: 272, and a CDR3 of SEQ ID NO: 273; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 274, a CDR2 of SEQ ID NO: 275, and a CDR3 of SEQ ID NO: 276. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 283, or a sequence that has at least 80% identity to SEQ ID NO: 283. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 284 or a sequence that has at least 80% identity to SEQ ID NO: 284. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 295; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 298. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 287, a CDR2 of SEQ ID NO: 288, and a CDR3 of SEQ ID NO: 289; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 290, a CDR2 of SEQ ID NO: 291, and a CDR3 of SEQ ID NO: 292. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 299, or a sequence

that has at least 80% identity to SEQ ID NO: 299. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 300 or a sequence that has at least 80% identity to SEQ ID NO: 300. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 311; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 314. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 303, a CDR2 of SEQ ID NO: 304, and a CDR3 of SEQ ID NO: 305; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 306, a CDR2 of SEQ ID NO: 307, and a CDR3 of SEQ ID NO: 308. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 315, or a sequence that has at least 80% identity to SEQ ID NO: 315. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 316 or a sequence that has at least 80% identity to SEQ ID NO: 316. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 327; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 330. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 319, a CDR2 of SEQ ID NO: 320, and a CDR3 of SEQ ID NO: 321; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 322, a CDR2 of SEQ ID NO: 323, and a CDR3 of SEQ ID NO: 324. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 331, or a sequence that has at least 80% identity to SEQ ID NO: 331. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 332 or a sequence that has at least 80% identity to SEQ ID NO: 332. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 343; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 346. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 335, a CDR2 of SEQ ID NO: 336, and a CDR3 of SEQ ID NO: 337; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 338, a CDR2 of SEQ ID NO: 339, and a CDR3 of SEQ ID NO: 340. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 347, or a sequence that has at least 80% identity to SEQ ID NO: 347. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 348 or a sequence that has at least 80% identity to SEQ ID NO: 348. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 359; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 362. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 351, a CDR2 of SEQ ID NO: 352, and a CDR3 of SEQ ID NO: 353; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 354, a CDR2 of SEQ ID NO: 355, and a CDR3 of SEQ ID NO: 356. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 363, or a sequence that has at least 80% identity to SEQ ID NO: 363. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 364 or a sequence that has at least 80% identity to SEQ ID NO: 364. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 375; and the TCR beta chain construct comprises a variable region having at least 80% sequence

identity to SEQ ID NO: 378. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 367, a CDR2 of SEQ ID NO: 368, and a CDR3 of SEQ ID NO: 369; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 370, a CDR2 of SEQ ID NO: 371, and a CDR3 of SEQ ID NO: 372. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 379, or a sequence that has at least 80% identity to SEQ ID NO: 379. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 380 or a sequence that has at least 80% identity to SEQ ID NO: 380. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 391; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 394. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 383, a CDR2 of SEQ ID NO: 384, and a CDR3 of SEQ ID NO: 385; the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 386, a CDR2 of SEQ ID NO: 387, and a CDR3 of SEQ ID NO: 388. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 395, or a sequence that has at least 80% identity to SEQ ID NO: 395. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 396 or a sequence that has at least 80% identity to SEQ ID NO: 396. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 407; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 410. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 399, a CDR2 of SEQ ID NO: 400, and a CDR3 of SEQ ID NO: 401; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 402, a CDR2 of SEQ ID NO: 403, and a CDR3 of SEQ ID NO: 404. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 411, or a sequence that has at least 80% identity to SEQ ID NO: 411. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 412 or a sequence that has at least 80% identity to SEQ ID NO: 412. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 423; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 426. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 415, a CDR2 of SEQ ID NO: 416, and a CDR3 of SEQ ID NO: 417; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 418, a CDR2 of SEQ ID NO: 419, and a CDR3 of SEQ ID NO: 420. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 427, or a sequence that has at least 80% identity to SEQ ID NO: 427. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 428 or a sequence that has at least 80% identity to SEQ ID NO: 428. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 391; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 394.

[0024] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from Tmprss2:ERG in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta

chain construct comprises a complementarity determining region 3 (CDR3) having a sequence of SEQ ID NO: 144 and SEQ ID NO: 147 or a sequence having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 144 and SEQ ID NO: 147. In some embodiments, the TCR comprises an alpha chain having a sequence of SEQ ID NO: 154, or a sequence that has at least 80% identity to SEQ ID NO: 154. In some embodiments, the TCR comprises a beta chain having a sequence of SEQ ID NO: 155 or a sequence that has at least 80% identity to SEQ ID NO: 155.

[0025] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the epitope from TMPRSS2:ERG comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 156.

[0026] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 150. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having a sequence of SEQ ID NO: 142 or a sequence having at least 90% sequence identity to SEQ ID NO: 142 and a sequence of SEQ ID NO: 145 or a sequence having at least 90% sequence identity to SEQ ID NO: 145 respectively. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to SEQ ID NO: 143 or SEQ ID NO: 146 respectively. In some embodiments, the TCR alpha chain construct comprises a variable region having a sequence of SEQ ID NO: 150 or at least 80% sequence identity to SEQ ID NO: 150; and the TCR beta chain construct comprises a variable region having a sequence of SEQ ID NO: 153 or at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 142, a CDR2 of SEQ ID NO: 143, and a CDR3 of SEQ ID NO: 144; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 145, a CDR2 of SEQ ID NO: 146, and a CDR3 of SEQ ID NO: 147.

[0027] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 129, 132, 191, 194, 206 and 209.

[0028] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant GATA3 peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[0029] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant GATA3 peptide in complex with an HLA-A02:01,

HLA-B07:02 or HLA-B08:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NOs: 129, 132, 191, 194, 206 or 209; and/or specifically binds to a mutant GATA3 peptide comprising a region having a sequence of or having a sequence with at least 70% sequence identity to SEQ ID NO: 141, 203 or 218.

[0030] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the epitope from GATA3 comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 141, 203 or 218.

[0031] In some embodiments, the TCR alpha chain construct comprises a variable region having a sequence of SEQ ID NO: 135, 197 or 212; or a sequence with at least 80% sequence identity to SEQ ID NO: 135, 197 or 212. In some embodiments, the TCR beta chain construct comprises a variable region having a sequence of SEQ ID NO: 138, 200 or 215; or a sequence having at least 80% sequence identity to SEQ ID NO: 138, 200 or 215. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having an amino acid sequence of, having or at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 127, 130, 189, 192, 204 and 207. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having an amino acid sequence of, or having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 128, 131, 190, 193, 205 and 208. In some embodiments, the GATA3 binding TCR alpha chain comprises a variable region having a sequence of SEQ ID NO: 135, or a sequence having at least 80% identity to SEQ ID NO: 135; and a beta chain having a variable region having a sequence of SEQ ID NO: 138, or a sequence having at least 80% identity to SEQ ID NO: 138. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 127, a CDR2 of SEQ ID NO: 128, and a CDR3 of SEQ ID NO: 129; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 130, a CDR2 of SEQ ID NO: 131, and a CDR3 of SEQ ID NO: 132. In some embodiments, the TCR has an alpha chain having a sequence of SEQ ID NO: 139, or a sequence having at least 80% identity to SEQ ID NO: 139. In some embodiments, the TCR has a beta chain having a sequence of SEQ ID NO: 140, or a sequence having at least 80% identity to SEQ ID NO: 140. In some embodiments, the TCR alpha chain construct comprises a variable region having an amino acid sequence of, or having at least 80% sequence identity to SEQ ID NO: 197; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 200. In some embodiments the TCR alpha chain has a sequence of SEQ ID NO: 201 or a sequence having at least 80% identity to SEQ ID NO: 201. In some embodiments the TCR beta chain has a sequence of SEQ ID NO: 202 or a sequence having at least 80% identity to SEQ ID NO: 202. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 189, a CDR2 of SEQ ID NO: 190, and a CDR3 of SEQ ID NO: 191; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 192, a CDR2 of SEQ ID NO: 193, and a CDR3 of SEQ ID NO: 194. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 212; and the

TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 215. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 204, a CDR2 of SEQ ID NO: 205, and a CDR3 of SEQ ID NO: 206; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 207, a CDR2 of SEQ ID NO: 208, and a CDR3 of SEQ ID NO: 209. In some embodiments, the TCR comprises of an alpha chain having a sequence of SEQ ID NO: 216 or a sequence having at least 80% identity to SEQ ID NO: 216. In some embodiments, the TCR comprises of a beta chain having a sequence of SEQ ID NO: 217 or a sequence having at least 80% identity to SEQ ID NO: 217.

[0032] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 161 and SEQ ID NO: 176, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 164 and SEQ ID NO: 179.

[0033] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant BTK peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[0034] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant BTK peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 161, 164, 176, or 179; and/or specifically binds to a mutant BTK peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 173 or 188.

[0035] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the epitope from BTK comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 173 or 188.

[0036] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or 182. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 159, 162, 174, and 177. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 160, 163, 175 and 178. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or

182; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 159 or 174, a CDR2 of SEQ ID NO: 160 or 175, and a CDR3 of SEQ ID NO: 161 or 176; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 162 or 177, a CDR2 of SEQ ID NO: 163 or 178, and a CDR3 of SEQ ID NO: 164 or 179.

[0037] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 449, SEQ ID NO: 466, SEQ ID NO: 483, SEQ ID NO: 500, and SEQ ID NO: 517, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 452, SEQ ID NO: 469, SEQ ID NO: 486, SEQ ID NO: 503, and SEQ ID NO: 520.

[0038] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant EGFR peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[0039] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant EGFR peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having a sequence of , or a sequence having at least 90% sequence identity to SEQ ID NO: 449, 466, 483, 500, 517, 452, 469, 486, 503, or 520; and/or specifically binds to a mutant EGFR peptide comprising a region having a sequence of, or having a sequence with at least 70% sequence identity to SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.

[0040] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the epitope from EGFR comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.

[0041] In some embodiments, the TCR alpha chain construct comprises a variable region having a sequence of, or a sequence having at least 80% sequence identity to SEQ ID NO: 449, 466, 483, 500 or 517. In some embodiments, the TCR beta chain construct comprises a variable region having a sequence of, or a sequence having at least 80% sequence identity to SEQ ID NO: 452, 469, 486, 503, or 520. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having a sequence of, or a sequence having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOS: 447, 464, 481, 498, 515, 450, 467, 484, 501, and 518. In some

embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having a sequence of, or a sequence having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 448, 465, 482, 499, 516, 451, 468, 485, 502, and 519. In some embodiments, the TCR alpha chain construct comprises a variable region having a sequence of, or a sequence having at least 80% sequence identity to SEQ ID NO: 455, 472, 489, 506, or 523; and the TCR beta chain construct comprises a variable region having a sequence of, or a sequence having at least 80% sequence identity to SEQ ID NO: 458, 475, 492, 509 or 526. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 447, 464, 481, 498 or 515, a CDR2 of SEQ ID NO: 448, 465, 482, 499 or 516, and a CDR3 of SEQ ID NO: 449, 466, 483, 500 or 517; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 450, 467, 484, 501 or 518, a CDR2 of SEQ ID NO: 451, 468, 485, 502, or 519, and a CDR3 of SEQ ID NO: 452, 469, 486, 503, or 520.

[0042] In some embodiments, the epitope comprises a mutation selected from the group consisting of a point mutation, a splice-site mutation, a frameshift mutation, a read-through mutation, a resistance mutation, a gene fusion mutation and any combination thereof. In some embodiments, the human MHC is encoded by either HLA-A02:01 allele, or HLA-A03:01 allele or HLA-A11:01 allele. In some embodiments, the RAS epitope comprises a point mutation. In some embodiments, the point mutation is a G12V mutation. In some embodiments, the point mutation is a G12C mutation. In some embodiments, the point mutation is a G12D mutation. In some embodiments, the human MHC is encoded by HLA-A02:01 allele. In some embodiments, the TMPRSS2:ERG epitope comprises a gene fusion mutation. In some embodiments, the human MHC is encoded by HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele. In some embodiments, the epitope comprises a frameshift mutation. In some embodiments, the human MHC is encoded by HLA-A02:01 allele. In some embodiments, the BTK epitope comprises a point mutation. In some embodiments, the point mutation is C481S mutation. In some embodiments, the human MHC is encoded by HLA-A02:01 allele. In some embodiments, the EGFR epitope comprises a point mutation. In some embodiments, the point mutation is T790M.

[0043] In some embodiments, the epitope has a length of at least 8 amino acids. In some embodiments, the epitope has a length of at least 16 amino acids. In some embodiments, the epitope has a length of from 8-25 amino acids. In some embodiments, the epitope has a length of from 8-12 amino acids. In some embodiments, the epitope has a length of from 16-25 amino acids. In some embodiments, the epitope has a length of 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids.

[0044] In some embodiments, the epitope binds to the human MHC with a greater affinity than a corresponding wild-type epitope. In some embodiments, the epitope binds to the human MHC with a K_D or an IC_{50} less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM.

[0045] In some embodiments, the mutation is not present in non-cancer cells of a subject. In some embodiments, the epitope is encoded by a gene or an expressed gene of a subject's cancer cells.

[0046] In some embodiments, the TCR binds to a MHC-peptide complex with a K_D or an IC_{50} of less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM.

[0047] In some embodiments, the nucleic acid is operably linked to a promoter.

[0048] Provided herein is a vector comprising a nucleic acid described herein. In some embodiments, the vector is a self-amplifying RNA replicon, plasmid, phage, transposon, cosmid, virus, or virion. In some embodiments, wherein the vector is a viral vector. In some embodiments, wherein the vector is derived from a retrovirus, lentivirus, adenovirus, adeno-associated virus, herpes virus, pox virus, alpha virus, vaccinia virus, hepatitis B virus, human papillomavirus or a pseudotype thereof. In some embodiments, the vector is a non-viral vector. In some embodiments, the non-viral vector is a nanoparticle, a cationic lipid, a cationic polymer, a metallic nanopolymer, a nanorod, a liposome, a micelle, a microbubble, a cell-penetrating peptide, or a liposphere.

[0049] Provided herein is a protein encoded by the nucleic acid of any one sections described above.

[0050] Provided herein is a host cell comprising the nucleic acid described above, the vector of described above, or the protein described above. In some embodiments, the host cell is a CD4⁺ T cell. In some embodiments, the host cell is a CD8⁺ T cell. In some embodiments, the host cell is an autologous cell. In some embodiments, the host cell is an allogeneic cell. In some embodiments, the host cell is a natural killer cell, a B cell, or an immortalized cell line. In some embodiments, the host cell is a human cell.

[0051] Provided herein is a pharmaceutical composition comprising a nucleic acid described herein, a vector described herein, a protein described herein, or a host cell described herein; and a pharmaceutically acceptable excipient or diluent. In some embodiments, the pharmaceutical composition further comprises an immunomodulatory agent or an adjuvant. In some embodiments, the immunomodulatory agent in the pharmaceutical composition is a cytokine. In some embodiments, the adjuvant in the pharmaceutical composition is poly I:C. In some embodiments, the pharmaceutical compositions are for use in treating an immune disease or cancer.

[0052] Provided herein is the use of the pharmaceutical composition described above, for treating an immune disease or cancer.

[0053] Provided herein is a vector described herein, a protein described herein, or a host cell described herein for manufacture of a medicament for treating an immune disease or cancer. In some embodiments, the medicament is an adoptive T cell therapy or a TCR gene therapy.

[0054] Provided herein is a method of treating a subject with a disease or condition, comprising administering to the subject a pharmaceutical composition disclosed herein.

[0055] Provided herein is a method of treating a subject with cancer, comprising administering to the subject a pharmaceutical composition disclosed herein.

[0056] Provided herein is a method of treating a subject with cancer comprising administering to the subject a pharmaceutical composition In some embodiments, ; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01 allele, an HLA-B07:02, an HLA-B08:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele of the subject's genome.

[0057] Provided herein is a method of treating a subject with cancer comprising administering a TCR or T cell expressing the TCR to the subject, wherein the TCR specifically binds to a mutant RAS peptide in complex with a protein encoded by an HLA-A02:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the subject expresses the HLA allele.

[0058] Provided herein is a method of treating a subject with cancer comprising administering to the subject a pharmaceutical composition described herein; wherein the TCR binds to a mutant RAS peptide comprising a mutation at G12 in complex with an HLA-A02:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01; wherein the subject is identified as expressing a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele.

[0059] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises at least one mutant amino acid and is fragment of at least 8 contiguous amino acids of a mutant GATA3 protein arising from a mutation in a GATA3 gene of a cancer cell; wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.

[0060] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises one or more mutant GATA3 amino acids encoded by a GATA3 neoORF sequence, wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.

[0061] Provided herein is a method of treating a subject with cancer comprising administering a TCR or T cell expressing the TCR to the subject; wherein the TCR specifically binds to a mutant GATA3 peptide in complex with a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.

[0062] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant TMPRSS2:ERG peptide in complex with an HLA protein; wherein the mutant TMPRSS2:ERG peptide comprises at least one mutant amino acid and is a fragment of a TMPRSS2:ERG gene fusion mutation; wherein the mutant TMPRSS2:ERG peptide binds to a protein encoded by an HLA-A02:01 allele.

[0063] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises at least one mutant amino acid; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0064] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a resistance mutation or a point mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0065] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a C481S mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0066] Provided herein is a method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) or a T cell expressing the TCR to the subject, wherein the TCR specifically binds to a mutant EGFR peptide in complex with a protein encoded by an HLA-A02:01; wherein the mutant EGFR peptide comprises a resistance mutation or a point mutation, wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01 allele. In some embodiments, the mutant EGFR peptide comprises a T790M mutation.

[0067] Provided herein is a method of preventing resistance to a cancer therapy, the method comprising administering to a subject in need thereof a pharmaceutical composition described herein.

[0068] Provided herein is a method of inducing an immune response, the method comprising administering to a subject in need thereof a pharmaceutical composition described herein.

[0069] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as a subject that expresses a protein encoded by an HLA-A02:01 allele, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the therapeutic is a pharmaceutical composition described herein.

[0070] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises at least one mutant amino acid and is fragment of at least 8 contiguous amino acids of a mutant GATA3 protein arising from a mutation in a GATA3 gene of a cancer cell; wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.

[0071] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A03:01 allele,

an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant RAS peptide comprising a mutation at G12 in complex with an HLA protein; wherein the mutant RAS peptide binds to a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele.

[0072] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant TMPRSS2:ERG peptide in complex with an HLA protein; wherein the mutant TMPRSS2:ERG peptide comprises at least one mutant amino acid and is a fragment of a TMPRSS2:ERG gene fusion mutation; wherein the mutant TMPRSS2:ERG peptide binds to a protein encoded by an HLA-A02:01 allele.

[0073] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises at least one mutant amino acid; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0074] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a resistance mutation or a point mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0075] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a C481S mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

[0076] Provided herein is a method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant EGFR peptide in complex with an HLA protein; wherein the mutant EGFR peptide comprises at least one mutant amino acid T790M; wherein the mutant EGFR peptide binds to a protein encoded by an HLA-A02:01 allele.

[0077] In some embodiments, the cancer is selected from the group consisting of breast cancer, lung cancer, non-small cell lung cancer, pancreatic cancer, colorectal cancer, uterine cancer, melanoma, ovarian cancer, prostate cancer, endometrial cancer, chronic lymphocytic leukemia (CLL) and liver cancer. In some embodiments, the subject has a breast cancer that is resistant to anti-estrogen therapy, is an MSI breast cancer,

is a metastatic breast cancer, is a Her2 negative breast cancer, is a Her2 positive breast cancer, is an ER negative breast cancer, is an ER positive breast cancer is a recurrent breast cancer, is a metastatic breast cancer, or any combination thereof. In some embodiments, the breast cancer expresses an estrogen receptor with a mutation.

[0078] In some embodiments, the subject has a breast cancer that is resistant to anti-estrogen therapy. In some embodiments, the breast cancer expresses an estrogen receptor with a mutation. In some embodiments, the subject has a CLL that is resistant to ibrutinib therapy. In some embodiments, the CLL expresses a Bruton tyrosine kinase (BTK) with a mutation, such as a C481S mutation. In some embodiments, the subject has a lung cancer that is resistant to a tyrosine kinase inhibitor. In some embodiments, the lung cancer expresses an epidermal growth factor receptor (EGFR) with a mutation, such as a T790M, L792F, or C797S mutation.

[0079] In some embodiments, an immune response is elicited in the subject. In some embodiments, the immune response is a humoral response. In some embodiments, the immune response is a cytotoxic T cell response.

[0080] In some embodiments, the method further comprises administering at least one additional therapeutic agent or modality. In some embodiments, the at least one additional therapeutic agent or modality is surgery, a checkpoint inhibitor, an antibody or fragment thereof, a chemotherapeutic agent, radiation, a vaccine, a small molecule, a T cell, a vector, and APC, a polynucleotide, an oncolytic virus or any combination thereof. In some embodiments, the at least one additional therapeutic agent is an anti-PD-1 agent and anti-PD-L1 agent, an anti-CTLA-4 agent, or an anti-CD40 agent. In some embodiments, the additional therapeutic agent is administered before, simultaneously, or after administering a pharmaceutical composition described herein.

[0081] In some embodiments, administering comprises administering subcutaneously or intravenously.

[0082] In some embodiments, the subject is a subject that has had disease progression following endocrine therapy in combination with a CDK 4/6 inhibitor.

[0083] Provided herein is a method comprising: identifying neoantigen-specific T cells from a sample comprising a population of T cells; identifying one or more peptides of a peptide-MHC complex that are presented by an antigen presenting cell (APC); identifying a variable sequence of a T cell receptor (TCR) from the neoantigen-specific T cells; expressing a recombinant TCR comprising the variable sequence of the TCR identified in a TCR cell; and performing a functional assay, wherein the functional assay comprises contacting the TCR cell to a peptide-MHC complex comprising a peptide of the one or more peptides identified.

[0084] In some embodiments, the method comprises obtaining the sample comprising the population of cells comprising the neoantigen-specific T cells. In some embodiments, obtaining the sample comprises obtaining a T cell sample from a healthy subject or from a subject with cancer. In some embodiments, the T cell sample is from a healthy donor. In some embodiments, the T cell sample is a peripheral blood mononuclear cell (PBMC) sample.

[0085] In some embodiments, in identifying neoantigen-specific T cells comprises contacting the population of T cells to at least one peptide-MHC multimer complex comprising a neoantigen peptide. In some embodiments, identifying neoantigen-specific T cells comprises contacting the population of T cells to a peptide-MHC complex comprising a neoantigen peptide. In some embodiments, identifying neoantigen-specific

T cells comprises contacting the population of T cells to an APC comprising the peptide-MHC complex. In some embodiments, identifying neoantigen-specific T cells further comprises isolating T cells of the T cell population specific to the peptide-MHC complex. In some embodiments, identifying neoantigen-specific T cells further comprises identifying or predicting T cells of the of the T cell population specific to the peptide-MHC complex based on TCR clonality. In some embodiments, identifying a variable sequence of a TCR from the neoantigen-specific T cells is performed before identifying neoantigen-specific T cells. In some embodiments, identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing DNA, RNA, or amplified products thereof from one or more neoantigen-specific T cells that encode the variable sequence. In some embodiments, identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing DNA, RNA, or amplified products thereof from a single neoantigen-specific T cell that encodes the variable sequence. In some embodiments, identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing barcoded DNA or barcoded RNA, or amplified products thereof, from one or more neoantigen-specific T cells that encode the variable sequence. In some embodiments, identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises pairing a TCR-alpha chain with a TCR-beta chain.

[0086] In some embodiments, expressing a recombinant TCR comprises expressing the variable sequence identified from a polynucleotide comprising a sequence encoding the variable sequence identified. In some embodiments, the polynucleotide is a vector. In some embodiments, the vector is a viral vector. In some embodiments, the viral vector is a lentiviral vector. In some embodiments, expressing a recombinant TCR comprises transducing or transfecting the polynucleotide into cells. In some embodiments, the cells are a T cell line or healthy donor PMBCs.

[0087] In some embodiments, identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises expressing the one or more peptides in cells. In some embodiments, identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises loading the one or more peptides onto MHCs of cells. In some embodiments, identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises eluting or isolating a peptide of the one or more peptides from a peptide MHC complex. In some embodiments, identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises performing mass spectrometry on a peptide of the one or more peptides that was isolated or eluted from a peptide-MHC complex. In some embodiments, performing a functional assay comprises determining expression of one or more cell markers. In some embodiments, the one or more cell markers comprise TNF- α , IFN- γ , LAMP-1, 4-1BB, IL-2, IL-17A, Granzyme B, PD-1, CD25, CD69, TIM3, LAG3, CTLA-4, CD62L, CD45RA, CD45RO, FoxP3, or any combination thereof.

INCORPORATION BY REFERENCE

[0088] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0089] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0090] FIG. 1 depicts a workflow for antigen-specific TCR identification and analysis. PBMCs from healthy donors can be stimulated with the antigen of interest, after which antigen-specific T cells can be identified with peptide-MHC multimers (left). Antigen-specific T cells can be isolated and the TCR can be sequenced and analyzed (middle left). The TCR can be synthesized and expressed in a cell line or PBMCs, and the specificity can be again confirmed by peptide-MHC multimer (middle right). The TCR-expressing cell line or PBMCs can then be co-cultured with antigen-expressing cell lines to confirm the functionality of the TCR (right).

[0091] FIG. 2 is an example schematic of an antigen-specific CD8⁺ T cell expansion. PBMCs can be stimulated with the antigen of interest and cytokines. After expansion antigen-specific CD8⁺ T cells can be identified with peptide-MHC multimers.

[0092] FIG. 3A is an example schematic of recombinant TCR constructs and vector design for expression of the TCR constructs in cells.

[0093] FIG. 3B is an example schematic of a viral vector encoding recombinant TCRs for transduction or transfection into cells.

[0094] FIG. 4A depicts an example flow cytometry analysis of RAS antigen specific CD8⁺ T cell expansion in response to stimulation with a RAS peptide.

[0095] FIG. 4B depicts an example flow cytometry analysis of RAS antigen specific Jurkat cells after sorting of top 10% of multimer positive cells expressing a recombinant TCR after puromycin selection.

[0096] FIG. 5 depicts an example flow cytometry analysis of RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12V peptide (left), RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12C peptide (middle), and RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12D peptide (right).

[0097] FIG. 6A depicts example flow cytometry analyses of RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with a G12V or G12C mutant RAS peptides (left), TCR clone abundance analysis after sequencing the TCR from pooled hits (middle), and confirmation of mutant versus wild-type specificity of the top 2 retrieved clones after recombinant TCR expression in Jurkat cells (right).

[0098] **FIG. 6B** depicts experimental results of TCR functional assays to assess the specificity (left) and avidity (right) of three RAS TCRs (RAS TCR-3, RAS TCR-4, RAS TCR-11). Graphs showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 loaded with either RAS wild-type or RAS-mutant peptide (left) or increasing amounts of RAS-mutant peptide (right).

[0099] **FIG. 7A** depicts experimental results of a TCR functional avidity assay (peptide titration). A graph showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 loaded with increasing amounts of RAS-wild type or RAS-mutant peptide.

[0100] **FIG. 7B** depicts an example graph showing IL-2 production after co-culturing RAS TCR-4-transduced Jurkat cells with A375 cells modified to express HLA-A11:01 only, modified to express HLA-A11:01 and the KRAS G12V mutation, or modified to express HLA-A11:01 and an irrelevant mutation.

[0101] **FIG. 8A** depicts an example graph showing IFN γ secretion from RAS TCR-4-transduced PBMCs after co-culture with the naturally RAS G12V mutant SW620 colon cancer cell line without manipulation, with expression of HLA-A11:01 plus RAS G12V peptide added, and with expression of HLA-A11:01 only.

[0102] **FIG. 8B** depicts an example graph showing Caspase-3 activation after co-culture with RAS TCR-transduced PBMCs in the naturally RAS G12V mutant SW620 colon cancer cell line without manipulation, with expression of HLA-A11:01 plus RAS G12V peptide added, and with expression of HLA-A11:01 only.

[0103] **FIG. 8C** depicts experimental results of a cytotoxicity assay in which PBMCs transduced with an irrelevant TCR (left) or RAS TCR-4 (right) are co-cultured with SW620 target tumor cells expressing HLA-A11:01 and GFP over an increasing range of PBMC to target ratios. Graphs depicting the growth of the target cells over 72 hours as measured by GFP signal (top) and the death of the target cells as measured by Annexin V signaling (bottom) show that the RAS TCR-transduced PBMCs kill the target cells effectively.

[0104] **FIG. 8D** depicts experimental results of a cytotoxicity assay in which PBMCs transduced with an irrelevant TCR (left) or RAS TCR-4 (right) are co-cultured with SNG-M target tumor cells over an increasing range of PBMC to target ratios. Graphs depicting the death of the target cells as measured by Annexin V signaling over 72 hours show that the RAS TCR-transduced PBMCs kill the target cells.

[0105] **FIG. 8E** depicts experimental results of a safety screen of RAS TCR-4. Depicted on the left is a graph showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 loaded with the cognate RAS G12V epitope or peptides in which one position of the cognate epitope is changed to an alanine. Depicted in the center is a graph showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 loaded with the RAS G12V epitope or peptides identified from the initial safety screen. Depicted on the right is a graph showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 transduced with Perilipin4 and loaded with RAS G12V peptide or Perilipin4 peptide or no peptide (right).

[0106] **FIG. 8F** depicts the workflow used to identify RAS TCR-26 and RAS TCR-27. Depicted on the top left is a flow cytometry analysis of RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12V peptide. Depicted on the top right is the measurement of the cell growth

of target A375 cells expressing HLA-A11:01 and GFP over 54 hours after co-culture with the expanded CD8⁺ T cells. In this experiment, T cells expanded in the presence of the peptides were incubated with the A375 cells that were loaded with indicated amounts of peptides. Depicted on the bottom left is the specific cytotoxicity calculated at 48 hours comparing target cells loaded with increasing amounts of mutant-RAS peptide normalized to a control with wild-type peptide. Depicted on the bottom right are the relative abundances of TCR alpha and TCR beta CDR3 regions after single-cell TCR sequencing the multimer-positive cells.

[00107] **FIG. 8G** depicts the workflow used to identify RAS TCR-28. Depicted on the top left is a flow cytometry analysis of RAS-peptide-HLA-A11:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12V peptide. Depicted on the top right is the measurement of the cell growth of target A375 cells expressing HLA-A11:01 and GFP and loaded with varying doses of the peptide, over 54 hours after co-culture with the expanded CD8⁺ T cells. The data show good inverse correlation of cell growth with peptide dose, which demonstrates the TCR specificity to the peptide. Depicted on the bottom left is the specific cytotoxicity calculated at 48 hours comparing target cells loaded with increasing amounts of mutant-RAS peptide normalized to a control with wild-type peptide. Depicted on the bottom right are the relative abundances of TCR alpha and TCR beta CDR3 regions after single-cell TCR sequencing the multimer-positive cells.

[00108] **FIG. 9** depicts an example flow cytometry analysis of RAS-peptide-HLA-A03:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12V peptide (left) and RAS-peptide-HLA-A03:01 complex specific CD8⁺ T cell expansion in response to stimulation with RAS G12C peptide (right).

[00109] **FIG. 10A** depicts a workflow for antigen-specific TCR identification and analysis of a sample depicted in **FIG. 9**.

[00110] **FIG. 10B** depicts a workflow for antigen-specific TCR identification of a sample depicted in **FIG. 9**.

[00111] **FIG. 10C** depicts experimental results of TCR functional avidity assays (peptide titration). Depicted on the left is a graph showing IL-2 production after co-culturing RAS TCR-5-transduced Jurkat cells with A375 cells expressing HLA-A03:01 loaded with increasing amounts of RAS-wild type or RAS-mutant peptide. Depicted on the right is a graph showing IL-2 production after co-culturing RAS TCR-6-transduced Jurkat cells with A375 cells expressing HLA-A03:01 loaded with increasing amounts of RAS-wild type or RAS-mutant peptide.

[00112] **FIG. 10D** depicts experimental results of a cytotoxicity assay in which PBMCs transduced with an irrelevant TCR (left), RAS TCR-5 (middle), or RAS TCR-6 (right) are co-cultured with A375 target tumor cells expressing HLA-A03:01 and GFP over an increasing range of PBMC to target ratios. Graphs of the growth of the target cells over 72 hours as measured by GFP signal show that the RAS TCR-transduced PBMCs kill the target cells effectively.

[00113] **FIG. 10E** depicts experimental results of a cytotoxicity assay in which PBMCs transduced with an irrelevant TCR, RAS TCR-5, or RAS TCR-6 are co-cultured with NCI-H441 target tumor cells. Increased Annexin V signal in target cells over 48 hours shows that the RAS TCRs are able to recognize and kill this target tumor cell.

[00114] **FIG. 10F** depicts experimental results of a safety screen of RAS TCR-5 (top) and RAS TCR-6 (bottom). Graphs showing IL-2 production after co-culturing RAS TCR-transduced Jurkat cells with A375 cells expressing HLA-A11:01 loaded with the cognate RAS G12V epitope or peptides in which one position of the cognate epitope is changed to an alanine.

[00115] **FIG. 11** depicts an example workflow for GATA3 antigen-specific TCR identification and analysis. Depicted on the left is an example flow cytometry analysis of GATA3-peptide-HLA-A02:01 complex specific CD8⁺ T cell expansion in response to stimulation with a GATA3 mutant peptide.

[00116] **FIG. 12A** depicts results of a TCR functional avidity assay (peptide titration). A graph showing IL-2 production after co-culturing GATA3 TCR-1-transduced T cells with cells loaded or transduced with increasing amounts of GATA3 mutant peptide.

[00117] **FIG. 12B** depicts a graph showing IL-2 production after co-culturing GATA3 TCR-transduced Jurkat cells with cells loaded with an irrelevant peptide or the mutant GATA3 peptide, and cells transduced with an irrelevant vector or a vector encoding the GATA3 neoORF mutation.

[00118] **FIG. 12C** depicts a graph showing upregulation of IFN γ production in 2 cell samples expressing control peptide or a GATA3 mutant peptide.

[00119] **FIG. 12D** depicts a graph showing percent CD8 and CD107a positive cells in 2 cell samples expressing control peptide or a GATA3 mutant peptide.

[00120] **FIG. 12E** depicts a graph showing percent live caspase 3 positive cells in 2 cell samples expressing control peptide or a GATA3 mutant peptide.

[00121] **FIG. 13** depicts an example workflow for TMPRSS2:ERG antigen-specific TCR identification and analysis. Depicted on the left is an example flow cytometry analysis of TMPRSS2:ERG-peptide-HLA-A02:01 complex specific CD8⁺ T cell expansion in response to stimulation with a TMPRSS2:ERG mutant peptide.

[00122] **FIG. 14** depicts an example graph showing IL-2 production after co-culturing TMPRSS2:ERG TCR-1-transduced Jurkat cells with 293T cells either unmanipulated, loaded with irrelevant peptide, or loaded with the TMPRSS2:ERG peptide.

[00123] **FIG. 15** depicts an example workflow for BTK antigen-specific TCR identification and analysis. Depicted on the left is an example flow cytometry analysis of BTK-peptide-HLA-A02:01 complex specific CD8⁺ T cell expansion in response to stimulation with a BTK mutant peptide.

[00124] **FIG. 16A** depicts an example flow cytometry analysis of EGFR-peptide-HLA-A02:01 complex specific CD8⁺ T cell expansion in response to stimulation with EGFR T790M peptide. Each plot on FIG. 16A represents a representative T cell expansion sample (well) with the EGFR T790M peptide. The TCRs from the cells were sequenced.

[00125] **FIG. 16B** depicts an example flow cytometry analysis of potential EGFR-peptide-HLA-A02:01 complex specific CD8⁺ T cell populations in response to stimulation with EGFR T790M peptide, the TCRs of which remain to be sequenced. Each plot on FIG. 16B represents a representative T cell expansion sample (well) in response to the EGFR T790M peptide.

DETAILED DESCRIPTION

[00126] The term “about” or “approximately” means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, i.e., the limitations of the measurement system. For example, “about” can mean within 1 or more than 1 standard deviation, per the practice in the art. Alternatively, “about” can mean a range of up to 20%, up to 10%, up to 5%, or up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5-fold, and more preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated the term “about” meaning within an acceptable error range for the particular value should be assumed.

[00127] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present disclosure, the preferred methods and materials are now described. The details of one or more particular embodiments are set forth in the description below.

I. Definitions

[00128] Unless otherwise stated, the term “TCR” should be understood to encompass full TCRs as well as antigen-binding portions or antigen-binding fragments (also called MHC-peptide binding fragments) thereof. In some embodiments, the TCR is an intact or full-length TCR. In some embodiments, the TCR is an antigen-binding portion that is less than a full-length TCR but that binds to a specific antigenic peptide bound to (i.e., in the context of) an MHC molecule, i.e., an MHC-peptide complex. In some cases, an antigen-binding portion or fragment of a TCR can contain only a portion of the structural domains of a full-length or intact TCR, but yet is able to bind the epitope (e.g., MHC-peptide complex) to which the full TCR binds. In some cases, an antigen-binding portion or fragment of a TCR contains the variable domains of a TCR, such as variable α chain and variable β chain of a TCR, sufficient to form a binding site for binding to a specific MHC-peptide complex, such as generally where each chain contains three complementarity determining regions. Polypeptides or proteins having a binding domain which is an antigen-binding domain or is homologous to an antigen-binding domain are included. Complementarity determining region (CDR) grafted TCRs and other humanized TCRs (including CDR modifications and framework region modifications) are also contemplated by these terms. It should be noted that while reference may be made only to immunoglobulin chains (e.g., heavy chains and light chains), the disclosed invention can be applied to multiple other different types of paired sequences, e.g., T cell receptor chain pairs (TCR α and TCR β chains and TCR γ and TCR δ chains), and is not limited to immunoglobulins.

[00129] The terms “complementarity determining region,” and “CDR,” synonymous with “hypervariable region” or “HVR,” are known in the art to refer to non-contiguous sequences of amino acids within TCR variable regions, which confer specificity and/or binding affinity to an MHC-peptide complex. In general, there are three CDRs in each alpha chain variable region (CDR-H1, CDR-H2, CDR-H3) and three CDRs in each beta chain

variable region (CDR-L1, CDR-L2, CDR-L3). “Framework regions” and “FR” are known in the art to refer to the non-CDR portions of the variable regions of the alpha and beta chains. In general, there are four FRs in each full-length alpha chain variable region (FR-H1, FR-H2, FR-H3, and FR-H4), and four FRs in each full-length beta chain variable region (FR-L1, FR-L2, FR-L3, and FR-L4).

[00130] The term “variable region” or “variable domain” refers to the domain of a TCR alpha, beta, gamma or delta chain, that is involved in binding the TCR to antigen-MHC complexes. The variable domains of the alpha chain and beta chain ($V\alpha$ and $V\beta$, respectively), and the gamma chain and delta chain ($V\gamma$ and $V\delta$, respectively) of a native TCR generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three CDRs. A single $V\alpha$ or $V\beta$ domain, or $V\gamma$ or $V\delta$ domain, may be sufficient to confer binding specificity to a peptide-MHC complex.

[00131] Also provided herein are TCR fragments, including antigen-binding fragments. In some embodiments, the TCR is an antigen-binding portion thereof, such as a variant of a full-length TCR not containing the transmembrane and/or cytoplasmic region(s) thereof, which may be referred to as a full soluble TCR. In some embodiments, the TCR is a dimeric TCR (dTCR). In some embodiments, the TCR is a single-chain TCR (scTCR), such as a scTCR having a structure as described in PCT patent publication numbers WO2003/020763, WO2004/033685, or WO2011/044186. In certain embodiments, the TCR is a single-chain TCR fragment comprising an alpha chain variable region linked to a beta chain variable region, such as a scTv. In some embodiments, a scTv is also referred to as a scFv. A single-chain Tv or scTv refers in some aspects TCR fragments that comprise the variable alpha or gamma chain ($V\alpha$ or $V\gamma$) and variable beta or delta chain ($V\beta$ or $V\delta$) domains of a TCR, wherein these domains are present in a single polypeptide chain. Generally, the Tv polypeptide further comprises a polypeptide linker between the $V\alpha$ and $V\beta$ domains or $V\gamma$ and $V\delta$ domains which enables the scTv to form the desired structure for antigen binding. A diabody refers in some aspects to TCR fragments with two antigen-binding sites, which fragments comprise a $V\alpha$ connected to a $V\beta$ in the same polypeptide chain ($V\alpha$ - $V\beta$) or a $V\gamma$ connected to a $V\delta$ in the same polypeptide chain ($V\gamma$ - $V\delta$). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Exemplary diabodies are described more fully in, for example, EP404097 and WO93111161. Fv refers in some aspects to a TCR fragment which contains a complete peptide-MHC complex recognition and peptide-MHC complex binding site. This region consists of a dimer of one TCR α chain and one TCR β chain or one TCR γ chain and one TCR δ chain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define a peptide-MHC complex binding site on the surface of the $V\alpha$ - $V\beta$ dimer or $V\gamma$ - $V\delta$ dimer. Collectively, a combination of one or more of the CDRs from each of the $V\alpha$ - $V\beta$ chains or $V\gamma$ - $V\delta$ chains confers peptide-MHC complex binding specificity to the TCR. For example, it would be understood that, for example, the CDR α 3 and CDR β 3 or CDR γ 3 and CDR δ 3 could be sufficient to confer antigen-binding specificity to a TCR when transferred to $V\alpha$ and $V\beta$ chains or $V\gamma$ - $V\delta$ chains of a recipient selected TCR or antigen-binding fragment thereof and this combination of CDRs can be tested for binding, affinity, etc. Furthermore, although

the two domains of a Tv fragment ($V\alpha$ and $V\beta$ or $V\gamma$ and $V\delta$), are coded for by separate genes, they can be joined using recombinant methods by a synthetic linker that enables them to be made as a single protein chain in which the $V\alpha$ and $V\beta$ or $V\gamma$ and $V\delta$ chain regions pair to form monovalent molecules (known as single chain Tv (scTv)). Such scTvs are also intended to be encompassed within the peptide-MHC complex binding portion of a TCR.

[00132] A “bispecific TCR” refers in some aspects to a TCR that shows specificities to two different peptide-MHC complexes or two different types of peptide-MHC complexes. The terms as used herein specifically include, without limitation, TCRs which show binding specificity for a target peptide-MHC complex and to another peptide-MHC complex that facilitates delivery to a particular tissue. Similarly, multi-specific TCRs have two or more binding specificities. A linear TCR refers in some aspects to a pair of tandem Fd segments (*e.g.*, $V\alpha$ - $C\alpha_1$ - $V\alpha$ - $C\alpha_1$) which form a pair of antigen binding regions. Linear TCRs can be bispecific or monospecific.

[00133] An “antigen-binding domain” refers in some aspects to one or more fragments of a TCR that retain the ability to specifically bind to a peptide-MHC complex. Non-limiting examples of TCR fragments included within such terms include, but are not limited to, (i) a Tab fragment, a monovalent fragment consisting of the $V\beta$, $V\alpha$, $C\beta$ and $C\alpha$ domains; (ii) a $T(ab')_2$ fragment, a bivalent fragment containing two Tab fragments linked by a disulfide bridge at the hinge region; (iii) a Td fragment consisting of the $V\alpha$ and $C\alpha_1$ domains; (iv) a Tv fragment containing the $V\beta$ and $V\alpha$ domains of a single arm of a TCR, including scTvs, (v) a dAb fragment (Ward et al., (1989) Nature 341:544 546), which contains a $V\alpha$ domain; and (vi) an isolated CDR. Included in this definition are TCRs with a single alpha chain or a single beta chain.

[00134] Among the provided TCRs are humanized and human TCRs. A “humanized” TCR is a TCR in which all or substantially all CDR amino acid residues are derived from non-human CDRs and all or substantially all FR amino acid residues are derived from human FRs. A humanized TCR optionally may include at least a portion of a TCR constant region derived from a human TCR. A “humanized form” of a non-human TCR, refers to a variant of the non-human TCR that has undergone humanization, typically to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human TCR. In some embodiments, some FR residues in a humanized TCR are substituted with corresponding residues from a non-human TCR (*e.g.*, the TCR from which the CDR residues are derived), *e.g.*, to restore or improve TCR specificity or affinity. A “human TCR” is a TCR with an amino acid sequence corresponding to that of a TCR produced by a human or a human cell, or non-human source that utilizes human TCR repertoires or other human TCR-encoding sequences, including human TCR libraries. The term excludes humanized forms of non-human TCRs comprising non-human peptide-MHC complex binding regions, such as those in which all or substantially all CDRs are non-human. Human TCRs may be prepared by administering an immunogen to a transgenic animal that has been modified to produce intact human TCRs or intact TCRs with human variable regions in response to antigenic challenge. Such animals typically contain all or a portion of the human TCR loci, which replace the endogenous TCR loci, or which are present extrachromosomally or integrated randomly into the animal’s

chromosomes. In such transgenic animals, the endogenous TCR loci have generally been inactivated. Human TCRs also may be derived from human TCR libraries, including phage display and cell-free libraries, containing TCR-encoding sequences derived from a human repertoire.

[00135] The term “cancer neoantigen” or “neoantigen” or “neoepitope” can refer to antigens that are not encoded in a normal, non-mutated host genome. A neoantigen can relate to an antigen including one or more amino acid modifications compared to the parental antigen. For example, a neoantigen may be a tumor-associated neoantigen, wherein the term “tumor-associated neoantigen” can include a peptide or protein including amino acid modifications due to tumor-specific mutations. In some instances, a neoantigen represents either oncogenic viral proteins or abnormal proteins that arise as a consequence of somatic mutations. For example, a neoantigen can arise by the disruption of cellular mechanisms through the activity of viral proteins. Another example can be an exposure of a carcinogenic compound, which in some cases can lead to a somatic mutation. This somatic mutation can ultimately lead to the formation of a tumor/cancer. A neoantigen can be a class of tumor antigens which arise from tumor-specific changes in proteins. Neoantigens encompass, but are not limited to, tumor antigens which arise from, for example, a substitution in a protein sequence, a frame shift mutation, a fusion polypeptide, an in-frame deletion, an insertion, and expression of an endogenous retroviral polypeptide. A neoepitope can be an epitope that is not present in a reference, such as a non-diseased cell, e.g., a non-cancerous cell or a germline cell, but is found in a diseased cell, e.g., a cancer cell. This includes situations where a corresponding epitope is found in a normal non-diseased cell or a germline cell but, due to one or more mutations in a diseased cell, e.g., a cancer cell, the sequence of the epitope is changed so as to result in the neoepitope.

[00136] An “epitope” refers in some aspects to a portion of an antigen or other macromolecule capable of forming a binding interaction with the variable region binding pocket of a TCR. In some aspects, an epitope refers to a portion of a peptide-MHC complex capable of forming a binding interaction with the variable region binding pocket of a TCR. Such binding interactions can be manifested as an intermolecular contact with one or more amino acid residues of one or more CDRs. Peptide-MHC complex binding can involve, for example, a CDR3, a CDR3 pair, or in some instances, interactions of up to all six CDRs of the $V\alpha$ and $V\beta$ chains or $V\gamma$ or $V\delta$ chains. An epitope can be a linear peptide sequence (i.e., “continuous”) or can be composed of noncontiguous amino acid sequences (i.e., “conformational” or “discontinuous”). A TCR can recognize one or more amino acid sequences. Therefore an epitope can define more than one distinct amino acid sequence. In some aspects, a TCR can recognize one or more amino acid sequences or epitopes in the context of an MHC. Epitopes recognized by TCRs can be determined by peptide mapping and sequence analysis techniques well known to one of skill in the art. Binding interactions are manifested as intermolecular contacts with one or more amino acid residues of a CDR. An epitope can refer to an antigenic determinant in a molecule such as an antigen, i.e., to a part in or fragment of the molecule that is recognized by the immune system, for example, that is recognized by a T cell, in particular when presented in the context of MHC molecules. An epitope of a protein such as a tumor antigen can comprise a continuous or discontinuous portion of the protein and can be between

5 and 100, 5 and 50, 8 and 30, or 10 and 25 amino acids in length, for example, the epitope may be 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids in length.

[00137] The term “binding” refers to a direct association between two molecules, due to, for example, covalent, electrostatic, hydrophobic, and ionic and/or hydrogen-bond interactions under physiological conditions, and includes interactions such as salt bridges and water bridges, as well as any other conventional means of binding.

[00138] In some embodiments, reference to a TCR with “specific binding” refers to a situation in which a TCR will not show any significant binding to molecules other than the peptide-MHC complex containing the epitope recognized by the TCR. The term is also applicable where for example, an antigen binding domain is specific for a particular epitope which is carried by a number of peptide-MHC complexes, in which case the selected TCR or peptide-MHC complex binding fragment thereof carrying the peptide-MHC complex binding domain will be able to bind to the various peptide-MHC complexes carrying the epitope. The terms “preferentially binds” or “specifically binds” mean that the TCRs or fragments thereof bind to an epitope with greater affinity than it binds unrelated amino acid sequences, and, if cross-reactive to other polypeptides containing the epitope, are not toxic at the levels at which they are formulated for administration to human use. In one aspect, such affinity is at least 1-fold greater, at least 2-fold greater, at least 3-fold greater, at least 4-fold greater, at least 5-fold greater, at least 6-fold greater, at least 7-fold greater, at least 8-fold greater, at least 9-fold greater, 10-fold greater, at least 20-fold greater, at least 30-fold greater, at least 40-fold greater, at least 50-fold greater, at least 60-fold greater, at least 70-fold greater, at least 80-fold greater, at least 90-fold greater, at least 100-fold greater, or at least 1000-fold greater than the affinity of the TCR or fragment thereof for unrelated amino acid sequences.

[00139] The term “affinity” refers to a measure of the strength of binding between two members of a binding pair (e.g., a human leukocyte antigen (HLA)-binding peptide and a class I or II HLA, or a peptide-HLA complex and a T cell receptor (TCR)). Affinity can be expressed as an equilibrium constant of the reversible binding of two agents and can be expressed as K_D , K_A , K_{off} or K_{on} . K_D refers to the dissociation constant between two members of a binding pair and has units of molarity. K_A refers to the affinity constant between two members of a binding pair is the inverse of the dissociation constant. Affinity may be determined experimentally, for example by surface plasmon resonance (SPR) using commercially available Biacore SPR units. K_{off} refers to the off-rate constant of two members of a binding pair, (e.g., the off-rate constant of an HLA-binding peptide and a class I or II HLA, or a peptide-HLA complex and a TCR). K_{on} refers to the on-rate constant of two members of a binding pair, (e.g., the on-rate constant of an HLA-binding peptide and a class I or II HLA, or a peptide-HLA complex and a TCR). Affinity of a binding protein to a ligand such as affinity of a TCR for an epitope can be, for example, from about 100 nanomolar (nM) to about 0.1 nM, from about 100 nM to about 1 picomolar (pM), or from about 100 nM to about 1 femtomolar (fM). The term “avidity” refers to the resistance of a complex of two or more agents to dissociation after dilution.

[00140] Throughout this disclosure, “binding data” results may be expressed in terms of an “ IC_{50} .” Affinity may also be expressed as the inhibitory concentration 50 (IC_{50}), or the concentration at which 50% of a first member of a binding pair (e.g., a peptide) is displaced. Likewise, $\ln(IC_{50})$ refers to the natural log of the IC_{50} .

For example, an IC_{50} may be the concentration of a tested peptide in a binding assay at which 50% inhibition of binding of a labeled reference peptide is observed. Given the conditions in which the assays are run (e.g., limiting HLA protein concentrations and/or labeled reference peptide concentrations), these values can approximate K_D values. Assays for determining binding are well known in the art and are described in detail, for example, in PCT publications WO 94/20127 and WO 94/03205, and other publications such as Sidney et al., *Current Protocols in Immunology* 18.3.1 (1998); Sidney, et al., *J. Immunol.* 154:247 (1995); and Sette, et al., *Mol. Immunol.* 31:813 (1994). Alternatively, binding can be expressed relative to binding by a reference standard peptide. Binding can also be determined using other assay systems including those using: live cells (e.g., Ceppellini et al., *Nature* 339:392 (1989); Christnick et al., *Nature* 352:67 (1991); Busch et al., *Int. Immunol.* 2:443 (1990); Hill et al., *J. Immunol.* 147:189 (1991); del Guercio et al., *J. Immunol.* 154:685 (1995)), cell free systems using detergent lysates (e.g., Cerundolo et al., *J. Immunol.* 21:2069 (1991)), immobilized purified MHC (e.g., Hill et al., *J. Immunol.* 152, 2890 (1994); Marshall et al., *J. Immunol.* 152:4946 (1994)), ELISA systems (e.g., Reay et al., *EMBO J.* 11:2829 (1992)), surface plasmon resonance (e.g., Khilko et al., *J. Biol. Chem.* 268:15425 (1993)); high flux soluble phase assays (Hammer et al., *J. Exp. Med.* 180:2353 (1994)), and measurement of class I MHC stabilization or assembly (e.g., Ljunggren et al., *Nature* 346:476 (1990); Schumacher et al., *Cell* 62:563 (1990); Townsend et al., *Cell* 62:285 (1990); Parker et al., *J. Immunol.* 149:1896 (1992)).

[00141] The terms “major histocompatibility complex” and the abbreviation “MHC” can include MHC class I and MHC class II molecules and relate to a complex of genes which occurs in all vertebrates. MHC proteins or molecules can be important for signaling between lymphocytes and antigen presenting cells or diseased cells in immune reactions, wherein the MHC proteins or molecules bind peptides and present them for recognition by T cell receptors. The proteins encoded by the MHC can be expressed on the surface of cells, and display both self-antigens (peptide fragments from the cell itself) and non-self-antigens (e.g., fragments of invading microorganisms) to a T cell. The MHC region can be divided into three subgroups, class I, class II, and class III. MHC class I proteins can contain an α -chain and β 2-microglobulin (not part of the MHC encoded by chromosome 15). They can present antigen fragments to cytotoxic T cells. MHC class II proteins can contain α - and β -chains and they can present antigen fragments to T-helper cells. MHC class III region can encode for other immune components, such as complement components and cytokines. The MHC can be both polygenic (there are several MHC class I and MHC class II genes) and polymorphic (there are multiple alleles of each gene).

[00142] The term “haplotype” can refer to the human leukocyte antigen (HLA) alleles found on one chromosome and the proteins encoded thereby. Haplotype may also refer to the allele present at any one locus within the MHC. Each class of MHC is represented by several loci: e.g., HLA-A (Human Leukocyte Antigen-A), HLA-B, HLA-C, HLA-E, HLA-F, HLA-G, HLA-H, HLA-J, HLA-K, HLA-L, HLA-P and HLA-V for class I and HLA-DRA, HLA-DRB1-9, HLA-DQA1, HLA-DQB1, HLA-DPA1, HLA-DPB1, HLA-DPB2, HLA-

DMA, HLA-DMB, HLA-DOA, and HLA-DOB for class II. The terms “HLA allele” and “MHC allele” are used interchangeably herein.

[00143] The terms “polynucleotide”, “nucleotide”, “nucleotide sequence”, “nucleic acid” and “oligonucleotide” are used interchangeably. They can refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise one or more modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. Polynucleotides can include nonstandard nucleotides, such as nucleotide analogs or modified nucleotides. In some embodiments, nonstandard nucleotides can stabilize hybrid formation. In some embodiments, nonstandard nucleotides can destabilize hybrid formation. In some embodiments, nonstandard nucleotides can enhance hybridization specificity. In some embodiments, nonstandard nucleotides can reduce hybridization specificity. Examples of nonstandard nucleotide modifications include 2' O-Me, 2' O-allyl, 2' O-propargyl, 2' O-alkyl, 2' fluoro, 2' arabino, 2' xylo, 2' fluoro arabino, phosphorothioate, phosphorodithioate, phosphoroamidates, 2' Amino, 5-alkyl-substituted pyrimidine, 3' deoxyguanosine, 5-halo-substituted pyrimidine, alkyl-substituted purine, halo-substituted purine, bicyclic nucleotides, 2'MOE, PNA molecules, LNA-molecules, LNA-like molecules, diaminopurine, S2T, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N⁶-adenine, 7-methyl guanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-D46-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, uracil-5-oxy acetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, 2,6-diaminopurine, and derivatives thereof. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[00144] “Complementarity” can refer to the ability of a nucleic acid to form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. A percent complementarity can indicate the percentage of residues in a nucleic acid molecule which can form hydrogen

bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary, respectively). “Perfectly complementary” can mean that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. “Substantially complementary” refers to a degree of complementarity that is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% over a region of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, or more nucleotides, or can refer to two nucleic acids that hybridize under stringent conditions. Sequence identity, such as for the purpose of assessing percent complementarity, may be measured by any suitable alignment algorithm, including but not limited to the Needleman-Wunsch algorithm (e.g., the EMBOSS Needle aligner available at www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html, optionally with default settings), the BLAST algorithm (see e.g., the BLAST alignment tool available at blast.ncbi.nlm.nih.gov/Blast.cgi, optionally with default settings), or the Smith-Waterman algorithm. Optimal alignment may be assessed using any suitable parameters of a chosen algorithm, including default parameters.

[00145] The terms “polypeptide” and “protein” are used interchangeably to refer to a polymer of amino acid residues, and, are not limited to a minimum length. For example, a polypeptide can comprise at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000 peptides or amino acids. Examples of polypeptides include, but are not limited to, amino acid chains, proteins, peptides, hormones, polypeptide saccharides, lipids, glycolipids, phospholipids, antibodies, enzymes, kinases, receptors, transcription factors, and ligands. Polypeptides, including the provided TCRs and TCR chains and other peptides, e.g., linkers and binding peptides, may include amino acid residues including natural and/or non-natural amino acid residues. The terms also include post-expression modifications of the polypeptide, for example, glycosylation, sialylation, acetylation, phosphorylation, and the like. In some aspects, the polypeptides may contain modifications with respect to a native or natural sequence, as long as the protein maintains the desired activity. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental, such as through mutations of hosts which produce the proteins or errors due to PCR amplification.

[00146] As used herein, the twenty conventional amino acids and their abbreviations known to one skilled in the art follow conventional usage. Stereoisomers (e.g., D-amino acids) of the twenty conventional amino acids, unnatural amino acids such as α -, α -disubstituted amino acids, N-alkyl amino acids, lactic acid, and other unconventional amino acids may also be suitable components for polypeptides of the present invention. Examples of unconventional amino acids include: 4-hydroxyproline, γ -carboxyglutamate, ϵ -N,N,N-trimethyllysine, ϵ -N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ -N-methylarginine, and other similar amino acids and imino acids (e.g., 4-hydroxyproline). In the polypeptide notation used herein, the left hand direction is the amino terminal direction and the right hand direction is the carboxy-terminal direction, in accordance with standard usage and convention. Percent (%) sequence identity with respect to a reference polypeptide sequence (or nucleic acid sequence) is the percentage

of amino acid residues (or nucleotides in case of nucleic acid sequence) in a candidate sequence that are identical with the amino acid residues (or nucleotides) in the reference polypeptide sequence (or nucleic acid sequence), after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, Calif., or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary. In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y , where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

[00147] A “germline sequence” refers to a genetic sequence from the haploid gametes and those diploid cells from which they are formed. Germline DNA contains multiple gene segments that encode a single TCR α or TCR β chain, or a single TCR γ or TCR δ chain. These gene segments are carried in the germ cells but cannot be transcribed and translated until they are arranged into functional genes. During T cell differentiation in the bone marrow, these gene segments are randomly shuffled by a dynamic genetic system capable of generating more than 10^8 specificities.

[00148] Inhibition, “treatment” and “treating” are used interchangeably and refer to, for example, stasis of symptoms, prolongation of survival, partial or full amelioration of symptoms, and partial or full eradication of a condition, disease or disorder associated with excess levels of protein or correlated with protein activity. For example, treatment of cancer includes, but is not limited to, stasis, partial or total elimination of a cancerous

growth or tumor. Treatment or partial elimination includes, for example, a fold reduction in growth or tumor size and/or volume such as about 2-fold, about 3-fold, about 4-fold, about 5-fold, about 10-fold, about 20-fold, about 50-fold, or any fold reduction in between. Similarly, treatment or partial elimination can include a percent reduction in growth or tumor size and/or volume of about 1%, 2%, 3%, 4%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or any percentage reduction in between. Prevention refers to prophylaxis, prevention of onset of symptoms, prevention of progression of a disease or disorder associated with excess levels of protein or correlated with protein activity.

[00149] A “subject”, “individual”, “host” or “patient” refers to living organisms such as mammals. Examples of subjects and hosts include, but are not limited to, horses, cows, camels, sheep, pigs, goats, dogs, cats, rabbits, guinea pigs, rats, mice (*e.g.*, humanized mice), gerbils, non-human primates (*e.g.*, macaques), humans and the like, non-mammals, including, *e.g.*, non-mammalian vertebrates, such as birds (*e.g.*, chickens or ducks) fish (*e.g.*, sharks) or frogs (*e.g.*, *Xenopus*), and non-mammalian invertebrates, as well as transgenic species thereof. In certain aspects, a subject refers to a single organism (*e.g.*, human). In certain aspects, or a group of individuals composing a small cohort having either a common immune factor to study and/or disease, and/or a cohort of individuals without the disease (*e.g.*, negative/normal control) are provided. A subject from whom samples are obtained can either be inflicted with a disease and/or disorder (*e.g.*, one or more allergies, infections, cancers or autoimmune disorders or the like) and can be compared against a negative control subject which is not affected by the disease.

[00150] A “kit” refers to a delivery system for delivering materials or reagents for carrying out a method disclosed herein. In some embodiments, kits include systems that allow for the storage, transport, or delivery of reaction reagents (*e.g.*, probes, enzymes, etc. in the appropriate containers) and/or supporting materials (*e.g.*, buffers, written instructions for performing the assay etc.) from one location to another. For example, kits include one or more enclosures (*e.g.*, boxes) containing the relevant reaction reagents and/or supporting materials. Such contents may be delivered to the intended recipient together or separately. For example, a first container may contain an enzyme for use in an assay, while a second container contains a plurality of primers. A packaging material refers to a physical structure housing the components of the kit. The packaging material can maintain the components sterile and can be made of material commonly used for such purposes (*e.g.*, paper, corrugated fiber, glass, plastic, foil, ampules, etc.). The label or packaging insert can include appropriate written instructions. Kits, therefore, can additionally include labels or instructions for using the kit components in any method of the invention. A kit can include a compound in a pack, or dispenser together with instructions for administering the compound in a method described herein.

[00151] The term “resistance mutation” refers to a mutation in a gene that allows the gene or the host cell containing the gene to become resistant to treatment with a drug. For example, BTK C481S mutation is a resistance mutation which can confer ibrutinib resistance.

II. Overview

[00152] The present disclosure provides T cell receptors (TCRs) against neoantigens, isolated nucleic acid molecules encoding TCRs against neoantigens, T cells expressing said TCRs, and pharmaceutical compositions for use in the treatment of diseases involving malignant cells expressing said neoantigens.

[00153] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3, 18, 33, 49, 65, 81, 97, and 113, and/or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6, 21, 36, 52, 68, 84, 100, and 116.

[00154] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the epitope from RAS comprises a region having at least 70% sequence identity to an amino acid sequence selected from SEQ ID NOs: 15, 30, 45, 46, 61, 62, 77, 78, 93, 94, 109, 110, 125, 126 and 219-222.

[00155] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele.

[00156] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 9, 24, 39, 55, 71, 87, 103, and 119. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 12, 27, 42, 58, 74, 90, 106, and 122. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 1, 16, 31, 47, 63, 79, 95, and 111. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 4, 19, 34, 50, 66, 82, 98, and 114. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 2, 17, 32, 48, 64, 80, 96, and 112. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 5, 20, 35, 51, 67, 83, 99, and 115. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 9; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 12. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 1, a CDR2 of SEQ ID NO: 2, and a CDR3 of SEQ ID NO: 3; and the TCR beta chain

construct comprises a CDR1 of SEQ ID NO: 4, a CDR2 of SEQ ID NO: 5, and a CDR3 of SEQ ID NO: 6. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 24; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 27. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 16, a CDR2 of SEQ ID NO: 17, and a CDR3 of SEQ ID NO: 18; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 19, a CDR2 of SEQ ID NO: 20, and a CDR3 of SEQ ID NO: 21. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 39; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 42. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 31, a CDR2 of SEQ ID NO: 32, and a CDR3 of SEQ ID NO: 33; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 34, a CDR2 of SEQ ID NO: 35, and a CDR3 of SEQ ID NO: 36. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 55; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 58. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 47, a CDR2 of SEQ ID NO: 48, and a CDR3 of SEQ ID NO: 49; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 50, a CDR2 of SEQ ID NO: 51, and a CDR3 of SEQ ID NO: 52.

[00157] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 144 and SEQ ID NO: 147.

[00158] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the epitope from TMPRSS2:ERG comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 156.

[00159] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 150. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to SEQ ID NO: 142 or SEQ ID NO: 145. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to SEQ ID NO: 143 or SEQ ID NO: 146. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 150; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO:

142, a CDR2 of SEQ ID NO: 143, and a CDR3 of SEQ ID NO: 144; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 145, a CDR2 of SEQ ID NO: 146, and a CDR3 of SEQ ID NO: 147.

[00160] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 129 and SEQ ID NO: 132.

[00161] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant GATA3 peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[00162] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant GATA3 peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 129 or SEQ ID NO: 132; and/or specifically binds to a mutant GATA3 peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 141.

[00163] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the epitope from GATA3 comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 141.

[00164] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 135. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 138. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 127 and SEQ ID NO: 130. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 128 and SEQ ID NO: 131. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 135; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 138. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 127, a CDR2 of SEQ ID NO: 128, and a CDR3 of SEQ ID NO: 129; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 130, a CDR2 of SEQ ID NO: 131, and a CDR3 of SEQ ID NO: 132.

[00165] In another aspect, provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the TCR alpha chain construct comprises a

complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 161 and SEQ ID NO: 176, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 164 and SEQ ID NO: 179. In another aspect, provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant BTK peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct. In another aspect, provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant BTK peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 161, 164, 176, or 179; and/or specifically binds to a mutant BTK peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 173 or 188. In another aspect, provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the epitope from BTK comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 173 or 188. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or 182. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 159, 162, 174, and 177. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 160, 163, 175 and 178. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or 182; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 159 or 174, a CDR2 of SEQ ID NO: 160 or 175, and a CDR3 of SEQ ID NO: 161 or 176; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 162 or 177, a CDR2 of SEQ ID NO: 163 or 178, and a CDR3 of SEQ ID NO: 164 or 179.

[00166] In yet another aspect, the present disclosure provides a host cell comprising the nucleic acid encoding a TCR against a neoantigen provided herein, a vector containing the nucleic acid sequence, or a protein encoded by the nucleic acid provided herein. In some embodiments, the host cell is a CD4⁺ T cell. In some embodiments, the host cell is a CD8⁺ T cell. The host cell may be a natural killer (NK) cell or a B cell. The host cell may be an immortalized cell line.

[00167] In yet another aspect, the present disclosure provides pharmaceutical compositions comprising the nucleic acid encoding a TCR against a neoantigen provided herein, a host cell comprising the nucleic acid

encoding a TCR against a neoantigen provided herein, a vector containing the nucleic acid sequence, or a protein encoded by the nucleic acid provided herein. In some embodiments, provided herein also comprises a method of using the pharmaceutical compositions disclosed herein.

[00168] Also provided herein in an additional aspect is a method of treating a subject with a disease or condition, comprising administering to the subject a pharmaceutical composition disclosed herein. In some embodiments, the subject has cancer.

III. T Cell Receptors (TCRs)

[00169] The ability of T cells to recognize antigens associated with various cancers or infectious organisms is conferred by its TCR, which is made up of both an alpha (α) chain and a beta (β) chain or a gamma (γ) and a delta (δ) chain. The proteins which make up these chains are encoded by DNA, which employs a unique mechanism for generating the tremendous diversity of the TCR. This multi-subunit immune recognition receptor associates with the CD3 complex and binds peptides presented by the MHC class I and II proteins on the surface of antigen-presenting cells (APCs). Binding of a TCR to the antigenic peptide on the APC is a central event in T cell activation, which occurs at an immunological synapse at the point of contact between the T cell and the APC.

[00170] Each TCR contains variable complementarity determining regions (CDRs), as well as framework regions (FRs) and a constant region. The amino acid sequence of the third complementarity-determining region (CDR3) loops of the α and β chain variable domains largely determines the sequence diversity of $\alpha\beta$ T cells arising from recombination between variable ($V\beta$), diversity ($D\beta$), and joining ($J\beta$) gene segments in the β chain locus, and between analogous $V\alpha$ and $J\alpha$ gene segments in the α chain locus, respectively. The existence of multiple such gene segments in the TCR α and β chain loci allows for a large number of distinct CDR3 sequences to be encoded. Independent addition and deletion of nucleotides at the $V\beta$ - $D\beta$, $D\beta$ - $J\beta$, and $V\alpha$ - $J\alpha$ junctions during the process of TCR gene rearrangement further increases CDR3 sequence diversity. In this respect, immunocompetence is reflected in the diversity of TCRs. The $\gamma\delta$ TCR is distinctive from the $\alpha\beta$ TCR in that it encodes a receptor that interacts closely with the innate immune system. TCR $\gamma\delta$, is expressed early in development, has specialized anatomical distribution, has unique pathogen and small-molecule specificities, and has a broad spectrum of innate and adaptive cellular interactions. Early in ontogeny, as the restricted subsets of TCR $\gamma\delta$ cells populate various tissues prenatally, a biased pattern of TCR γ V and J segment expression is established.

[00171] The TCRs provided herein target may be engineered TCRs, for example, chimeric antigen receptors (CARs). CARs can be composed of three regions: an ectodomain, a transmembrane domain and an endodomain.

[00172] An ectodomain can be the region of the receptor that is exposed to the extracellular fluid and can consist of an antigen recognition region. In some embodiments, an ectodomain further comprises a spacer. In some embodiments, an ectodomain further comprises a signal peptide. A signal peptide can direct the nascent protein into the endoplasmic reticulum. A signal protein in a CAR may be a single-chain variable fragment (scFv). A fusion protein may be a protein that is formed by merging two or more genes that code

originally for different proteins but when they are translated in the cell, the translation produces one or more polypeptides with functional properties derived for each of the original genes. A scFv is a chimeric protein made up of a light chain domain and heavy chain variable domain connected with a short linker peptide. The linker may comprise hydrophilic residues with stretches of glycine and/or serine residues. The linker may comprise stretches of glutamate and lysine residues, which can improve solubility.

[00173] A transmembrane domain can be a hydrophobic domain that spans the membrane. In some embodiments, a transmembrane domain comprises an alpha-helical domain. A transmembrane domain may be functional for the stability of the receptor as a whole. In some embodiments, a transmembrane domain comprises a transmembrane domain from the most membrane proximal component of an endodomain. In some embodiments, a transmembrane domain comprises a CD3-zeta transmembrane domain. In some embodiments, a transmembrane domain allows for incorporation of an artificial TCR into a native TCR complex. In some embodiments, a transmembrane domain comprises a CD28 transmembrane domain.

[00174] An endodomain can be a functional intracellular portion of a receptor, such as a TCR or CAR. After antigen recognition, receptors cluster and a signal may be transmitted to the cell. In some embodiments, an endodomain comprises a CD3-zeta intracellular domain. In some embodiments, an endodomain comprises at least one ITAM. In some embodiments, an endodomain comprises at least 3 or at least 3 ITAMs. In some embodiments, an endodomain comprises a CD28 intracellular domain. In some embodiments, an endodomain comprises an OX40 intracellular domain. In some embodiments, an endodomain comprises a chimeric intracellular domain. For example, an endodomain can comprise a CD28 intracellular domain, an OX40 intracellular domain and a CD3-zeta intracellular domain.

IV. T cells

[00175] T cells belong to a group of white blood cells known as lymphocytes, and play a central role in cell-mediated immunity. T cells include CD4⁺ T cells (helper T cells) and CD8⁺ T cells (cytotoxic T cells). CD4⁺ T cells can assist other white blood cells in immunologic processes, including maturation of B-cells and activation of cytotoxic T cells and macrophages. CD4⁺ T cells are activated when presented with peptide antigens by MHC class II molecules expressed on the surface of antigen presenting cells (APCs). Once activated, the T cells can divide rapidly and secrete cytokines that regulate the active immune response. CD8⁺ T cells can destroy virally infected cells and tumor cells, and, can also be implicated in transplant rejection. CD8⁺ T cells can recognize their targets by binding to antigen associated with MHC class I, which is present on the surface of nearly every cell of the body. Most T cells have a T cell receptor (TCR). The ability of T cells to recognize antigens associated with various cancers or infectious organisms is conferred by its TCR, which is made up of both an alpha (α) chain and a beta (β) chain or a gamma (γ) and a delta (δ) chain. The proteins which make up these chains are encoded by DNA, which employs a unique mechanism for generating the diversity of the TCR. This multi-subunit immune recognition receptor can associate with the CD3 complex and bind peptides presented by the MHC class I and II proteins on the surface of antigen-presenting cells (APCs). The first signal in activation of T cells can be provided by binding of the T cell receptor to a short peptide presented by the MHC on another

cell. This ensures that only a T cell with a TCR specific to that peptide is activated. The partner cell is usually an antigen presenting cell such as a professional antigen presenting cell, usually a dendritic cell in the case of naive responses, although B-cells and macrophages can be important APCs. Binding of a TCR to the antigenic peptide on the APC can be a central event in T cell activation, which occurs at an immunological synapse at the point of contact between the T cell and the APC.

[00176] T cells can be prepared according to methods known in the art. T cells can be an enriched T cell preparation, an APC-depleted cell preparation, or a substantially purified T cell preparation. T cells can be a mixed T cell population or a purified T cell subset. T cells can be an enriched T cell preparation containing a number or percentage of T cells that is increased with respect to an isolated population of T cells.

[00177] T cells, or a subset of T cells, can be obtained from various lymphoid tissues. T cells can be obtained from a number of sources, including peripheral blood mononuclear cells (PBMCs), bone marrow, thymus, tissue biopsy, tumor, lymph node tissue, gut associated lymphoid tissue, mucosa associated lymphoid tissue, spleen tissue, lymphoid tissue, and tumors. The term “peripheral blood lymphocytes” (PBL) and its grammatical equivalents as used herein can refer to lymphocytes that circulate in the blood (e.g., peripheral blood). Peripheral blood lymphocytes can refer to lymphocytes that are not localized to organs. Peripheral blood lymphocytes can comprise T cells, NK cells, B cell, or any combinations thereof.

[00178] The method can comprise isolating T cells from a subject. The method can comprise obtaining T cells isolated from a subject. T cells can be obtained from T cell lines. T cells can be obtained from autologous sources. T cells can be obtained from allogeneic sources. T cells may also be obtained from a xenogeneic source, for example, from mouse, rat, non-human primate, and pig.

[00179] T cells can be an APC-depleted cell preparation. T cells can be substantially free of APCs. For example, T cells can comprise T cells separated from over 75% of APCs. In an exemplary embodiment, peripheral blood mononuclear cells (PBMCs) can be obtained from blood, e.g., in heparinized vials. PBMCs can be separated from red blood cells by centrifugation and PBMCs recovered from the interface. The recovered PBMCs optionally can be washed (e.g., with PBS).

[00180] T cell purification can be achieved, for example, by positive or negative selection including, but not limited to, the use of antibodies directed to CD2, CD3, CD4, CD5, CD8, CD14, CD19, and/or MHC class II molecules. A specific T cell subset, such as CD28⁺, CD4⁺, CD8⁺, CD45RA⁺, and/or CD45RO⁺ T cells, can be isolated by positive or negative selection techniques. For example, CD3⁺, CD28⁺ T cells can be positively selected using CD3/CD28 conjugated magnetic beads. In one aspect of the present invention, enrichment of a T cell population by negative selection can be accomplished with a combination of antibodies directed to surface markers unique to the negatively selected cells.

[00181] For example, a T cell sample can comprise cells from a subject's circulating blood and can be obtained by apheresis or leukopheresis. A T cell sample may contain lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and/or platelets. Undesirable components of the T cell sample can be removed and the remaining T cells can be suspended in culture media.

For example, cells can be washed to remove the plasma fraction. For example, T cells can be isolated from peripheral blood lymphocytes by lysing the red blood cells and by centrifugation through a PERCOLL™ gradient.

[00182] In some embodiments, a T cell comprises at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC. In some embodiments, a T cell comprises at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC. In some embodiments, a T cell comprises at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC. In some embodiments, a host cell comprises at least one TCR disclosed herein, wherein the host cell is a CD4+ T cell. In some embodiments, the host cell is a CD8+ T cell. In some embodiments, the host cell is an autologous cell. In some embodiments, the host cell is an allogeneic cell. In some embodiments, the host cell is a human cell. In some other cases, a host cell may be natural killer (NK) cell, a B cell, or an immortalized cell line.

[00183] In some embodiments, T cells can be obtained by positive selection and/or negative selection. In positive selection, an affinity agent (such as an antibody, an antibody fragment, and aptamer) can be used to bind a cell surface marker expressed on the population of cells, for example, CD3 for T cells. Using the affinity agent, the T cells can be labeled. The labeled T cells can then be enriched using various methods that are well-known in the art. Non-limiting examples of those methods include fluorescent-activated cell sorting (FACS) and (para)magnetic particle-based cell separation (e.g. MACS cell separation kits from Miltenyi Biotec).

[00184] In negative selection, affinity agents can be used to bind cell surface markers expressed on blood cells other than the desired population. For example, when attempting to isolate T cells, a cocktail of affinity agents can be used to label B cells, NK cells, monocytes, platelets, dendritic cells, granulocytes and erythrocytes. The labeled cells can then be depleted, leaving the T cells enriched. The exemplary methods to deplete labeled cells include FACS and (para)magnetic particle-based cell separation.

[00185] In addition to labeling-based isolation, special growth condition may be used to promote the growth of one particular cell population. For example, the special growth condition can be obtained using special cytokines or growth factors. For another example, in culture media containing phytohemagglutinin (PHA), IL-2, and/or IL-15, T cells may preferentially proliferate.

[00186] In some situations, non-functional markers may be used to isolate T cells since binding of functional markers such as binding of CD3 by anti-CD3 antibody (alone or conjugated to magnetic particles) may trigger unwanted signaling events on T cells. Therefore, a cocktail of antibodies against CD14, CD15, CD16, CD19, CD34, CD36, CD56, CD123, and CD235a (glycophorin A) can be used to isolate T cells.

[00187] Detailed protocol can be found in published literatures (e.g. see Lefort et al., *J Vis Exp.* 2010; (40): 2017) which are incorporated by reference herein. T cell isolation kits can be obtained from, for example, STEMCELL Technologies, Thermofisher, and Miltenyi Biotec.

[00188] The T cell described herein may be an allogeneic T cell.

[00189] In some embodiments, the T cell may be a genetically-modified cell comprising in its genome a modified human T cell receptor (TCR) alpha chain gene and/or a modified human TCR beta chain gene, wherein the cell has reduced cell-surface expression of the endogenous TCR.

[00190] Gene-editing nucleases may be employed in order to disrupt components of the TCR. The TCR alpha chain (TCR α) is encoded by a single TRAC gene and pairs with the TCR beta chain (TCR β) encoded by two TCRB genes. Since the TCR α/β dimer can produce a fully functioning TCR complex, disrupting TCR α and/or TCR β function may reduce (even eliminate) endogenous TCR expression.

[00191] Various methods may be used to disrupt endogenous TCR α or TCR β genes. For example, four classes of gene editing proteins exist that share a common mode of action in binding a user defined sequence of DNA and mediating a double stranded DNA break (DSB). Zinc finger nucleases (ZFN) are heterodimeric arrays that co-localize at a target DNA site. ZFNs include individual finger subunits that bind DNA and are tethered to the FokI nuclease domain that cleaves DNA. Transcription activator-like effector nucleases (TALEN) include repeating units that bind DNA by virtue of a hypervariable two amino acid sequence (repeat variable diresidue; RVD) that governs DNA base recognition. Similar to ZFNs, TALENs function as dimeric proteins that are fused to the FokI endonuclease domain for DSB generation. Meganucleases (MN) are monomeric proteins with innate nuclease activity that are derived from bacterial homing endonucleases and engineered for a unique target site. The clustered regularly interspaced short palindromic repeats (CRISPR) and associated Cas9 nuclease platform involves a small guide RNA (gRNA) transcript that contacts a target DNA sequence via Watson-Crick base pairing and the Cas9 nuclease that cleaves the DNA.

[00192] In some embodiments, introducing the genome-editing nuclease into the T cell includes introducing into the T cell a polynucleotide that encodes the genome-editing nuclease.

[00193] In some embodiments, introducing the genome-editing nuclease into the T cell includes introducing into the T cell a Cas9 polypeptide. In some embodiments, the genome-editing nuclease includes a TALEN nuclease, a CRISPR/Cas9 nuclease, or a megaTAL nuclease.

[00194] In some embodiments, the CRISPR/Cas9 nuclease is derived from either *Streptococcus pyogenes* or *Staphylococcus aureus*. In some of these embodiments, the CRISPR/Cas9 nuclease includes a nuclease-resistant gRNA such as, for example, at least one 2'-OMe-phosphorothioate modified base, at least one 2'-O-methyl modified base, or at least one 2'-O-methyl 3' thioPACE modified base.

[00195] In some embodiments, the TALEN nuclease or the megaTAL nuclease is encoded by an RNA that has an exogenous polyadenylation signal.

[00196] In some embodiments, the method described herein may further include culturing the T cell under conditions effective for expanding the population of genome-modified T cells.

[00197] In some embodiments, disrupting expression of TCR α and/or TCR β further disrupts assembly of TCR α and TCR β . In some embodiments, disrupting expression of TCR α further disrupts formation of a complex

between TCR and CD3. In some embodiments, disrupting expression of TCR α involves further disrupting assembly of TCR α and TCR β .

[00198] In some embodiments, a genetically-modified T cell comprises a disrupted TCR alpha chain and/or beta chain and an inactivated gene encoding immune checkpoint protein such as PD1 and CTLA-4. This may be made possible by gene inactivation using specific TALE-nucleases directed against TCRalpha or TCRbeta coupled with inactivation of genes encoding immune checkpoint protein such as PD1 and CTLA-4.

[00199] In some embodiments, the genetic modification relies on the inactivation of one gene, or two genes selected from the group consisting of PD1, CTLA-4, LAG3, Tim3, BTLA, BY55, TIGIT, B7H5, LAIR1, SIGLEC10, 2B4, TCR alpha and TCR beta. In some embodiments, the genetic modification relies on the inactivation of two genes selected from the group consisting of PD1 and TCR alpha, PD1 and TCR beta, CTLA-4 and TCR alpha, CTLA-4 and TCR beta, LAG 3 and TCR alpha, LAG 3 and TCR beta, Tim3 and TCR alpha, Tim3 and TCR beta, BTLA and TCR alpha, BTLA and TCR beta, BY55 and TCR alpha, BY55 and TCR beta, TIGIT and TCR alpha, TIGIT and TCR beta, B7H5 and TCR alpha, B7H5 and TCR beta, LAIR1 and TCR alpha, LAIR1 and TCR beta, SIGLEC10 and TCR alpha, SIGLEC10 and TCR beta, 2B4 and TCR alpha, 2B4 and TCR beta. In some embodiments, the genetic modification relies on the inactivation of more than two genes. The genetic modification may be operated ex-vivo.

V. TCRs Specific to RAS peptide-MHC complexes

[00200] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3, 18, 33, 49, 65, 81, 97, 113, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 401, 417, and 433 and/or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6, 21, 36, 52, 68, 84, 100, 116, 244, 260, 276, 292, 308, 324, 340, 356, 372, 388, 404, 420, and 436.

[00201] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the epitope from RAS comprises a region having at least 70% sequence identity to an amino acid sequence selected from SEQ ID NOs: 15, 30, 45, 46, 61, 62, 77, 78, 93, 94, 109, 110, 125, 126, 219-222, 253, 254, 269, 270, 285, 286, 301, 302, 317, 318, 333, 334, 349, 350, 365, 366, 381, 382, 397, 398, 413, 414, 429, 430, 445 and 446.

[00202] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele. In some embodiments, the alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 71, 87,

103, 295, 311, 327, 343, 359 and 391, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 74, 90, 106, 298, 314, 330, 346, 362 and 394, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele.

[00203] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 63, 79, 95, 287, 303, 319, 335, 351 and 383. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 66, 82, 98, 290, 306, 322, 338, 354 and 386. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 64, 80, 96, 288, 304, 320, 336, 352 and 384. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 67, 83, 99, 291, 307, 323, 339, 355 and 387. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 65, 81, 97, 289, 305, 321, 337, 353 and 385. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 68, 84, 100, 292, 308, 324, 340, 356 and 388.

[00204] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele. In some embodiments, the alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 9 and 24 wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 12 and 27, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele.

[00205] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 1 and 16. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 4 and 19. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 2 and 17. In some embodiments TCR beta chain construct comprises a

complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 5 and 20. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3 and 18. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6 and 21.

[00206] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct; wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 39, 55, 122, 247, 263, 279, 375, 407, 423 and 439, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to an amino acid sequence selected from SEQ ID NOs: 42, 58, 125, 250, 266, 282, 378, 413, 426 and 442, wherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele.

[00207] In some embodiments, the TCR alpha chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 31, 47, 111, 239, 255, 271, 367, 399, 415, and 431. In some embodiments, the TCR beta chain construct as described above comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 34, 50, 114, 242, 258, 274, 370, 402, 418, and 434. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 32, 48, 112, 240, 256, 272, 368, 400, 416, and 432. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 35, 51, 115, 243, 259, 275, 371, 403, 419, and 435. In some embodiments, the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 33, 49, 113, 241, 257, 273, 369, 401, 417, and 433. In some embodiments, the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 36, 52, 116, 228, 244, 260, 276, 372, 404, 420, and 434. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 9; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 12. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 1, a CDR2 of SEQ ID NO: 2, and a CDR3 of SEQ ID NO: 3; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 4, a CDR2 of SEQ ID NO: 5, and a CDR3 of SEQ ID NO: 6. In some embodiments, the TCR alpha

chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 24; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 27. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 16, a CDR2 of SEQ ID NO: 17, and a CDR3 of SEQ ID NO: 18; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 19, a CDR2 of SEQ ID NO: 20, and a CDR3 of SEQ ID NO: 21. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 39; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 42. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 31, a CDR2 of SEQ ID NO: 32, and a CDR3 of SEQ ID NO: 33; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 34, a CDR2 of SEQ ID NO: 35, and a CDR3 of SEQ ID NO: 36. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 55; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 58. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 47, a CDR2 of SEQ ID NO: 48, and a CDR3 of SEQ ID NO: 49; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 50, a CDR2 of SEQ ID NO: 51, and a CDR3 of SEQ ID NO: 52. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 71; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 74. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 63, a CDR2 of SEQ ID NO: 64, and a CDR3 of SEQ ID NO: 65; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 66, a CDR2 of SEQ ID NO: 67, and a CDR3 of SEQ ID NO: 68. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 87; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 90. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 79, a CDR2 of SEQ ID NO: 80, and a CDR3 of SEQ ID NO: 81; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 82, a CDR2 of SEQ ID NO: 83, and a CDR3 of SEQ ID NO: 84. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 103; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 106. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 95, a CDR2 of SEQ ID NO: 96, and a CDR3 of SEQ ID NO: 97; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 98, a CDR2 of SEQ ID NO: 99, and a CDR3 of SEQ ID NO: 100. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 119; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 122. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 111, a CDR2 of SEQ ID NO: 112, and a CDR3 of SEQ ID NO: 113; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 114, a CDR2 of SEQ ID NO: 115, and a CDR3 of SEQ ID NO: 116. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO:

263; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 266. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 255, a CDR2 of SEQ ID NO: 256, and a CDR3 of SEQ ID NO: 257; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 258, a CDR2 of SEQ ID NO: 259, and a CDR3 of SEQ ID NO: 260. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 279; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 282. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 271, a CDR2 of SEQ ID NO: 272, and a CDR3 of SEQ ID NO: 273; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 274, a CDR2 of SEQ ID NO: 275, and a CDR3 of SEQ ID NO: 276. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 295; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 298. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 287, a CDR2 of SEQ ID NO: 288, and a CDR3 of SEQ ID NO: 289; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 290, a CDR2 of SEQ ID NO: 291, and a CDR3 of SEQ ID NO: 292. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 311; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 314. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 303, a CDR2 of SEQ ID NO: 304, and a CDR3 of SEQ ID NO: 305; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 306, a CDR2 of SEQ ID NO: 307, and a CDR3 of SEQ ID NO: 308. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 327; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 330. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 319, a CDR2 of SEQ ID NO: 320, and a CDR3 of SEQ ID NO: 321; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 322, a CDR2 of SEQ ID NO: 323, and a CDR3 of SEQ ID NO: 324. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 343; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 346. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 335, a CDR2 of SEQ ID NO: 336, and a CDR3 of SEQ ID NO: 337; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 338, a CDR2 of SEQ ID NO: 339, and a CDR3 of SEQ ID NO: 340. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 343; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 346. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 351, a CDR2 of SEQ ID NO: 352, and a CDR3 of SEQ ID NO: 353; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 354, a CDR2 of SEQ ID NO: 355, and a CDR3 of SEQ ID NO: 356. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 343; and the TCR beta chain

construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 346. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 367, a CDR2 of SEQ ID NO: 368, and a CDR3 of SEQ ID NO: 369; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 370, a CDR2 of SEQ ID NO: 371, and a CDR3 of SEQ ID NO: 372. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 391; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 394. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 383, a CDR2 of SEQ ID NO: 384, and a CDR3 of SEQ ID NO: 385; the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 386, a CDR2 of SEQ ID NO: 387, and a CDR3 of SEQ ID NO: 388. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 391; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 394. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 399, a CDR2 of SEQ ID NO: 400, and a CDR3 of SEQ ID NO: 401; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 402, a CDR2 of SEQ ID NO: 403, and a CDR3 of SEQ ID NO: 404. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 423; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 426. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 415, a CDR2 of SEQ ID NO: 416, and a CDR3 of SEQ ID NO: 417; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 418, a CDR2 of SEQ ID NO: 419, and a CDR3 of SEQ ID NO: 420. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 391; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 394. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 431, a CDR2 of SEQ ID NO: 432, and a CDR3 of SEQ ID NO: 433; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 434, a CDR2 of SEQ ID NO: 435, and a CDR3 of SEQ ID NO: 426.

[00208] In various embodiments, the nucleic acid sequence encoding a TCR is codon optimized.

[00209] Mutations in any one of the three *ras* genes, *H-ras*, *K-ras* and *N-ras* are one of the most common events in human tumorigenesis. About 30% of all human tumors are found to carry at least one mutation in any of the canonical *ras* genes. Ras mutations are evident in, for example, adenocarcinoma of the biliary tract, transitional cell carcinoma of the bladder, breast carcinoma, cervical adenocarcinoma, colon adenocarcinoma, colon adenoma, neuroblastoma (autonomic ganglia), acute myeloid leukemia, chronic myeloid leukemia, chronic myelomonocytic leukemia, juvenile myelomonocytic leukemia, acute lymphoblastic leukemia, Burkitt's lymphoma, Hodgkin's lymphoma, plasma cell myeloma, hepatocellular carcinoma, large cell carcinoma, non-small cell carcinoma, ductal carcinoma, endocrine tumor, prostrate adenocarcinoma, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, angiosarcoma, leiomyosarcoma, liposarcoma, rhabdomyosarcoma, myxoma, malignant fibrous histiocytoma, pleomorphic sarcoma, germinoma, seminoma, anaplastic carcinoma, follicular carcinoma, papillary carcinoma and Hurthle cell carcinoma. Ras mutations are

found in cancers affecting many tissues and organs of the body, for example, lung, liver, breast, bladder, colon, cervix, pancreas, prostate gland, stomach, thyroid, testis, soft tissue, skin and blood.

[00210] In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the RAS peptide comprises a G12V mutation. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the RAS peptide comprises a G12C mutation. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the RAS peptide comprises a G12D mutation. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the RAS peptide comprises a mutation at Q61. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the RAS peptide comprises a sequence of VVGAVGVGK, VVVGAVGVGK, VVGADGVGK, VVVGADGVGK, VVGACGVGK, VVVGACGVGK, KLVVVGACGV, LVVVGACGV, KLVVVGADGV, LVVVGADGV, KLVVVGAVGV or LVVVGAVGV.

[00211] In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A03:01 allele. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A11:01 allele.

[00212] In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele and wherein the RAS peptide comprises a sequence of VVGAVGVGK, VVVGAVGVGK, VVGADGVGK, VVVGADGVGK, VVGACGVGK, VVVGACGVGK, KLVVVGACGV, LVVVGACGV, KLVVVGADGV, LVVVGADGV, KLVVVGAVGV or LVVVGAVGV. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A03:01 allele and wherein the RAS peptide comprises a sequence of VVGAVGVGK, VVVGAVGVGK, VVGADGVGK, VVVGADGVGK, VVGACGVGK, VVVGACGVGK, KLVVVGACGV, LVVVGACGV, KLVVVGADGV, LVVVGADGV, KLVVVGAVGV or LVVVGAVGV. In various embodiments, the TCR binds to an MHC:RAS peptide complex, wherein the human MHC is encoded by an HLA-A11:01 allele and wherein the RAS peptide comprises a sequence of VVGAVGVGK, VVVGAVGVGK, VVGADGVGK, VVVGADGVGK, VVGACGVGK, VVVGACGVGK, KLVVVGACGV, LVVVGACGV, KLVVVGADGV, LVVVGADGV, KLVVVGAVGV or LVVVGAVGV.

[00213] In some embodiments, one TCR as disclosed herein, exhibits a specific binding affinity to an epitope peptide containing a point mutation found in cancer when the epitope peptide is in complex with an MHC encoded by the specific allele; and additionally the TCR may exhibit a different binding affinity to another epitope peptide containing a different point mutation of the same cancer protein, when the epitope peptide is in complex with an MHC encoded by the specific allele, but do not exhibit binding affinity to the WT peptide which does not contain any mutation.

VI. TCRs Specific to TMPRSS2:ERG peptide-MHC complexes

[00214] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from

TMPRSS2:ERG in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 144 and SEQ ID NO: 147.

[00215] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the epitope from TMPRSS2:ERG comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 156.

[00216] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 150. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to SEQ ID NO: 142 or SEQ ID NO: 145. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to SEQ ID NO: 143 or SEQ ID NO: 146. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 150; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 153. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 142, a CDR2 of SEQ ID NO: 143, and a CDR3 of SEQ ID NO: 144; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 145, a CDR2 of SEQ ID NO: 146, and a CDR3 of SEQ ID NO: 147.

[00217] In some embodiments, a TCR comprises a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 144 or 147.

[00218] In some embodiments, a TCR comprises a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the epitope from TMPRSS2:ERG comprises a region having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 156.

[00219] In some embodiments, the TCR alpha chain construct and or TCR beta chain construct comprises a variable region having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 150 or 153.

[00220] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 142 or 145.

[00221] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to SEQ ID NO: 143 or 146.

[00222] In some embodiments, the nucleic acid encoding a TCR alpha chain construct and/or TCR beta chain comprises a nucleic acid sequence with at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to any one of SEQ ID NOs: 148, 149, 151, and 152. In various embodiments, the nucleic acid sequence encoding a TCR is codon optimized.

[00223] In various embodiments, the TCR binds to an MHC:TMPRSS2::ERG peptide complex, wherein the TMPRSS2::ERG peptide comprises a gene fusion mutation. In various embodiments, the TCR binds to an MHC:TMPRSS2::ERG peptide complex, wherein the TMPRSS2::ERG peptide comprises a gene fusion mutation comprising at least two consecutive amino acids wherein the at least two consecutive amino acids comprise at least one amino acid of TMPRSS2 and at least one amino acid of ERG. In various embodiments, the TCR binds to an MHC:TMPRSS2::ERG peptide complex, wherein the TMPRSS2::ERG peptide comprises a sequence of ALNSEALSV.

[00224] In various embodiments, the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:TMPRSS2::ERG peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele.

[00225] In various embodiments, the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:TMPRSS2::ERG peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele wherein the TMPRSS2::ERG peptide comprises a sequence of ALNSEALSV.

VII. TCRs Specific to GATA3 peptide-MHC complexes

[00226] In some other embodiments, a TCR comprises a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 129, 132, 191, 194, 206 or 209.

[00227] In some embodiments, a TCR comprises a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the epitope from GATA3 comprises a region having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 141, 203 or 218.

[00228] In some embodiments, the TCR alpha chain construct and or TCR beta chain construct comprises a variable region having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 135, 138, 197, 200, 212 or 215.

[00229] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 127, 130, 189, 192, 204 or 207.

[00230] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to SEQ ID NO: 128, 131, 190, 193, 205 or 208.

[00231] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 129, 132, 191, 194, 206 or 209.

[00232] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant GATA3 peptide in complex with a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[00233] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant GATA3 peptide in complex with an HLA-A02:01, HLA-B07:02 or HLA-B08:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 129, 132, 191, 194, 206 or 209; and/or specifically binds to a mutant GATA3 peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 141, 203 or 218.

[00234] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the epitope from GATA3 comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 141, 203 or 218.

[00235] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 135, 197 or 212. In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 138, 200 or 215. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 127, 130, 189, 192, 204 and 207. In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 128, 131, 190, 193, 205 and 208.

[00236] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 135; and the TCR beta chain construct comprises a variable region having at

least 80% sequence identity to SEQ ID NO: 138. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 197; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 200. In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 212; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 215.

[00237] In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 127, a CDR2 of SEQ ID NO: 128, and a CDR3 of SEQ ID NO: 129; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 130, a CDR2 of SEQ ID NO: 131, and a CDR3 of SEQ ID NO: 132. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 189, a CDR2 of SEQ ID NO: 190, and a CDR3 of SEQ ID NO: 191; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 192, a CDR2 of SEQ ID NO: 193, and a CDR3 of SEQ ID NO: 194. In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 204, a CDR2 of SEQ ID NO: 205, and a CDR3 of SEQ ID NO: 206; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 207, a CDR2 of SEQ ID NO: 208, and a CDR3 of SEQ ID NO: 209.

[00238] In some embodiments, the nucleic acid encoding a TCR alpha chain construct and/or TCR beta chain comprises a nucleic acid sequence with at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to any one of SEQ ID NOs: 133, 134, 136 or 137. In some embodiments, the nucleic acid encoding a TCR alpha chain construct and/or TCR beta chain comprises a nucleic acid sequence with at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to any one of SEQ ID NOs: 195, 196, 198 or 199. In some embodiments, the nucleic acid encoding a TCR alpha chain construct and/or TCR beta chain comprises a nucleic acid sequence with at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 98% sequence identity to any one of SEQ ID NOs: 210, 211, 213 or 214.

[00239] In various embodiments, the nucleic acid sequence encoding a TCR is codon optimized.

[00240] In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA peptide comprises at least one amino acid encoded by a GATA3 neoORF sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA peptide comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids encoded by a GATA3 neoORF sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA peptide comprises at least one amino acid encoded by a GATA3 neoORF sequence and at least one amino acid encoded by a GATA3 wild type sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA peptide comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids encoded by a GATA3 neoORF sequence and at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids encoded by a GATA3 wild type sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex,

wherein the GATA peptide comprises at least one amino acid encoded by a GATA3 neoORF sequence and at least one amino acid not encoded by a GATA3 neoORF sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA peptide comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids encoded by a GATA3 neoORF sequence and at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 amino acids not encoded by a GATA3 neoORF sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein each amino acid of the GATA peptide is an amino acid encoded by a GATA3 neoORF sequence. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the GATA3 peptide comprises a sequence of MLTGPPARV, KPKRDGYMF or ESKIMFATL.

[00241] In various embodiments, the human MHC is encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the human MHC is encoded by an HLA-B07:02 allele. In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the human MHC is encoded by an HLA-B08:01 allele.

[00242] In various embodiments, the TCR binds to an MHC:GATA3 peptide complex, wherein the human MHC is encoded by an HLA-B08:01 allele and wherein the GATA3 peptide comprises a sequence of MLTGPPARV, KPKRDGYMF or ESKIMFATL.

VIII. TCRs Specific to BTK peptide-MHC complexes

[00243] The *BTK* gene can encode a Bruton tyrosine kinase (BTK) protein, which can be related to the development and maturation of B cells. The BTK protein can transmit chemical signals that instruct B cells to mature and produce antibodies.

[00244] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 161 and SEQ ID NO: 176, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 164 and SEQ ID NO: 179.

[00245] Also provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant BTK peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 161, 164, 176, or 179; and/or specifically binds to a mutant BTK peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 173 or 188.

[00246] Also provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK

in complex with a human MHC, wherein the epitope from BTK comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 173 or 188.

[00247] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or 182.

[00248] In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185.

[00249] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 159, 162, 174, and 177.

[00250] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 160, 163, 175 and 178.

[00251] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 167 or 182; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 170 or 185.

[00252] In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 159 or 174, a CDR2 of SEQ ID NO: 160 or 175, and a CDR3 of SEQ ID NO: 161 or 176; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 162 or 177, a CDR2 of SEQ ID NO: 163 or 178, and a CDR3 of SEQ ID NO: 164 or 179.

[00253] In some embodiments, the epitope comprises a point mutation. In some embodiments, the point mutation is C481S mutation.

[00254] In various embodiments, the nucleic acid sequence encoding a TCR is codon optimized.

[00255] In various embodiments, the TCR binds to an MHC:BTK peptide complex, wherein the BTK peptide comprises a point mutation. In various embodiments, the TCR binds to an MHC:BTK peptide complex, wherein the BTK peptide comprises a C481S point mutation. In various embodiments, the TCR binds to an MHC:BTK peptide complex, wherein the BTK peptide comprises a sequence of SLLNYLREM.

[00256] In some embodiments, the human MHC is encoded by HLA-A02:01 allele. In various embodiments, the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:BTK peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele.

[00257] In various embodiments, the TCR binds to an MHC:BTK peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele and wherein the BTK peptide comprises a sequence of SLLNYLREM.

IX. TCRs Specific to EGFR peptide-MHC complexes

[00258] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO:

449, SEQ ID NO: 466, SEQ ID NO: 483, SEQ ID NO: 500, and SEQ ID NO: 517, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 452, SEQ ID NO: 469, SEQ ID NO: 486, SEQ ID NO: 503, and SEQ ID NO: 520.

[00259] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant EGFR peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises a TCR alpha chain construct and/or a TCR beta chain construct.

[00260] Provided herein is an isolated nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR specifically binds to a mutant EGFR peptide in complex with an HLA-A02:01 protein; comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to SEQ ID NO: 449, 466, 483, 500, 517, 452, 469, 486, 503, or 520; and/or specifically binds to a mutant EGFR peptide comprising a region with at least 70% sequence identity to SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.

[00261] Provided herein is a nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the epitope from EGFR comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.

[00262] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 449, 466, 483, 500 or 517.

[00263] In some embodiments, the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 452, 469, 486, 503, or 520.

[00264] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 447, 464, 481, 498, 515, 450, 467, 484, 501, and 518.

[00265] In some embodiments, the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NOs: 448, 465, 482, 499, 516, 451, 468, 485, 502, and 519.

[00266] In some embodiments, the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 455, 472, 489, 506, or 523; and the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 458, 475, 492, 509 or 526.

[00267] In some embodiments, the TCR alpha chain construct comprises a CDR1 of SEQ ID NO: 447, 464, 481, 498 or 515, a CDR2 of SEQ ID NO: 448, 465, 482, 499 or 516, and a CDR3 of SEQ ID NO: 449, 466, 483, 500 or 517; and the TCR beta chain construct comprises a CDR1 of SEQ ID NO: 450, 467, 484, 501 or

518, a CDR2 of SEQ ID NO: 451, 468, 485, 502, or 519, and a CDR3 of SEQ ID NO: 452, 469, 486, 503, or 520.

[00268] In some embodiments, the epitope comprises a point mutation. In some embodiments, the point mutation is a T790M mutation. In some embodiments, the human MHC is encoded by an HLA-A02:01 allele.

[00269] In various embodiments, the nucleic acid sequence encoding a TCR is codon optimized.

[00270] In various embodiments, the TCR binds to an MHC:EGFR peptide complex, wherein the EGFR peptide comprises a point mutation. In various embodiments, the TCR binds to an MHC:EGFR peptide complex, wherein the EGFR peptide comprises a T790M point mutation. In various embodiments, the TCR binds to an MHC:EGFR peptide complex, wherein the EGFR peptide comprises a sequence of QLIMQLMPF, LIMQLMPFGC or MQLMPFGCLL.

[00271] In various embodiments, the human MHC is encoded by an HLA-A02:01 allele. In various embodiments, the TCR binds to an MHC:EGFR peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele.

[00272] In various embodiments, the TCR binds to an MHC:EGFR peptide complex, wherein the human MHC is encoded by an HLA-A02:01 allele and wherein the EGFR peptide comprises a sequence of QLIMQLMPF, LIMQLMPFGC or MQLMPFGCLL.

[00273] Delivery of Nucleic Acid or Vector

[00274] Nucleic acids encoding TCRs or vectors containing such nucleic acids can be delivered to host cells for expression and processing.

[00275] Terms such as “transferring”, “introducing” or “transfecting” are used interchangeably herein and relate to the introduction of nucleic acids, in particular exogenous or heterologous nucleic acids, into a cell.

[00276] Cells can be transfected with any carriers with which nucleic acid can be associated, e.g., by forming complexes with the nucleic acid or forming vesicles in which the nucleic acid is enclosed or encapsulated, resulting in increased stability of the nucleic acid compared to naked nucleic acid. Carriers useful according to the present disclosure include, for example, lipid-containing carriers such as cationic lipids, liposomes, in particular cationic liposomes, and micelles, and nanoparticles. Cationic lipids may form complexes with negatively charged nucleic acids. Any cationic lipid may be used according to the present disclosure.

[00277] In various embodiments, a nucleic acid encoding a TCR disclosed herein is operably linked to a promoter. Furthermore, the present disclosure provides a vector, e.g. a plasmid, shuttle vector, phagemide, cosmid, expression vector, retroviral vector, adenoviral vector or particle and/or vector to be used in gene therapy, which comprises one or more of the nucleic acids as disclosed above. A “vector” is a nucleic acid molecule that is capable of transporting another nucleic acid. The vector comprises the nucleic acid insert, which encodes the polypeptide or protein desired for expression in a cell, such as a host cell. For the purposes of the disclosure, an insert may be a nucleic acid encoding a TCR; an alpha chain or a beta chain or both of a TCR. The term “incorporating” a nucleic acid sequence in a vector may mean preparing a suitable expression vector with an insert comprising said nucleic acid sequence. An “expression vector” is a vector that can direct the expression

of a protein encoded by one or more genes carried by the vector when it is present in the appropriate environment. "Retroviruses" are viruses having an RNA genome. "Gammaretrovirus" refers to a genus of the retroviridae family. Exemplary gammaretroviruses include, but are not limited to, mouse stem cell virus, murine leukemia virus, feline leukemia virus, feline sarcoma virus, and avian reticuloendotheliosis viruses. "Lentivirus" refers to a genus of retroviruses that are capable of infecting dividing and non-dividing cells. Several examples of lentiviruses include HIV (human immunodeficiency virus: including HIV type 1, and HIV type 2); equine infectious anemia virus; feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV). A vector that encodes a core virus is also known as a "viral vector." There are a large number of available viral vectors that are suitable for use with the invention, including those identified for human gene therapy applications, such as those described by Pfeifer and Verma (Pfeifer, A. and I. M. Verma. 2001. *Ann. Rev. Genomics Hum. Genet.* 2:177-211). Suitable viral vectors include vectors based on RNA viruses, such as retrovirus-derived vectors, e.g., Moloney murine leukemia virus (MLV)-derived vectors, and include more complex retrovirus-derived vectors, e.g., lentivirus-derived vectors. HIV-1-derived vectors belong to this category. Other examples include lentivirus vectors derived from HIV-2, FIV, equine infectious anemia virus, SIV, and maedi/visna virus. Methods of using retroviral and lentiviral viral vectors and packaging cells for transducing mammalian target cells with viral particles containing TCRs transgenes are well known in the art and have been previously described, for example, in U.S. Pat. No. 8,119,772; Walchli et al., 2011, *PLoS One* 6:327930; Zhao et al., *J. Immunol.*, 2005, 174:4415-4423; Engels et al., 2003, *Hum. Gene Ther.* 14:1155-68; Frecha et al., 2010, *Mol. Ther.* 18:1748-57; Verhoeyen et al., 2009, *Methods Mol. Biol.* 506:97-114. Retroviral and lentiviral vector constructs and expression systems are also commercially available. In some embodiments, a viral vector is used to introduce the non-endogenous nucleic acid sequence encoding TCR α chain specific for the peptide antigen into the hematopoietic progenitor cells. The viral vector may be a retroviral vector or a lentiviral vector. The viral vector may also include a nucleic acid sequence encoding a marker for transduction. Transduction markers for viral vectors are known in the art and include selection markers, which may confer drug resistance, or detectable markers, such as fluorescent markers or cell surface proteins that can be detected by methods such as flow cytometry. Where the viral vector genome comprises more than one nucleic acid sequence to be expressed in the host cell as separate transcripts, the viral vector may also comprise additional sequence between the two (or more) transcripts allowing bicistronic or multicistronic expression. Examples of such sequences used in viral vectors include internal ribosome entry sites (IRES), furin cleavage sites, viral 2A peptide. Other vectors also can be used for polynucleotide delivery including DNA viral vectors, including, for example adenovirus-based vectors and adeno-associated virus (AAV)-based vectors; vectors derived from herpes simplex viruses (HSVs), including amplicon vectors, replication-defective HSV and attenuated HSV (Krisky et al., 1998, *Gene Ther.* 5: 1517-30). Other vectors include those derived from baculoviruses and alpha-viruses. (Jolly D J. 1999. *Emerging viral vectors*. pp 209-40 in Friedmann T. ed. 1999. *The development of human gene therapy*. New York: Cold Spring Harbor Lab).

[00278] A vector may include nucleic acid sequences that permit the nucleic acid to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker genes and other genetic elements known to those of ordinary skill in the art. A vector preferably is an expression vector that includes a nucleic acid according to the present invention operably linked to sequences allowing for the expression of said nucleic acid.

[00279] In some embodiments, provided herein is a vector comprising a nucleic acid encoding a TCR disclosed herein. In some embodiments, the vector is a self-amplifying RNA replicon, plasmid, phage, transposon, cosmid, virus, or virion. In some embodiments, the vector is a viral vector. In some embodiments, the vector is derived from a retrovirus, lentivirus, adenovirus, adeno-associated virus, herpes virus, pox virus, alpha virus, vaccinia virus, hepatitis B virus, human papillomavirus or a pseudotype thereof. In some embodiments, the vector is a non-viral vector. In some embodiments, the non-viral vector is a nanoparticle, a cationic lipid, a cationic polymer, a metallic nanopolymer, a nanorod, a liposome, a micelle, a microbubble, a cell-penetrating peptide, or a liposphere.

[00280] Presented herein are constructs, for example, nucleic acid constructs that encode an alpha chain and a beta chain of a TCR for expression in a cell. In some embodiments, the constructs comprise one or more polynucleotides encoding a TCR alpha chain and a TCR beta chain. In some embodiments, the polynucleotides are incorporated in a suitable vector. In some embodiments, the polynucleotides encoding the alpha chain and the beta chain are incorporated in the same vector. In some embodiments, the polynucleotides encoding the alpha chain and the beta chain are incorporated in different vectors, and both vectors are delivered for expression in the single cell.

[00281] In some embodiments, a cell may be transduced or transfected with a nucleic acid encoding a TCR, wherein the cell is capable of expressing the TCR and the cell is used as a therapeutic. In some embodiments the cell is derived from a subject or a host, wherein the subject or the host is a human. In some embodiments, the subject or the host comprises a cell having a mutation in an epitope, and the TCR expressed in the cell is capable of binding specifically to the epitope having the mutation. In some embodiments, the cell is a lymphocyte cell. In some embodiments, the T-lymphocyte. In some embodiments, the cell is a lymphocytic precursor cell. In some embodiments, the cell is a T lymphocyte precursor cell. In some embodiments, the cell is a T lymphocyte progenitor cell. In some embodiments the cell is a thymocyte.

[00282] In some embodiments, the T cells are immature T cells. In some embodiments, the T cells are antigen naive T cells. The host cell may be cultured *ex vivo* for 1, 2, 3, 4, 5 or more days for monitoring and recover after transfection or transduction with the polynucleotide(s) encoding the TCR.

X. Neoantigens

[00283] The TCRs disclosed herein are specific to immunogenic neoantigens. In some embodiments, the neoantigen peptide is from RAS. In some embodiments, the neoantigen peptide is from GATA3. In some embodiments, the neoantigen peptide is from BTK. In some embodiments, the neoantigen peptide is from Tmprss2:ERG. In some embodiments, one or more neoantigen peptides are loaded on to APCs, wherein the

peptide loaded APCs are then used to stimulate T cells to produce antigen specific T cells. In some embodiments, the APCs used for peptide loading are dendritic cells. Immunogenic neoantigen sequences can be identified by any suitable method known in the art.

[00284] In various embodiments, the neoantigen comprises an epitope. In both animals and humans, mutated epitopes can be potentially effective in inducing an immune response or activating T cells. In some embodiments, the epitope comprises a mutation. In some embodiments, the mutation is selected from the group consisting of a point mutation, a splice-site mutation, a frameshift mutation, a read-through mutation, a gene fusion mutation and any combination thereof.

[00285] In some embodiments, the epitope has a length of at least 8 amino acids. In some embodiments, the epitope has a length of at least 16 amino acids. In some embodiments, the epitope has a length of from 8-25 amino acids. In some embodiments, the epitope has a length of from 8-12 amino acids. In some embodiments, the epitope has a length of from 16-25 amino acids. In some embodiments, the epitope has a length of 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids.

[00286] In certain embodiments, a neoantigen or epitope thereof can comprise, but is not limited to, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 41, about 42, about 43, about 44, about 45, about 46, about 47, about 48, about 49, about 50, about 60, about 70, about 80, about 90, about 100, about 110, about 120 or greater amino acid residues, and any range derivable therein. In specific embodiments, a neoantigen or epitope thereof is equal to or less than 100 amino acids.

[00287] In some embodiments, a neoantigen or epitope thereof for MHC Class I is 13 residues or less in length and usually consists of between about 8 and about 11 residues, particularly 9 or 10 residues. In some embodiments, a neoantigen or epitope thereof for MHC Class II is 9-24 residues in length.

[00288] In some embodiments, neoantigens bind an HLA protein (e.g., HLA class I or HLA class II). In specific embodiments neoantigens bind an HLA protein with greater affinity than a corresponding wild-type peptide. In specific embodiments, the neoantigenic peptide or polypeptide has an IC₅₀ of at least less than 5000 nM, at least less than 500 nM, at least less than 100 nM, at least less than 50 nM or less.

[00289] In some embodiments, the epitope binds to the human MHC with a greater affinity than a corresponding wild-type epitope. In some embodiments, the epitope binds to the human MHC with a K_D or an IC₅₀ less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM. In some embodiments, the epitope comprises a mutation, wherein the mutation is not present in non-cancer cells of a subject. In some embodiments, the epitope is encoded by a gene or an expressed gene of a subject's cancer cells. In some embodiments, the TCR binds to an HLA-peptide complex with a K_D or an IC₅₀ of less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM.

[00290] In some embodiments, the neoantigenic peptide can be from about 8 and about 50 amino acid residues in length, or from about 8 and about 30, from about 8 and about 20, from about 8 and about 18, from about 8 and about 15, or from about 8 and about 12 amino acid residues in length. In some embodiments, the neoantigenic peptide can be from about 8 and about 500 amino acid residues in length, or from about 8 and about 450, from about 8 and about 400, from about 8 and about 350, from about 8 and about 300, from about 8 and about 250, from about 8 and about 200, from about 8 and about 150, from about 8 and about 100, from about 8 and about 50, or from about 8 and about 30 amino acid residues in length.

[00291] In some embodiments, the neoantigenic peptide can be at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or more amino acid residues in length. In some embodiments, the neoantigenic peptide can be at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more amino acid residues in length. In some embodiments, the neoantigenic peptide can be at most 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or less amino acid residues in length. In some embodiments, the neoantigenic peptide can be at most 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, or less amino acid residues in length.

[00292] In some embodiments, the neoantigenic peptide has a total length of at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350, at least 400, at least 450, or at least 500 amino acids.

[00293] In some embodiments, the neoantigenic peptide has a total length of at most 8, at most 9, at most 10, at most 11, at most 12, at most 13, at most 14, at most 15, at most 16, at most 17, at most 18, at most 19, at most 20, at most 21, at most 22, at most 23, at most 24, at most 25, at most 26, at most 27, at most 28, at most 29, at most 30, at most 40, at most 50, at most 60, at most 70, at most 80, at most 90, at most 100, at most 150, at most 200, at most 250, at most 300, at most 350, at most 400, at most 450, or at most 500 amino acids.

[00294] In some embodiments, the neoantigenic peptide can have a pI value of about 0.5 and about 12, about 2 and about 10, or about 4 and about 8. In some embodiments, the neoantigenic peptide can have a pI value of at least 4.5, 5, 5.5, 6, 6.5, 7, 7.5, or more. In some embodiments, the neoantigenic peptide can have a pI value of at most 4.5, 5, 5.5, 6, 6.5, 7, 7.5, or less.

[00295] In some embodiments, the neoantigenic peptide can have an HLA binding affinity of between about 1pM and about 1mM, about 100pM and about 500μM, about 500pM and about 10μM, about 1nM and about 1μM, or about 10nM and about 1μM. In some embodiments, the neoantigenic peptide can have an HLA binding affinity of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100,

150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 700, 800, 900 μ M, or more. In some embodiments, the neoantigenic peptide can have an HLA binding affinity of at most 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 700, 800, 900 μ M.

[00296] In some embodiments, a neoantigenic peptide described herein can comprise carriers such as those well known in the art, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acid residues such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like.

[00297] In some embodiments, a neoantigenic peptide described herein can be modified by terminal-NH₂ acylation, e.g., by alkanoyl (C1-C20) or thioglycolyl acetylation, terminal-carboxyl amidation, e.g., ammonia, methylamine, etc. In some embodiments, these modifications can provide sites for linking to a support or other molecule.

[00298] In some embodiments, a neoantigenic peptide described herein can contain modifications such as but not limited to glycosylation, side chain oxidation, biotinylation, phosphorylation, addition of a surface active material, e.g. a lipid, or can be chemically modified, e.g., acetylation, etc. Moreover, bonds in the peptide can be other than peptide bonds, e.g., covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds, etc.

[00299] In some embodiments, a neoantigenic peptide described herein can contain substitutions to modify a physical property (e.g., stability or solubility) of the resulting peptide. For example, neoantigenic peptides can be modified by the substitution of a cysteine (C) with α -amino butyric acid ("B"). Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding and cross-binding capability in certain instances. Substitution of cysteine with α -amino butyric acid can occur at any residue of a neoantigenic peptide, e.g., at either anchor or non-anchor positions of an epitope or analog within a peptide, or at other positions of a peptide.

[00300] In some embodiments, a neoantigenic peptide described herein can comprise amino acid mimetics or unnatural amino acid residues, e.g. D- or L-naphylalanine; D- or L-phenylglycine; D- or L-2-thieneylalanine; D- or L-1, -2, 3-, or 4-pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoro-methyl)-phenylalanine; D-.rho.-fluorophenylalanine; D- or L-.rho.-biphenyl-phenylalanine; D- or L-.rho.-methoxybiphenylphenylalanine; D- or L-2-indole(allyl)alanines; and, D- or L-alkylalanines, where the alkyl group can be a substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acid residues. Aromatic rings of a non-natural amino acid include, e.g., thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings. Modified peptides that have various amino acid mimetics or unnatural amino acid

residues are particularly useful, as they tend to manifest increased stability in vivo. Such peptides can also possess improved shelf-life or manufacturing properties.

[00301] Peptide stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef, et al., *Eur. J. Drug Metab. Pharmacokinetics* 11:291 (1986). Half-life of the peptides described herein is conveniently determined using a 25% human serum (v/v) assay. The protocol is as follows: pooled human serum (Type AB, non-heat inactivated) is dilapidated by centrifugation before use. The serum is then diluted to 25% with RPMI-1640 or another suitable tissue culture medium. At predetermined time intervals, a small amount of reaction solution is removed and added to either 6% aqueous trichloroacetic acid (TCA) or ethanol. The cloudy reaction sample is cooled (4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

[00302] In some embodiments, a neoantigenic peptide described herein can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or can be isolated from natural sources such as native tumors or pathogenic organisms. Epitopes can be synthesized individually or joined directly or indirectly in a peptide. Although a neoantigenic peptide described herein will be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments, the peptide can be synthetically conjugated to be joined to native fragments or particles.

[00303] In some embodiments, a neoantigenic peptide described herein can be prepared in a wide variety of ways. In some embodiments, the peptides can be synthesized in solution or on a solid support according to conventional techniques. Various automatic synthesizers are commercially available and can be used according to known protocols. (See, for example, Stewart & Young, *SOLID PHASE PEPTIDE SYNTHESIS*, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptides can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

[00304] Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes a peptide inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1989). Thus, recombinant peptides, which comprise or consist of one or more epitopes described herein, can be used to present the appropriate T cell epitope.

XI. Pharmaceutical Compositions

[00305] Pharmaceutical compositions can be formulated using one or more physiologically acceptable carriers including excipients and auxiliaries which facilitate processing of the active agents into preparations which can be used pharmaceutically. Proper formulation can be dependent upon the route of administration chosen. Any of the well-known techniques, carriers, and excipients can be used as suitable and as understood in the art.

[00306] In some cases, a pharmaceutical composition is formulated as cell based therapeutic, e.g., a T cell therapeutics. In some embodiments, a pharmaceutical composition comprises a peptide-based therapy, a nucleic

acid-based therapy, an antibody-based therapy, and/or a cell-based therapy. In some embodiments, a pharmaceutical composition comprises a peptide-based therapeutic, or nucleic acid based therapeutic in which the nucleic acid encodes the polypeptides. A composition can comprise T cells specific for two or more immunogenic antigen or neoantigen peptides. In some embodiments, the T cell specific therapeutic may be supplemented by one or more additional therapies.

[00307] In some embodiments, a pharmaceutical composition comprising: a nucleic acid encoding a TCR targeting a neoantigen disclosed herein, a vector containing the nucleic acid, the protein encoded by the nucleic acid, or a host cell comprising the nucleic acid, the protein or the vector; and a pharmaceutically acceptable excipient or diluent. In some embodiments, the pharmaceutical composition further comprises an immunomodulatory agent or an adjuvant. In some embodiments, the immunomodulatory agent is a cytokine. In some embodiments, the adjuvant is poly I:C.

[00308] Also provided herein is the use of the pharmaceutical compositions in treating an immune disease or cancer.

[00309] Pharmaceutical compositions can include, in addition to active ingredient, a pharmaceutically acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The precise nature of the carrier or other material will depend on the route of administration. Acceptable carriers, excipients, or stabilizers are those that are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG).

[00310] Acceptable carriers are physiologically acceptable to the administered patient and retain the therapeutic properties of the compounds with/in which it is administered. Acceptable carriers and their formulations are generally described in, for example, Remington's Pharmaceutical Sciences (18th ed. A. Gennaro, Mack Publishing Co., Easton, PA 1990). One example of carrier is physiological saline. A pharmaceutically acceptable carrier is a pharmaceutically acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, involved in carrying or transporting the subject compounds from the administration site of one organ, or portion of the body, to another organ, or portion of the body, or in an in vitro assay system. Acceptable carriers are compatible with the other ingredients of the

formulation and not injurious to a subject to whom it is administered. Nor should an acceptable carrier alter the specific activity of the other ingredients.

[00311] In one aspect, provided herein are pharmaceutically acceptable or physiologically acceptable compositions including solvents (aqueous or non-aqueous), solutions, emulsions, dispersion media, coatings, isotonic and absorption promoting or delaying agents, compatible with pharmaceutical administration. Pharmaceutical compositions or pharmaceutical formulations therefore refer to a composition suitable for pharmaceutical use in a subject. Compositions can be formulated to be compatible with a particular route of administration (i.e., systemic or local). Thus, compositions include carriers, diluents, or excipients suitable for administration by various routes.

[00312] In some embodiments, a pharmaceutical composition can further comprise an acceptable additive in order to improve the stability of the composition. Acceptable additives may not alter the specific activity of the active agent, *e.g.* immune cells. Examples of acceptable additives include, but are not limited to, a sugar such as mannitol, sorbitol, glucose, xylitol, trehalose, sorbose, sucrose, galactose, dextran, dextrose, fructose, lactose and mixtures thereof. Acceptable additives can be combined with acceptable carriers and/or excipients such as dextrose. Alternatively, examples of acceptable additives include, but are not limited to, a surfactant such as polysorbate 20 or polysorbate 80 to increase stability of the peptide and decrease gelling of the solution. The surfactant can be added to the composition in an amount of 0.01% to 5% of the solution. Addition of such acceptable additives increases the stability and half-life of the composition in storage.

[00313] In some embodiments the pharmaceutical composition comprises a therapeutic which is a T cell expressing one or more polynucleotides, encoding a T cell receptor. In some embodiments, the pharmaceutical composition comprises physiologically acceptable carrier suitable for a cell suspension.

[00314] The pharmaceutical composition can be administered, for example, by injection. Pharmaceutical compositions for injection include aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, or phosphate buffered saline (PBS). The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. Fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Antibacterial and antifungal agents include, for example, parabens, chlorobutanol, phenol, ascorbic acid and thimerosal. Isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, and sodium chloride can be included in the composition. The resulting solutions can be packaged for use as is, or lyophilized; the lyophilized preparation can later be combined with a sterile solution prior to administration. For intravenous, injection, or injection at the site of affliction, the active ingredient will be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's

Injection, Lactated Ringer's Injection. Preservatives, stabilizers, buffers, antioxidants and/or other additives can be included, as needed. Sterile injectable solutions can be prepared by incorporating an active ingredient in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active ingredient into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation can be vacuum drying and freeze drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00315] Pharmaceutical compositions can be conventionally administered intravenously, such as by injection of a unit dose, for example. For injection, an active ingredient can be in the form of a parenterally acceptable aqueous solution which is substantially pyrogen-free and has suitable pH, isotonicity and stability. One can prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilizers, buffers, antioxidants and/or other additives can be included, as required. Additionally, compositions can be administered via aerosolization.

[00316] When the pharmaceutical compositions are considered for use in medicaments or any of the methods provided herein, it is contemplated that the composition can be substantially free of pyrogens such that the composition will not cause an inflammatory reaction or an unsafe allergic reaction when administered to a human patient. Testing compositions for pyrogens and preparing compositions substantially free of pyrogens are well understood to one of ordinary skill of the art and can be accomplished using commercially available kits.

[00317] Acceptable carriers can contain a compound that stabilizes, increases or delays absorption, or increases or delays clearance. Such compounds include, for example, carbohydrates, such as glucose, sucrose, or dextrans; low molecular weight proteins; compositions that reduce the clearance or hydrolysis of peptides; or excipients or other stabilizers and/or buffers. Agents that delay absorption include, for example, aluminum monostearate and gelatin. Detergents can also be used to stabilize or to increase or decrease the absorption of the pharmaceutical composition, including liposomal carriers. To protect from digestion the compound can be complexed with a composition to render it resistant to acidic and enzymatic hydrolysis, or the compound can be complexed in an appropriately resistant carrier such as a liposome. Means of protecting compounds from digestion are known in the art (e.g., Fix (1996) Pharm Res. 13:1760 1764; Samanen (1996) J. Pharm. Pharmacol. 48:119 135; and U.S. Pat. No. 5,391,377).

[00318] The pharmaceutical compositions can be administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered depends on the subject to be treated, capacity of the subject's immune system to utilize the active ingredient, and degree of binding capacity desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. Suitable regimes for initial administration and booster shots are also variable, but, are typified by an initial administration followed by repeated doses at one or more hour

intervals by a subsequent injection or other administration. Alternatively, continuous intravenous infusions sufficient to maintain concentrations in the blood are contemplated.

[00319] In some embodiments, the present disclosure is directed to an immunogenic composition, e.g., a pharmaceutical composition capable of raising a neoantigen-specific response (e.g., a humoral or cell-mediated immune response). In some embodiments, the immunogenic composition comprises neoantigen therapeutics (e.g., peptides, polynucleotides, TCR, CAR, cells containing TCR or CAR, dendritic cell containing polypeptide, dendritic cell containing polynucleotide, antibody, etc.) described herein corresponding to a tumor specific antigen or neoantigen.

[00320] In some embodiments, a pharmaceutical composition described herein is capable of raising a specific cytotoxic T cells response, specific helper T cell response, or a B cell response.

[00321] In some embodiments, antigen polypeptides or polynucleotides can be provided as antigen presenting cells (e.g., dendritic cells) containing such polypeptides or polynucleotides. In other embodiments, such antigen presenting cells are used to stimulate T cells for use in patients. In some embodiments, the antigen presenting cells are dendritic cells. In related embodiments, the dendritic cells are autologous dendritic cells that are pulsed with the neoantigen peptide or nucleic acid. The neoantigen peptide can be any suitable peptide that gives rise to an appropriate T cell response. In some embodiments, the T cell is a CTL. In some embodiments, the T cell is an HTL. Thus, one embodiment of the present disclosure is an immunogenic composition containing at least one antigen presenting cell (e.g., a dendritic cell) that is pulsed or loaded with one or more neoantigen polypeptides or polynucleotides described herein. In some embodiments, such APCs are autologous (e.g., autologous dendritic cells). Alternatively, peripheral blood mononuclear cells (PBMCs) isolated from a patient can be loaded with neoantigen peptides or polynucleotides ex vivo. In related embodiments, such APCs or PBMCs are injected back into the patient. The polynucleotide can be any suitable polynucleotide that is capable of transducing the dendritic cell, thus resulting in the presentation of a neoantigen peptide and induction of immunity. In some embodiments, such antigen presenting cells (APCs) (e.g., dendritic cells) or peripheral blood mononuclear cells (PBMCs) are used to stimulate a T cell (e.g., an autologous T cell, or an allogeneic T cell). In related embodiments, the T cell is a CTL. In other related embodiments, the T cell is an HTL. In some embodiments, the T cells are CD8⁺ T cells. In some embodiments, the T cells are CD4⁺ T cells. Such T cells are then injected into the patient. In some embodiments, CTL is injected into the patient. In some embodiments, HTL is injected into the patient. In some embodiments, both CTL and HTL are injected into the patient. Administration of either therapeutic can be performed simultaneously or sequentially and in any order.

[00322] In some embodiments, pharmaceutical compositions (e.g., immunogenic compositions) described herein for therapeutic treatment can be formulated for parenteral, topical, nasal, oral or local administration. In some embodiments, the pharmaceutical compositions described herein are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. In some embodiments, the composition can be administered intratumorally. The compositions can be administered at the site of surgical excision to induce a local immune response to the tumor. In some embodiments, described herein are compositions for parenteral

administration which comprise a solution of the neoantigen peptides and immunogenic compositions are dissolved or suspended in an acceptable carrier, for example, an aqueous carrier. A variety of aqueous carriers can be used, e.g., water, buffered water, 0.9% saline, 0.3% glycine, hyaluronic acid and the like. These compositions can be sterilized by conventional, well known sterilization techniques, or can be sterile filtered. The resulting aqueous solutions can be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions can contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

[00323] The ability of an adjuvant to increase the immune response to an antigen is typically manifested by a significant increase in immune-mediated reaction, or reduction in disease symptoms. For example, an increase in humoral immunity can be manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T cell activity can be manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant can also alter an immune response, for example, by changing a primarily humoral or T helper 2 response into a primarily cellular, or T helper 1 response.

[00324] Suitable adjuvants are known in the art (see, WO 2015/095811) and include, but are not limited to poly(I:C), poly-ICLC, STING agonist, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel® vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, β -glucan, Pam3Cys, Pam3CSK4, Aquila's QS21 stimulon (Aquila Biotech, Worcester, Mass., USA) which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox. Quil or Superfos. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described (Dupuis M, et al., Cell Immunol. 1998; 186(1):18-27; Allison A C; Dev Biol Stand. 1998; 92:3-11) (Mosca et al. Frontiers in Bioscience, 2007; 12:4050-4060) (Gamvrellis et al. Immunol & Cell Biol. 2004; 82: 506-516). Also cytokines can be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF- α), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, PGE1, PGE2, IL-1, IL-1 β , IL-4, IL-6 and CD40L) (U.S. Pat. No. 5,849,589 incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12) (Gabrilovich D I, et al., J Immunother Emphasis Tumor Immunol. 1996 (6):414-418).

[00325] CpG immunostimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a therapeutic setting. Without being bound by theory, CpG oligonucleotides act by activating the innate (non-adaptive) immune system via Toll-like receptors (TLR), mainly TLR9. CpG triggered TLR9 activation

enhances antigen-specific humoral and cellular responses to a wide variety of antigens, including peptide or protein antigens, live or killed viruses, dendritic cell immunogenic pharmaceutical compositions, autologous cellular immunogenic pharmaceutical compositions and polysaccharide conjugates in both prophylactic and therapeutic immunogenic pharmaceutical compositions. Importantly, it enhances dendritic cell maturation and differentiation, resulting in enhanced activation of TH1 cells and strong cytotoxic T-lymphocyte (CTL) generation, even in the absence of CD4⁺ T cell help. The TH1 bias induced by TLR9 stimulation is maintained even in the presence of adjuvants such as alum or incomplete Freund's adjuvant (IFA) that normally promote a TH2 bias. CpG oligonucleotides show even greater adjuvant activity when formulated or co-administered with other adjuvants or in formulations such as microparticles, nanoparticles, lipid emulsions or similar formulations, which are especially useful for inducing a strong response when the antigen is relatively weak. They can also accelerate the immune response and enabled the antigen doses to be reduced with comparable antibody responses to the full-dose immunogenic pharmaceutical composition without CpG in some experiments (Arthur M. Krieg, *Nature Reviews, Drug Discovery*, 5, June 2006, 471-484). U.S. Pat. No. 6,406,705 describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen-specific immune response. A commercially available CpG TLR9 antagonist is dSLIM (double Stem Loop Immunomodulator) by Mologen (Berlin, DE), which is a component of the pharmaceutical composition described herein. Other TLR binding molecules such as RNA binding TLR7, TLR8 and/or TLR9 can also be used.

[00326] Other examples of useful adjuvants include, but are not limited to, chemically modified CpGs (e.g. CpR, Idera), Poly(I:C)(e.g., polyI:C12U), polyIC:LC, non-CpG bacterial DNA or RNA, ssRNA40 for TLR8, as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, bevacizumab, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafenib, XL-999, CP-547632, pazopanib, ZD2171, AZD2171, ipilimumab, tremelimumab, and SC58175, which can act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives useful in the context of the present invention can readily be determined by the skilled artisan without undue experimentation. Additional adjuvants include colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim).

[00327] In some embodiments, an immunogenic composition according to the present disclosure can comprise more than one different adjuvant. Furthermore, the invention encompasses a pharmaceutical composition comprising any adjuvant substance including any of the above or combinations thereof. In some embodiments, the immunogenic composition comprises neoantigen therapeutics (e.g., peptides, polynucleotides, TCR, CAR, cells containing TCR or CAR, dendritic cell containing polypeptide, dendritic cell containing polynucleotide, antibody, etc.) and the adjuvant can be administered separately in any appropriate sequence.

[00328] Lipidation can be classified into several different types, such as N-myristoylation, palmitoylation, GPI-anchor addition, prenylation, and several additional types of modifications. N-myristoylation is the covalent attachment of myristate, a C14 saturated acid, to a glycine residue. Palmitoylation is thioester linkage of long-chain fatty acids (C16) to cysteine residues. GPI-anchor addition is glycosyl-phosphatidylinositol (GPI) linkage

via amide bond. Prenylation is the thioether linkage of an isoprenoid lipid (e.g. farnesyl (C-15), geranylgeranyl (C-20)) to cysteine residues. Additional types of modifications can include attachment of S-diacylglycerol by a sulfur atom of cysteines, O-octanoyl conjugation via serine or threonine residues, S-archaeol conjugation to cysteine residues, and cholesterol attachment.

[00329] Fatty acids for generating a lipidated peptides can include C2 to C30 saturated, monounsaturated, or polyunsaturated fatty acyl groups. Exemplary fatty acids can include palmitoyl, myristoyl, stearoyl and decanoyl groups. In some instances, a lipid moiety that has adjuvant property is attached to a polypeptide of interest to elicit or enhance immunogenicity in the absence of an extrinsic adjuvant. A lipidated peptide or lipopeptide can be referred to as a self-adjuvant lipopeptide. Any of the fatty acids described above and elsewhere herein can elicit or enhance immunogenicity of a polypeptide of interest. A fatty acid that can elicit or enhance immunogenicity can include palmitoyl, myristoyl, stearoyl, lauroyl, octanoyl, and decanoyl groups.

[00330] Polypeptides such as naked peptides or lipidated peptides can be incorporated into a liposome. Sometimes, lipidated peptides can be incorporated into a liposome. For example, the lipid portion of the lipidated peptide can spontaneously integrate into the lipid bilayer of a liposome. Thus, a lipopeptide can be presented on the “surface” of a liposome.

[00331] Liposome can also be used to deliver nucleic acids into a cell. The nucleic acid of interest comprises one or more sequences encoding a T cell receptor. Liposomes may be used to deliver a DNA or an RNA. Liposomes may be used to deliver a nucleic acid incorporated in a vector. The nucleic acid may be 50-200,000 nucleotides long, or may be 100-500,000 nucleotides long, or may be 20-500,000 nucleotides long. Exemplary liposomes suitable for incorporation in the formulations include, and are not limited to, multilamellar vesicles (MLV), oligolamellar vesicles (OLV), unilamellar vesicles (UV), small unilamellar vesicles (SUV), medium-sized unilamellar vesicles (MUV), large unilamellar vesicles (LUV), giant unilamellar vesicles (GUV), multivesicular vesicles (MVV), single or oligolamellar vesicles made by reverse-phase evaporation method (REV), multilamellar vesicles made by the reverse-phase evaporation method (MLV-REV), stable plurilamellar vesicles (SPLV), frozen and thawed MLV (FATMLV), vesicles prepared by extrusion methods (VET), vesicles prepared by French press (FPV), vesicles prepared by fusion (FUV), dehydration-rehydration vesicles (DRV), and bubblesomes (BSV).

[00332] Depending on the method of preparation, liposomes can be unilamellar or multilamellar, and can vary in size with diameters ranging from about 0.02 μm to greater than about 10 μm . Liposomes can adsorb many types of cells and then release an incorporated agent (e.g., a peptide described herein). In some cases, the liposomes fuse with the target cell, whereby the contents of the liposome then empty into the target cell. A liposome can be endocytosed by cells that are phagocytic. Endocytosis can be followed by intralysosomal degradation of liposomal lipids and release of the encapsulated agents.

[00333] The liposomes provided herein can also comprise carrier lipids. In some embodiments, the carrier lipids are phospholipids. Carrier lipids capable of forming liposomes include, but are not limited to dipalmitoylphosphatidylcholine (DPPC), phosphatidylcholine (PC; lecithin), phosphatidic acid (PA),

phosphatidylglycerol (PG), phosphatidylethanolamine (PE), phosphatidylserine (PS). Other suitable phospholipids further include distearoylphosphatidylcholine (DSPC), dimyristoylphosphatidylcholine (DMPC), dipalmitoylphosphatidylglycerol (DPPG), distearoylphosphatidylglycerol (DSPG), dimyristoylphosphatidylglycerol (DMPG), dipalmitoylphosphatidic acid (DPPA); dimyristoylphosphatidic acid (DMPA), distearoylphosphatidic acid (DSPA), dipalmitoylphosphatidylserine (DPPS), dimyristoylphosphatidylserine (DMPS), distearoylphosphatidylserine (DSPS), dipalmitoylphosphatidylethanolamine (DPPE), dimyristoylphosphatidylethanolamine (DMPE), distearoylphosphatidylethanolamine (DSPE) and the like, or combinations thereof. In some embodiments, the liposomes further comprise a sterol (e.g., cholesterol) which modulates liposome formation. The carrier lipids can be any known non-phosphate polar lipids.

[00334] A pharmaceutical composition can be encapsulated within liposomes using well-known technology. Biodegradable microspheres can also be employed as carriers for the pharmaceutical compositions of this invention.

[00335] The pharmaceutical composition can be administered in liposomes or microspheres (or microparticles). Methods for preparing liposomes and microspheres for administration to a patient are well known to those of skill in the art. Essentially, material is dissolved in an aqueous solution, the appropriate phospholipids and lipids added, along with surfactants if required, and the material dialyzed or sonicated, as necessary.

[00336] Microspheres formed of polymers or proteins are well known to those skilled in the art, and can be tailored for passage through the gastrointestinal tract directly into the blood stream. Alternatively, the compound can be incorporated and the microspheres, or composite of microspheres, implanted for slow release over a period of time ranging from days to months.

[00337] Cell-based immunogenic pharmaceutical compositions can also be administered to a subject. For example, an antigen presenting cell (APC) based immunogenic pharmaceutical composition can be formulated using any of the well-known techniques, carriers, and excipients as suitable and as understood in the art. APCs include monocytes, monocyte-derived cells, macrophages, and dendritic cells. Sometimes, an APC based immunogenic pharmaceutical composition can be a dendritic cell-based immunogenic pharmaceutical composition.

[00338] A dendritic cell-based immunogenic pharmaceutical composition can be prepared by any methods well known in the art. In some cases, dendritic cell-based immunogenic pharmaceutical compositions can be prepared through an ex vivo or in vivo method. The ex vivo method can comprise the use of autologous DCs pulsed ex vivo with the polypeptides described herein, to activate or load the DCs prior to administration into the patient. The in vivo method can comprise targeting specific DC receptors using antibodies coupled with the polypeptides described herein. The DC-based immunogenic pharmaceutical composition can further comprise DC activators such as TLR3, TLR-7-8, and CD40 agonists. The DC-based immunogenic pharmaceutical composition can further comprise adjuvants, and a pharmaceutically acceptable carrier.

[00339] An adjuvant can be used to enhance the immune response (humoral and/or cellular) elicited in a patient receiving the immunogenic pharmaceutical composition. Sometimes, adjuvants can elicit a Th1-type response. Other times, adjuvants can elicit a Th2-type response. A Th1-type response can be characterized by the production of cytokines such as IFN- γ as opposed to a Th2-type response which can be characterized by the production of cytokines such as IL-4, IL-5 and IL-10.

[00340] In some aspects, lipid-based adjuvants, such as MPLA and MDP, can be used with the immunogenic pharmaceutical compositions disclosed herein. Monophosphoryl lipid A (MPLA), for example, is an adjuvant that causes increased presentation of liposomal antigen to specific T Lymphocytes. In addition, a muramyl dipeptide (MDP) can also be used as a suitable adjuvant in conjunction with the immunogenic pharmaceutical formulations described herein.

[00341] Adjuvant can also comprise stimulatory molecules such as cytokines. Non-limiting examples of cytokines include: CCL20, α -interferon (IFN α), β -interferon (IFN β), γ -interferon (IFN γ), platelet derived growth factor (PDGF), TNF α , GM-CSF, epidermal growth factor (EGF), cutaneous T cell-attracting chemokine (CTACK), epithelial thymus-expressed chemokine (TECK), mucosae-associated epithelial chemokine (MEC), IL-12, IL-15, IL-28, MHC, CD80, CD86, IL-1, IL-2, IL-4, IL-5, IL-6, IL-10, IL-18, MCP-1, MIP-1a, MIP-1-, IL-8, L- selectin, P-selectin, E-selectin, CD34, GlyCAM-1, MadCAM-1, LFA-1, VLA-1, Mac-1, p150.95, PECAM, ICAM-1, ICAM-2, ICAM-3, CD2, LFA-3, M-CSF, G-CSF, mutant forms of IL-18, CD40, CD40L, vascular growth factor, fibroblast growth factor, IL-7, nerve growth factor, vascular endothelial growth factor, Fas, TNF receptor, Fit, Apo-1, p55, WSL-1, DR3, TRAMP, Apo-3, AIR, LARD, NGRF, DR4, DRS, KILLER, TRAIL-R2, TRICK2, DR6, Caspase ICE, Fos, c-jun, Sp-1, Ap-1, Ap-2, p38, p65Rel, MyD88, IRAK, TRAF6, I κ B, Inactive NIK, SAP K, SAP-I, JNK, interferon response genes, NF κ B, Bax, TRAIL, TRAILrec, TRAILrecDRC5, TRAIL-R3, TRAIL-R4, RANK, RANK LIGAND, Ox40, Ox40 LIGAND, NKG2D, MICA, MICB, NKG2A, NKG2B, NKG2C, NKG2E, NKG2F, TAPI, and TAP2.

[00342] Additional adjuvants include: MCP-1, MIP-1a, MIP-1p, IL-8, RANTES, L-selectin, P-selectin, E-selectin, CD34, GlyCAM-1, MadCAM-1, LFA-1, VLA-1, Mac-1, p150.95, PECAM, ICAM-1, ICAM-2, ICAM-3, CD2, LFA-3, M-CSF, G-CSF, IL-4, mutant forms of IL-18, CD40, CD40L, vascular growth factor, fibroblast growth factor, IL-7, IL-22, nerve growth factor, vascular endothelial growth factor, Fas, TNF receptor, Fit, Apo-1, p55, WSL-1, DR3, TRAMP, Apo-3, AIR, LARD, NGRF, DR4, DR5, KILLER, TRAIL-R2, TRICK2, DR6, Caspase ICE, Fos, c-jun, Sp-1, Ap-1, Ap-2, p38, p65Rel, MyD88, IRAK, TRAF6, I κ B, Inactive NIK, SAP K, SAP-1, JNK, interferon response genes, NF κ B, Bax, TRAIL, TRAILrec, TRAILrecDRC5, TRAIL-R3, TRAIL-R4, RANK, RANK LIGAND, Ox40, Ox40 LIGAND, NKG2D, MICA, MICB, NKG2A, NKG2B, NKG2C, NKG2E, NKG2F, TAP1, TAP2 and functional fragments thereof.

[00343] In some aspects, an adjuvant can be a modulator of a toll like receptor. Examples of modulators of toll-like receptors include TLR9 agonists and are not limited to small molecule modulators of toll-like receptors such as Imiquimod. Sometimes, an adjuvant is selected from bacteria toxoids, polyoxypropylene-polyoxyethylene block polymers, aluminum salts, liposomes, CpG polymers, oil-in-water emulsions, or a

combination thereof. Sometimes, an adjuvant is an oil-in-water emulsion. The oil-in-water emulsion can include at least one oil and at least one surfactant, with the oil(s) and surfactant(s) being biodegradable (metabolizable) and biocompatible. The oil droplets in the emulsion can be less than 5 μm in diameter, and can even have a sub-micron diameter, with these small sizes being achieved with a microfluidiser to provide stable emulsions. Droplets with a size less than 220 nm can be subjected to filter sterilization.

[00344] In some instances, an immunogenic pharmaceutical composition can include carriers and excipients (including but not limited to buffers, carbohydrates, mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents, suspending agents, thickening agents and/or preservatives), water, oils including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like, saline solutions, aqueous dextrose and glycerol solutions, flavoring agents, coloring agents, and other acceptable additives, adjuvants, or binders, other pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH buffering agents, tonicity adjusting agents, emulsifying agents, wetting agents and the like. Examples of excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. In another instances, the pharmaceutical preparation is substantially free of preservatives. In other instances, the pharmaceutical preparation can contain at least one preservative. It will be recognized that, while any suitable carrier known to those of ordinary skill in the art can be employed to administer the pharmaceutical compositions described herein, the type of carrier will vary depending on the mode of administration.

[00345] An immunogenic pharmaceutical composition can include preservatives such as thiomersal or 2-phenoxyethanol. In some instances, the immunogenic pharmaceutical composition is substantially free from (e.g., $<10\text{ }\mu\text{g/mL}$) mercurial material e.g. thiomersal-free. α -Tocopherol succinate may be used as an alternative to mercurial compounds.

[00346] For controlling the tonicity, a physiological salt such as sodium salt can be included in the immunogenic pharmaceutical composition. Other salts can include potassium chloride, potassium dihydrogen phosphate, disodium phosphate, and/or magnesium chloride, or the like.

[00347] An immunogenic pharmaceutical composition can have an osmolality of between 200 mOsm/kg and 400 mOsm/kg, between 240-360 mOsm/kg, or within the range of 290-310 mOsm/kg.

[00348] An immunogenic pharmaceutical composition can comprise one or more buffers, such as a Tris buffer; a borate buffer; a succinate buffer; a histidine buffer (particularly with an aluminum hydroxide adjuvant); or a citrate buffer. Buffers, in some cases, are included in the 5-20 or 10-50 mM range.

[00349] The pH of the immunogenic pharmaceutical composition can be between about 5.0 and about 8.5, between about 6.0 and about 8.0, between about 6.5 and about 7.5, or between about 7.0 and about 7.8.

[00350] An immunogenic pharmaceutical composition can be sterile. The immunogenic pharmaceutical composition can be non-pyrogenic e.g. containing <1 EU (endotoxin unit, a standard measure) per dose, and can be <0.1 EU per dose. The composition can be gluten free.

[00351] An immunogenic pharmaceutical composition can include detergent e.g. a polyoxyethylene sorbitan ester surfactant (known as ‘Tweens’), or an octoxynol (such as octoxynol-9 (Triton X-100) or t-octylphenoxypolyethoxyethanol). The detergent can be present only at trace amounts. The immunogenic pharmaceutical composition can include less than 1 mg/mL of each of octoxynol-10 and polysorbate 80. Other residual components in trace amounts can be antibiotics (e.g. neomycin, kanamycin, polymyxin B).

[00352] An immunogenic pharmaceutical composition can be formulated as a sterile solution or suspension, in suitable vehicles, well known in the art. The pharmaceutical compositions can be sterilized by conventional, well-known sterilization techniques, or can be sterile filtered. The resulting aqueous solutions can be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

[00353] Pharmaceutical compositions comprising, for example, an active agent such as immune cells disclosed herein, in combination with one or more adjuvants can be formulated to comprise certain molar ratios. For example, molar ratios of about 99:1 to about 1:99 of an active agent such as an immune cell described herein, in combination with one or more adjuvants can be used. In some instances, the range of molar ratios of an active agent such as an immune cell described herein, in combination with one or more adjuvants can be selected from about 80:20 to about 20:80; about 75:25 to about 25:75, about 70:30 to about 30:70, about 66:33 to about 33:66, about 60:40 to about 40:60; about 50:50; and about 90:10 to about 10:90. The molar ratio of an active agent such as an immune cell described herein, in combination with one or more adjuvants can be about 1:9, and in some cases can be about 1:1. The active agent such as an immune cell described herein, in combination with one or more adjuvants can be formulated together, in the same dosage unit e.g., in one vial, suppository, tablet, capsule, an aerosol spray; or each agent, form, and/or compound can be formulated in separate units, e.g., two vials, suppositories, tablets, two capsules, a tablet and a vial, an aerosol spray, and the like.

[00354] In some instances, an immunogenic pharmaceutical composition can be administered with an additional agent. The choice of the additional agent can depend, at least in part, on the condition being treated. The additional agent can include, for example, a checkpoint inhibitor agent such as an anti-PD1, anti-CTLA4, anti-PD-L1, anti CD40, or anti-TIM3 agent (e.g., an anti-PD1, anti-CTLA4, anti-PD-L1, anti CD40, or anti-TIM3 antibody); or any agents having a therapeutic effect for a pathogen infection (e.g. viral infection), including, e.g., drugs used to treat inflammatory conditions such as an NSAID, e.g., ibuprofen, naproxen, acetaminophen, ketoprofen, or aspirin. For example, the checkpoint inhibitor can be a PD-1/PD-L1 antagonist selected from the group consisting of: nivolumab (ONO-4538/BMS-936558, MDX1 106, OPDIVO), pembrolizumab (MK-3475, KEYTRUDA), pidilizumab (CT-011), and MPDL3280A (ROCHE). As another example, formulations can additionally contain one or more supplements, such as vitamin C, E or other anti-oxidants.

[00355] A pharmaceutical composition comprising an active agent such as an immune cell described herein, in combination with one or more adjuvants can be formulated in conventional manner using one or more physiologically acceptable carriers, comprising excipients, diluents, and/or auxiliaries, e.g., which facilitate

processing of the active agents into preparations that can be administered. Proper formulation can depend at least in part upon the route of administration chosen. The agent(s) described herein can be delivered to a patient using a number of routes or modes of administration, including oral, buccal, topical, rectal, transdermal, transmucosal, subcutaneous, intravenous, and intramuscular applications, as well as by inhalation.

[00356] The active agents can be formulated for parenteral administration (e.g., by injection, for example bolus injection or continuous infusion) and can be presented in unit dose form in ampoules, pre-filled syringes, small volume infusion or in multi-dose containers with an added preservative. The compositions can take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, for example solutions in aqueous polyethylene glycol.

[00357] For injectable formulations, the vehicle can be chosen from those known in art to be suitable, including aqueous solutions or oil suspensions, or emulsions, with sesame oil, corn oil, cottonseed oil, or peanut oil, as well as elixirs, mannitol, dextrose, or a sterile aqueous solution, and similar pharmaceutical vehicles. The formulation can also comprise polymer compositions which are biocompatible, biodegradable, such as poly(lactic-co-glycolic)acid. These materials can be made into micro or nanospheres, loaded with drug and further coated or derivatized to provide superior sustained release performance. Vehicles suitable for periocular or intraocular injection include, for example, suspensions of therapeutic agent in injection grade water, liposomes and vehicles suitable for lipophilic substances. Other vehicles for periocular or intraocular injection are well known in the art.

[00358] In some instances, pharmaceutical composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

[00359] When administration is by injection, the active agent can be formulated in aqueous solutions, specifically in physiologically compatible buffers such as Hanks solution, Ringer's solution, or physiological saline buffer. The solution can contain formulatory agents such as suspending, stabilizing and/or dispersing agents. In another embodiment, the pharmaceutical composition does not comprise an adjuvant or any other substance added to enhance the immune response.

[00360] In addition to the formulations described previously, the active agents can also be formulated as a depot preparation. Such long acting formulations can be administered by implantation or transcutaneous delivery (for example subcutaneously or intramuscularly), intramuscular injection or use of a transdermal patch.

Thus, for example, the agents can be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[00361] In some cases, pharmaceutical compositions comprising one or more agents exert local and regional effects when administered topically or injected at or near particular sites of infection. Direct topical application, e.g., of a viscous liquid, solution, suspension, dimethylsulfoxide (DMSO)-based solutions, liposomal formulations, gel, jelly, cream, lotion, ointment, suppository, foam, or aerosol spray, can be used for local administration, to produce for example local and/or regional effects. Pharmaceutically appropriate vehicles for such formulation include, for example, lower aliphatic alcohols, polyglycols (e.g., glycerol or polyethylene glycol), esters of fatty acids, oils, fats, silicones, and the like. Such preparations can also include preservatives (e.g., p-hydroxybenzoic acid esters) and/or antioxidants (e.g., ascorbic acid and tocopherol). See also *Dermatological Formulations: Percutaneous absorption*, Barry (Ed.), Marcel Dekker Incl, 1983. In another embodiment, local/topical formulations comprising a transporter, carrier, or ion channel inhibitor are used to treat epidermal or mucosal viral infections.

[00362] Pharmaceutical compositions can contain adjuvants such as hydrophilic or lipophilic gelling agents, hydrophilic or lipophilic active agents, preserving agents, antioxidants, solvents, fragrances, fillers, sunscreens, odor-absorbers and dyestuffs. The amounts of these various adjuvants are those conventionally used in the fields considered and, for example, are from about 0.01% to about 20% of the total weight of the composition. Depending on their nature, these adjuvants can be introduced into the fatty phase, into the aqueous phase and/or into the lipid vesicles.

XII. Methods of Treatment

[00363] Provided herein are method of using any of the nucleic acid disclosed above, the vector containing any of the nucleic acid sequence disclosed above, the protein encoded by any of the nucleic acid disclosed above, or the host cell disclosed above, for manufacture of a medicament for treating an immune disease or cancer.

[00364] Also provided herein are methods of treating a subject with a disease, disorder or condition. A method of treatment can comprise administering a pharmaceutical composition disclosed herein to a subject with a disease, disorder or condition. The present disclosure provides methods of treatment comprising an immunogenic therapy. Methods of treatment for a disease (such as cancer or a viral infection) are provided. A method can comprise administering to a subject an effective amount of a pharmaceutical composition comprising an immunogenic antigen specific T cells. In some embodiments, the antigen comprises a tumor antigen.

[00365] In some embodiments, the method of treating a subject with a disease or condition comprises administering to the subject the pharmaceutical composition disclosed herein. In some embodiments, the method is a method of preventing resistance to a cancer therapy, wherein the method comprises administering to a subject in need thereof the pharmaceutical composition disclosed herein. In some embodiments, the method

is a method of inducing an immune response, wherein the method comprises administering to a subject in need thereof the pharmaceutical composition disclosed herein. In some embodiments, the immune response is a humoral response. In some embodiments, the immune response is a cytotoxic T cell response.

[00366] In some embodiments, the subject has cancer, wherein the cancer is selected from the group consisting of melanoma, ovarian cancer, lung cancer, prostate cancer, breast cancer, colorectal cancer, endometrial cancer, and chronic lymphocytic leukemia (CLL).

[00367] In some embodiments, the subject has a breast cancer that is resistant to anti-estrogen therapy. In some embodiments, the breast cancer expresses an estrogen receptor with a mutation. In some embodiments, the subject has a CLL that is resistant to ibrutinib therapy. In some embodiments, the CLL expresses a Bruton tyrosine kinase with a mutation, such as a C481S mutation. In some embodiments, the subject has a lung cancer that is resistant to a tyrosine kinase inhibitor. In some embodiments, the lung cancer expresses an epidermal growth factor receptor (EGFR) with a mutation, such as a T790M, L792F, or C797S mutation.

[00368] In some embodiments, the method further comprises administering at least one additional therapeutic agent or modality. In some embodiments, the at least one additional therapeutic agent or modality is surgery, a checkpoint inhibitor, an antibody or fragment thereof, a chemotherapeutic agent, radiation, a vaccine, a small molecule, a T cell, a vector, and APC, a polynucleotide, an oncolytic virus or any combination thereof. In some embodiments, the at least one additional therapeutic agent is an anti-PD-1 agent and anti-PD-L1 agent, an anti-CTLA-4 agent, or an anti-CD40 agent. In some embodiments, the additional therapeutic agent is administered before, simultaneously, or after administering the pharmaceutical composition disclosed herein.

[00369] In some other aspects, provided here is use of a pharmaceutical composition for the manufacture of a medicament for use in therapy. In some embodiments, a method of treatment comprises administering to a subject an effective amount of T cells specifically recognizing an immunogenic neoantigen peptide. In some embodiments, a method of treatment comprises administering to a subject an effective amount of a TCR that specifically recognizes an immunogenic neoantigen peptide, such as a TCR expressed in a T cell.

[00370] In some embodiments, the cancer is selected from the group consisting of carcinoma, lymphoma, blastoma, sarcoma, leukemia, squamous cell cancer, lung cancer (including small cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer (including gastrointestinal cancer), pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, melanoma, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, head and neck cancer, colorectal cancer, rectal cancer, soft-tissue sarcoma, Kaposi's sarcoma, B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL), small lymphocytic (SL) NHL, intermediate grade/follicular NHL, intermediate grade diffuse NHL, high grade immunoblastic NHL, high grade lymphoblastic NHL, high grade small non-cleaved cell NHL, bulky disease NHL, mantle cell lymphoma, AIDS-related lymphoma, and Waldenstrom's macroglobulinemia), chronic lymphocytic leukemia (CLL), acute lymphoblastic leukemia

(ALL), myeloma, Hairy cell leukemia, chronic myeloblasts leukemia, and post-transplant lymphoproliferative disorder (PTLD), abnormal vascular proliferation associated with phakomatoses, edema, Meigs' syndrome, and combinations thereof.

[00371] The methods of the disclosure can be used to treat any type of cancer known in the art. Non-limiting examples of cancers to be treated by the methods of the present disclosure can include melanoma (e.g., metastatic malignant melanoma), renal cancer (e.g., clear cell carcinoma), prostate cancer (e.g., hormone refractory prostate adenocarcinoma), pancreatic adenocarcinoma, breast cancer, colon cancer, lung cancer (e.g., non-small cell lung cancer), esophageal cancer, squamous cell carcinoma of the head and neck, liver cancer, ovarian cancer, cervical cancer, thyroid cancer, glioblastoma, glioma, leukemia, lymphoma, and other neoplastic malignancies.

[00372] Additionally, the disease or condition provided herein includes refractory or recurrent malignancies whose growth may be inhibited using the methods of treatment of the present disclosure. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is selected from the group consisting of carcinoma, squamous carcinoma, adenocarcinoma, sarcomata, endometrial cancer, breast cancer, ovarian cancer, cervical cancer, fallopian tube cancer, primary peritoneal cancer, colon cancer, colorectal cancer, squamous cell carcinoma of the anogenital region, melanoma, renal cell carcinoma, lung cancer, non-small cell lung cancer, squamous cell carcinoma of the lung, stomach cancer, bladder cancer, gall bladder cancer, liver cancer, thyroid cancer, laryngeal cancer, salivary gland cancer, esophageal cancer, head and neck cancer, glioblastoma, glioma, squamous cell carcinoma of the head and neck, prostate cancer, pancreatic cancer, mesothelioma, sarcoma, hematological cancer, leukemia, lymphoma, neuroma, and combinations thereof. In some embodiments, a cancer to be treated by the methods of the present disclosure include, for example, carcinoma, squamous carcinoma (for example, cervical canal, eyelid, tunica conjunctiva, vagina, lung, oral cavity, skin, urinary bladder, tongue, larynx, and gullet), and adenocarcinoma (for example, prostate, small intestine, endometrium, cervical canal, large intestine, lung, pancreas, gullet, rectum, uterus, stomach, mammary gland, and ovary). In some embodiments, a cancer to be treated by the methods of the present disclosure further include sarcomata (for example, myogenic sarcoma), leukosis, neuroma, melanoma, and lymphoma. In some embodiments, a cancer to be treated by the methods of the present disclosure is breast cancer. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is triple negative breast cancer (TNBC). In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is ovarian cancer. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is colorectal cancer.

[00373] In some embodiments, a patient or population of patients to be treated with a pharmaceutical composition of the present disclosure have a solid tumor. In some embodiments, a solid tumor is a melanoma, renal cell carcinoma, lung cancer, bladder cancer, breast cancer, cervical cancer, colon cancer, gall bladder cancer, laryngeal cancer, liver cancer, thyroid cancer, stomach cancer, salivary gland cancer, prostate cancer, pancreatic cancer, or Merkel cell carcinoma. In some embodiments, a patient or population of patients to be treated with a pharmaceutical composition of the present disclosure have a hematological cancer. In some embodiments, the patient has a hematological cancer such as Diffuse large B cell lymphoma (“DLBCL”), Hodgkin’s lymphoma (“HL”), Non-Hodgkin’s lymphoma (“NHL”), Follicular lymphoma (“FL”), acute myeloid leukemia (“AML”), or Multiple myeloma (“MM”). In some embodiments, a patient or population of patients to be treated having the cancer selected from the group consisting of ovarian cancer, lung cancer and melanoma.

[00374] Specific examples of cancers that can be prevented and/or treated in accordance with present disclosure include, but are not limited to, the following: renal cancer, kidney cancer, glioblastoma multiforme, metastatic breast cancer; breast carcinoma; breast sarcoma; neurofibroma; neurofibromatosis; pediatric tumors; neuroblastoma; malignant melanoma; carcinomas of the epidermis; leukemias such as but not limited to, acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemias such as myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia leukemias and myelodysplastic syndrome, chronic leukemias such as but not limited to, chronic myelocytic (granulocytic) leukemia, chronic lymphocytic leukemia, hairy cell leukemia; polycythemia vera; lymphomas such as but not limited to Hodgkin’s disease, non-Hodgkin’s disease; multiple myelomas such as but not limited to smoldering multiple myeloma, nonsecretory myeloma, osteosclerotic myeloma, plasma cell leukemia, solitary plasmacytoma and extramedullary plasmacytoma; Waldenstrom’s macroglobulinemia; monoclonal gammopathy of undetermined significance; benign monoclonal gammopathy; heavy chain disease; bone cancer and connective tissue sarcomas such as but not limited to bone sarcoma, myeloma bone disease, multiple myeloma, cholesteatoma-induced bone osteosarcoma, Paget’s disease of bone, osteosarcoma, chondrosarcoma, Ewing’s sarcoma, malignant giant cell tumor, fibrosarcoma of bone, chordoma, periosteal sarcoma, soft-tissue sarcomas, angiosarcoma (hemangiosarcoma), fibrosarcoma, Kaposi’s sarcoma, leiomyosarcoma, liposarcoma, lymphangio sarcoma, neurilemmoma, rhabdomyosarcoma, and synovial sarcoma; brain tumors such as but not limited to, glioma, astrocytoma, brain stem glioma, ependymoma, oligodendroglioma, nonglial tumor, acoustic neurinoma, craniopharyngioma, medulloblastoma, meningioma, pineocytoma, pineoblastoma, and primary brain lymphoma; breast cancer including but not limited to adenocarcinoma, lobular (small cell) carcinoma, intraductal carcinoma, medullary breast cancer, mucinous breast cancer, tubular breast cancer, papillary breast cancer, Paget’s disease (including juvenile Paget’s disease) and inflammatory breast cancer; adrenal cancer such as but not limited to pheochromocytom and adrenocortical carcinoma; thyroid cancer such as but not limited to papillary or follicular thyroid cancer, medullary thyroid cancer and anaplastic thyroid cancer; pancreatic cancer such as but not limited

to, insulinoma, gastrinoma, glucagonoma, vipoma, somatostatin-secreting tumor, and carcinoid or islet cell tumor; pituitary cancers such as but limited to Cushing's disease, prolactin-secreting tumor, acromegaly, and diabetes insipidus; eye cancers such as but not limited to ocular melanoma such as iris melanoma, choroidal melanoma, and ciliary body melanoma, and retinoblastoma; vaginal cancers such as squamous cell carcinoma, adenocarcinoma, and melanoma; vulvar cancer such as squamous cell carcinoma, melanoma, adenocarcinoma, basal cell carcinoma, sarcoma, and Paget's disease; cervical cancers such as but not limited to, squamous cell carcinoma, and adenocarcinoma; uterine cancers such as but not limited to endometrial carcinoma and uterine sarcoma; ovarian cancers such as but not limited to, ovarian epithelial carcinoma, borderline tumor, germ cell tumor, and stromal tumor; cervical carcinoma; esophageal cancers such as but not limited to, squamous cancer, adenocarcinoma, adenoid cystic carcinoma, mucoepidermoid carcinoma, adenosquamous carcinoma, sarcoma, melanoma, plasmacytoma, verrucous carcinoma, and oat cell (small cell) carcinoma; stomach cancers such as but not limited to, adenocarcinoma, fungating (polypoid), ulcerating, superficial spreading, diffusely spreading, malignant lymphoma, liposarcoma, fibrosarcoma, and carcinosarcoma; colon cancers; colorectal cancer, KRAS mutated colorectal cancer; colon carcinoma; rectal cancers; liver cancers such as but not limited to hepatocellular carcinoma and hepatoblastoma, gallbladder cancers such as adenocarcinoma; cholangiocarcinomas such as but not limited to papillary, nodular, and diffuse; lung cancers such as KRAS-mutated non-small cell lung cancer, non-small cell lung cancer, squamous cell carcinoma (epidermoid carcinoma), adenocarcinoma, large-cell carcinoma and small-cell lung cancer; lung carcinoma; testicular cancers such as but not limited to germinal tumor, seminoma, anaplastic, classic (typical), spermatocytic, nonseminoma, embryonal carcinoma, teratoma carcinoma, choriocarcinoma (yolk-sac tumor), prostate cancers such as but not limited to, androgen-independent prostate cancer, androgen-dependent prostate cancer, adenocarcinoma, leiomyosarcoma, and rhabdomyosarcoma; penile cancers; oral cancers such as but not limited to squamous cell carcinoma; basal cancers; salivary gland cancers such as but not limited to adenocarcinoma, mucoepidermoid carcinoma, and adenoidcystic carcinoma; pharynx cancers such as but not limited to squamous cell cancer, and verrucous; skin cancers such as but not limited to, basal cell carcinoma, squamous cell carcinoma and melanoma, superficial spreading melanoma, nodular melanoma, lentigo malignant melanoma, acral lentiginous melanoma; kidney cancers such as but not limited to renal cell cancer, adenocarcinoma, hypernephroma, fibrosarcoma, transitional cell cancer (renal pelvis and/or uterus); renal carcinoma; Wilms' tumor; bladder cancers such as but not limited to transitional cell carcinoma, squamous cell cancer, adenocarcinoma, carcinosarcoma. In addition, cancers include myxosarcoma, osteogenic sarcoma, endotheliosarcoma, lymphangioendotheliosarcoma, mesothelioma, synovioma, hemangioblastoma, epithelial carcinoma, cystadenocarcinoma, bronchogenic carcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma and papillary adenocarcinomas.

[00375] Cancers include, but are not limited to, B cell cancer, *e.g.*, multiple myeloma, Waldenstrom's macroglobulinemia, the heavy chain diseases, such as, for example, alpha chain disease, gamma chain disease, and mu chain disease, benign monoclonal gammopathy, and immunocytic amyloidosis, melanomas, breast

cancer, lung cancer, bronchus cancer, colorectal cancer, prostate cancer (*e.g.*, metastatic, hormone refractory prostate cancer), pancreatic cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or central nervous system cancer, peripheral nervous system cancer, esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer of the oral cavity or pharynx, liver cancer, kidney cancer, testicular cancer, biliary tract cancer, small bowel or appendix cancer, salivary gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma, chondrosarcoma, cancer of hematological tissues, and the like. Other non-limiting examples of types of cancers applicable to the methods encompassed by the present disclosure include human sarcomas and carcinomas, *e.g.*, fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, colorectal cancer, pancreatic cancer, breast cancer, ovarian cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, liver cancer, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, cervical cancer, bone cancer, brain tumor, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, retinoblastoma; leukemias, *e.g.*, acute lymphocytic leukemia and acute myelocytic leukemia (myeloblastic, promyelocytic, myelomonocytic, monocytic and erythroleukemia); chronic leukemia (chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia); and polycythemia vera, lymphoma (Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, and heavy chain disease. In some embodiments, the cancer whose phenotype is determined by the method of the present disclosure is an epithelial cancer such as, but not limited to, bladder cancer, breast cancer, cervical cancer, colon cancer, gynecologic cancers, renal cancer, laryngeal cancer, lung cancer, oral cancer, head and neck cancer, ovarian cancer, pancreatic cancer, prostate cancer, or skin cancer. In other embodiments, the cancer is breast cancer, prostate cancer, lung cancer, or colon cancer. In still other embodiments, the epithelial cancer is non-small-cell lung cancer, nonpapillary renal cell carcinoma, cervical carcinoma, ovarian carcinoma (*e.g.*, serous ovarian carcinoma), or breast carcinoma. The epithelial cancers may be characterized in various other ways including, but not limited to, serous, endometrioid, mucinous, clear cell, brenner, or undifferentiated. In some embodiments, the present disclosure is used in the treatment, diagnosis, and/or prognosis of lymphoma or its subtypes, including, but not limited to, mantle cell lymphoma. Lymphoproliferative disorders are also considered to be proliferative diseases.

[00376] In some embodiments, the subject has a breast cancer that is resistant to anti-estrogen therapy, is an MSI breast cancer, is a metastatic breast cancer, is a Her2 negative breast cancer, is a Her2 positive breast cancer, is an ER negative breast cancer, is an ER positive breast cancer or any combination thereof.

[00377] In some embodiments, the breast cancer expresses an estrogen receptor with a mutation.

[00378] In some embodiments, the cancer is recurrent or metastatic breast cancer. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is triple negative breast cancer (TNBC).

[00379] The pharmaceutical compositions provided herein may be used alone or in combination with conventional therapeutic regimens such as surgery, irradiation, chemotherapy and/or bone marrow transplantation (autologous, syngeneic, allogeneic or unrelated).

[00380] In some embodiments, at least one or more chemotherapeutic agents may be administered in addition to the pharmaceutical composition comprising an immunogenic therapy. In some embodiments, the one or more chemotherapeutic agents may belong to different classes of chemotherapeutic agents.

[00381] In practicing the methods of treatment or use provided herein, therapeutically-effective amounts of the pharmaceutical compositions can be administered to a subject having a disease or condition. A therapeutically-effective amount can vary widely depending on the severity of the disease, the age and relative health of the subject, the potency of the compounds used, and other factors.

[00382] Subjects can be, for example, mammal, humans, pregnant women, elderly adults, adults, adolescents, pre-adolescents, children, toddlers, infants, newborn, or neonates. A subject can be a patient. In some cases, a subject can be a human. In some cases, a subject can be a child (i.e. a young human being below the age of puberty). In some cases, a subject can be an infant. In some cases, the subject can be a formula-fed infant. In some cases, a subject can be an individual enrolled in a clinical study. In some cases, a subject can be a laboratory animal, for example, a mammal, or a rodent. In some cases, the subject can be a mouse. In some cases, the subject can be an obese or overweight subject.

[00383] In some embodiments, the subject has previously been treated with one or more different cancer treatment modalities. In some embodiments, the subject has previously been treated with one or more of radiotherapy, chemotherapy, or immunotherapy. In some embodiments, the subject has been treated with one, two, three, four, or five lines of prior therapy. In some embodiments, the prior therapy is a cytotoxic therapy.

[00384] In some embodiments, the disease or condition that can be treated with the methods disclosed herein is abnormal growth of cells. In some embodiments, the disease or condition that can be treated with the methods disclosed herein is cancer. In some embodiments, the cancer is a malignant cancer. In some embodiments, the cancer is a benign cancer. In some embodiments, the cancer is an invasive cancer. In some embodiments, the cancer is a solid tumor. In some embodiments, the cancer is a liquid cancer.

[00385] The methods of the disclosure can be used to treat any type of cancer known in the art. Non-limiting examples of cancers to be treated by the methods of the present disclosure include melanoma (e.g., metastatic malignant melanoma), renal cancer (e.g., clear cell carcinoma), prostate cancer (e.g., hormone refractory prostate adenocarcinoma), pancreatic adenocarcinoma, breast cancer, colon cancer, lung cancer (e.g., non-small cell lung cancer), esophageal cancer, squamous cell carcinoma of the head and neck, liver cancer, ovarian cancer, cervical cancer, thyroid cancer, glioblastoma, glioma, leukemia, lymphoma, and other neoplastic malignancies.

[00386] Additionally, the disease or condition provided herein includes refractory or recurrent malignancies whose growth may be inhibited using the methods of treatment of the present disclosure. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is selected from the group consisting of carcinoma, squamous carcinoma, adenocarcinoma, sarcomata, endometrial cancer, breast cancer, ovarian cancer, cervical cancer, fallopian tube cancer, primary peritoneal cancer, colon cancer, colorectal cancer, squamous cell carcinoma of the anogenital region, melanoma, renal cell carcinoma, lung cancer, non-small cell lung cancer, squamous cell carcinoma of the lung, stomach cancer, bladder cancer, gall bladder cancer, liver cancer, thyroid cancer, laryngeal cancer, salivary gland cancer, esophageal cancer, head and neck cancer, glioblastoma, glioma, squamous cell carcinoma of the head and neck, prostate cancer, pancreatic cancer, mesothelioma, sarcoma, hematological cancer, leukemia, lymphoma, neuroma, and combinations thereof. In some embodiments, a cancer to be treated by the methods of the present disclosure include, for example, carcinoma, squamous carcinoma (for example, cervical canal, eyelid, tunica conjunctiva, vagina, lung, oral cavity, skin, urinary bladder, tongue, larynx, and gullet), and adenocarcinoma (for example, prostate, small intestine, endometrium, cervical canal, large intestine, lung, pancreas, gullet, rectum, uterus, stomach, mammary gland, and ovary). In some embodiments, a cancer to be treated by the methods of the present disclosure further include sarcomata (for example, myogenic sarcoma), leukosis, neuroma, melanoma, and lymphoma. In some embodiments, a cancer to be treated by the methods of the present disclosure is breast cancer. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is triple negative breast cancer (TNBC). In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is ovarian cancer. In some embodiments, a cancer to be treated by the methods of treatment of the present disclosure is colorectal cancer.

[00387] In some embodiments, a patient or population of patients to be treated with a pharmaceutical composition of the present disclosure have a solid tumor. In some embodiments, a solid tumor is a melanoma, renal cell carcinoma, lung cancer, bladder cancer, breast cancer, cervical cancer, colon cancer, gall bladder cancer, laryngeal cancer, liver cancer, thyroid cancer, stomach cancer, salivary gland cancer, prostate cancer, pancreatic cancer, or Merkel cell carcinoma. In some embodiments, a patient or population of patients to be treated with a pharmaceutical composition of the present disclosure have a hematological cancer. In some embodiments, the patient has a hematological cancer such as Diffuse large B cell lymphoma (“DLBCL”), Hodgkin’s lymphoma (“HL”), Non-Hodgkin’s lymphoma (“NHL”), Follicular lymphoma (“FL”), acute myeloid leukemia (“AML”), or Multiple myeloma (“MM”). In some embodiments, a patient or population of patients to be treated having the cancer selected from the group consisting of ovarian cancer, lung cancer and melanoma.

[00388] Specific examples of cancers that can be prevented and/or treated in accordance with present disclosure include, but are not limited to, the following: renal cancer, kidney cancer, glioblastoma multiforme, metastatic breast cancer; breast carcinoma; breast sarcoma; neurofibroma; neurofibromatosis; pediatric tumors; neuroblastoma; malignant melanoma; carcinomas of the epidermis; leukemias such as but not limited to, acute

leukemia, acute lymphocytic leukemia, acute myelocytic leukemias such as myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia leukemias and myelodysplastic syndrome, chronic leukemias such as but not limited to, chronic myelocytic (granulocytic) leukemia, chronic lymphocytic leukemia, hairy cell leukemia; polycythemia vera; lymphomas such as but not limited to Hodgkin's disease, non-Hodgkin's disease; multiple myelomas such as but not limited to smoldering multiple myeloma, nonsecretory myeloma, osteosclerotic myeloma, plasma cell leukemia, solitary plasmacytoma and extramedullary plasmacytoma; Waldenstrom's macroglobulinemia; monoclonal gammopathy of undetermined significance; benign monoclonal gammopathy; heavy chain disease; bone cancer and connective tissue sarcomas such as but not limited to bone sarcoma, myeloma bone disease, multiple myeloma, cholesteatoma-induced bone osteosarcoma, Paget's disease of bone, osteosarcoma, chondrosarcoma, Ewing's sarcoma, malignant giant cell tumor, fibrosarcoma of bone, chordoma, periosteal sarcoma, soft-tissue sarcomas, angiosarcoma (hemangiosarcoma), fibrosarcoma, Kaposi's sarcoma, leiomyosarcoma, liposarcoma, lymphangio sarcoma, neurilemmoma, rhabdomyosarcoma, and synovial sarcoma; brain tumors such as but not limited to, glioma, astrocytoma, brain stem glioma, ependymoma, oligodendroglioma, nonglial tumor, acoustic neurinoma, craniopharyngioma, medulloblastoma, meningioma, pineocytoma, pineoblastoma, and primary brain lymphoma; breast cancer including but not limited to adenocarcinoma, lobular (small cell) carcinoma, intraductal carcinoma, medullary breast cancer, mucinous breast cancer, tubular breast cancer, papillary breast cancer, Paget's disease (including juvenile Paget's disease) and inflammatory breast cancer; adrenal cancer such as but not limited to pheochromocytom and adrenocortical carcinoma; thyroid cancer such as but not limited to papillary or follicular thyroid cancer, medullary thyroid cancer and anaplastic thyroid cancer; pancreatic cancer such as but not limited to, insulinoma, gastrinoma, glucagonoma, vipoma, somatostatin-secreting tumor, and carcinoid or islet cell tumor; pituitary cancers such as but limited to Cushing's disease, prolactin-secreting tumor, acromegaly, and diabetes insipidus; eye cancers such as but not limited to ocular melanoma such as iris melanoma, choroidal melanoma, and ciliary body melanoma, and retinoblastoma; vaginal cancers such as squamous cell carcinoma, adenocarcinoma, and melanoma; vulvar cancer such as squamous cell carcinoma, melanoma, adenocarcinoma, basal cell carcinoma, sarcoma, and Paget's disease; cervical cancers such as but not limited to, squamous cell carcinoma, and adenocarcinoma; uterine cancers such as but not limited to endometrial carcinoma and uterine sarcoma; ovarian cancers such as but not limited to, ovarian epithelial carcinoma, borderline tumor, germ cell tumor, and stromal tumor; cervical carcinoma; esophageal cancers such as but not limited to, squamous cancer, adenocarcinoma, adenoid cystic carcinoma, mucoepidermoid carcinoma, adenosquamous carcinoma, sarcoma, melanoma, plasmacytoma, verrucous carcinoma, and oat cell (small cell) carcinoma; stomach cancers such as but not limited to, adenocarcinoma, fungating (polypoid), ulcerating, superficial spreading, diffusely spreading, malignant lymphoma, liposarcoma, fibrosarcoma, and carcinosarcoma; colon cancers; colorectal cancer, RAS mutated colorectal cancer; colon carcinoma; rectal cancers; liver cancers such as but not limited to hepatocellular carcinoma and hepatoblastoma, gallbladder cancers such as adenocarcinoma; cholangiocarcinomas such as but not limited to pappillary, nodular, and diffuse; lung cancers such as RAS-

mutated non-small cell lung cancer, non-small cell lung cancer, squamous cell carcinoma (epidermoid carcinoma), adenocarcinoma, large-cell carcinoma and small-cell lung cancer; lung carcinoma; testicular cancers such as but not limited to germinal tumor, seminoma, anaplastic, classic (typical), spermatocytic, nonseminoma, embryonal carcinoma, teratoma carcinoma, choriocarcinoma (yolk-sac tumor), prostate cancers such as but not limited to, androgen-independent prostate cancer, androgen-dependent prostate cancer, adenocarcinoma, leiomyosarcoma, and rhabdomyosarcoma; penal cancers; oral cancers such as but not limited to squamous cell carcinoma; basal cancers; salivary gland cancers such as but not limited to adenocarcinoma, mucoepidermoid carcinoma, and adenoidcystic carcinoma; pharynx cancers such as but not limited to squamous cell cancer, and verrucous; skin cancers such as but not limited to, basal cell carcinoma, squamous cell carcinoma and melanoma, superficial spreading melanoma, nodular melanoma, lentigo malignant melanoma, acral lentiginous melanoma; kidney cancers such as but not limited to renal cell cancer, adenocarcinoma, hypernephroma, fibrosarcoma, transitional cell cancer (renal pelvis and/or uterine); renal carcinoma; Wilms' tumor; bladder cancers such as but not limited to transitional cell carcinoma, squamous cell cancer, adenocarcinoma, carcinosarcoma. In addition, cancers include myxosarcoma, osteogenic sarcoma, endotheliosarcoma, lymphangioendotheliosarcoma, mesothelioma, synovioma, hemangioblastoma, epithelial carcinoma, cystadenocarcinoma, bronchogenic carcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma and papillary adenocarcinomas.

[00389] In some embodiments, a subject with a mutation in a RAS gene is treated for cancer by administering a pharmaceutical composition comprising a TCR that recognizes a RAS mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, the pharmaceutical composition comprises a nucleic acid sequence encoding the TCR. In some embodiments, the nucleic acid is a DNA or an RNA. In some embodiments, the nucleic acid is a messenger RNA encoding the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, the pharmaceutical composition comprises a vector that comprises a nucleic acid sequence encoding the TCR and is capable of driving the expression of the TCR, wherein the TCR recognizes a RAS mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, and wherein the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, the pharmaceutical composition comprises a cell that comprises a nucleic acid sequence encoding the TCR that recognizes a RAS mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, the subject having a cancer is administered a pharmaceutical composition comprising a TCR that recognizes a RAS mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein, wherein the cancer is selected from adenocarcinoma of the biliary tract, transitional

cell carcinoma of the bladder, breast carcinoma, cervical adenocarcinoma, colon adenocarcinoma, colon adenoma, neuroblastoma (autonomic ganglia), acute myeloid leukemia, chronic myeloid leukemia, chronic myelomonocytic leukemia, juvenile myelomonocytic leukemia, acute lymphoblastic leukemia, Burkitt's lymphoma, Hodgkin's lymphoma, plasma cell myeloma, hepatocellular carcinoma, large cell carcinoma, non-small cell carcinoma, ductal carcinoma, endocrine tumor, prostate adenocarcinoma, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, angiosarcoma, leiomyosarcoma, liposarcoma, rhabdomyosarcoma, myxoma, malignant fibrous histiocytoma, pleomorphic sarcoma, germinoma, seminoma, anaplastic carcinoma, follicular carcinoma, papillary carcinoma and Hurthle cell carcinoma.

[00390] In some embodiments, a subject with a mutation in a GATA3 gene is treated for cancer by administering a pharmaceutical composition comprising a TCR that recognizes a GATA3 mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, the subject with a mutation in a GATA3 gene is treated for breast cancer.

[00391] In some embodiments, a subject with a mutation in EGFR gene is treated for cancer by administering a pharmaceutical composition comprising a TCR that recognizes a EGFR mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein. In some embodiments, a subject with a mutation in TMPRSS2:ERG gene is treated for cancer by administering a pharmaceutical composition comprising a TCR that recognizes a TMPRSS2:ERG mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein.

[00392] In some embodiments, a subject with a mutation in BTK gene is treated for cancer by administering a pharmaceutical composition comprising a TCR that recognizes a BTK mutant epitope in complex with an MHC protein encoded by the HLA allele of the subject, the TCR having a TCR alpha chain variable region and a TCR beta chain variable region having an amino acid sequence disclosed herein.

[00393] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

EXAMPLES

Example 1: Workflow for antigen-specific T cell identification and validation

[00394] In this example, an exemplary workflow to generate and use antigen peptide specific TCRs is described. **FIG. 1** demonstrates a graphical representation of the workflow. **FIG. 2** details an exemplary timeline for the workflow process, starting with obtaining and culturing PBMCs from a subject, the PBMCs are then stabilized in overnight culture, and incubated in the presence of peptides and cytokines; the monocyte- and DC-derived antigen presenting cells (APCs) help induce T cells in response to the peptide antigens presented by the APCs; between 10 days to 2 weeks, antigen specific T cells expand and are sorted for antigen specificity and activation (for example, CD8⁺ marker expression indicating generation of cytotoxic T lymphocytes). The activated antigen responsive T cells contain antigen specific TCRs.

[00395] Briefly, Mutated peptides containing mutant target epitopes (e.g., mutant TMPRSS2:ERG, RAS, BTK and GATA3 peptides) were synthesized using a peptide synthesizer. The synthesized peptides were used to load APCs to stimulate T cells from a sample of healthy donor peripheral blood mononuclear cells (PBMCs). PBMCs from patients harboring neoantigens of interest can also be used to obtain neoantigen-specific T cells. After incubation with the peptide loaded APCs, T cell populations were analyzed by flow cytometry. Antigen-specific T cells were isolated using flow cytometry (**FIGs. 1, 2, 4A, 5, 6, 8F, 8G, 9, 10A, 10B, 11, 13, 15, 16A and 16B**). Single cell TCR sequencing was performed for the isolated antigen-specific T cells using 10x Genomics Single Cell V(D)J system to profile the sequences of isolated antigen-specific TCRs. Sequencing reads were analyzed using the Cell RangerTM analysis pipeline, and candidate sequences of TCRs were selected for further analysis and functional assays (**FIGs. 1, 6A, 10A, 10B, 11, 13, 15 and 16A and 16B**).

[00396] For analysis of TCR functionality, vectors or mRNA encoding TMPRSS2:ERG, RAS, BTK or GATA3 peptides containing target mutant epitopes were transduced into HEK293T or A375 cells to produce antigen expressing cell lines. Jurkat cells, TCR β deficient Jurkat cells or PBMCs from healthy donors were transduced with nucleic acids (**FIG. 3A**) encoding candidate TCRs in a lentiviral vector. An exemplary vector is shown in **FIG. 3B**. **FIGs. 4B, 6A and 6B, 10C-10F, 11 and 13** show functional assays for TCR-expressing vector transduced cells. TMPRSS2:ERG, RAS, BTK and GATA3 antigen expressing cell lines were cocultured with TCR transduced Jurkat cells, TCR β deficient Jurkat cells or PBMCs from healthy donors for antigen recognition assays to analyze the functionality of candidate TCRs (**FIGs. 7A-7B, 8A-8E, 10A-10F, 12B and 14**).

Example 2: Obtaining antigen specific T cells

[00397] In vitro T cell inductions were used to expand antigen specific T cells. The healthy human donor PBMCs were seeded in each well of 24 well plate in AIM V media (Invitrogen). Mutant peptides (TMPRSS2:ERG, RAS, BTK or GATA3), TNF- α , IL-1 β , PGE1, and IL-7 were added into wells after 24 hours incubation. The culture media was exchanged every 2 days with fresh media. The antigen specific T cells were evaluated and isolated at day 10 to 20 (**FIG. 2**).

Example 3: HLA-multimer staining and sorting

[00398] Neoantigen specific T cells were detected by combining HLA-multimer staining with 2 different fluorochrome conjugated recombinant HLA (HLA-A02.01, HLA-A03.01, or HLA-A11.01) multimer with

neoantigen peptides. Anti-CD8, anti-CD4, anti-CD19, anti-CD16, anti-CD14, anti-CD56 and antibodies and Live/Dead IR dye (Invitrogen) were used for cell surface staining. CD8⁺ T cells were identified as CD8⁺CD4⁻CD19⁻CD16⁻CD14⁻CD56⁻IR⁻ (FIGs. 1, 2, 4A, 5, 6A, 8F, 8G, 9, 10A, 10B, 11, 13, 15, 16A and 16B). For sorting, up to 5×10⁶ cells were incubated with 1-20 µg multimer in 100 µL PBS + 0.5% human serum. Antibodies and Live/Dead IR dye were used to stain the cells for an additional 30 min. After staining, cells were washed twice and diluted in PBS + 0.5% human serum. Live/Dead IR dye-negative cells were gated and CD8⁺/multimer⁺ T cells were sorted on a FACS Aria cell sorter (BD Biosciences).

Example 4: Deep sequencing of antigen-specific TCRs

[00399] Antigen-specific T cells were sorted into a mixture of PBS and 2% FBS (Hyclone Defined), and 10x Genomics V(D)J kit was used to genetically barcode the RNAs from single T cells. RNA libraries were prepared according to the manufacturer's protocols. The resulting libraries were sequenced using ILLUMINA's MiSeq platform. 10x Genomics analysis software was then used to analyze the sequencing data to obtain paired TCR alpha and beta sequences. Dominant clones were identified based on the frequency of cells with a common TCR alpha and/or TCR beta (FIGs. 1, 6, 8F, 8G, 10A, 10B, 11, 13, 15 and 16A).

Example 5: Antigen-specific TCR gene synthesis and cloning

[00400] FIG. 3A represents a graphical diagram of an exemplary vector design, incorporating a TCR alpha chain and a TCR beta chain construct; wherein the TCR alpha- and beta- chain constructs comprise nucleic acid sequences encoding a variable (V), a diversity ((D), only in beta chain construct) a joining (J) and a constant (C) region for each of a TCR alpha (α) chain and a TCR beta (β) chain as shown in the diagram, in a vector with an upstream regulatory element comprising elements necessary for expression of the incorporated nucleic acid sequence, including, for example, a promoter (example EF1a region as shown in the diagram), further incorporating F2A and P2A proteolytic cleavage sites and a sequence encoding for Puromycin resistance (Puro) for Puromycin mediated selection. The lentiviral vectors were constructed from pCDH-EF1-T2A-Puro (SBI system bioscience). Antigen-specific TCR lentiviral vectors were generated by inserting a TCR beta variable region, followed by a TCR beta mouse constant region, furin cleavage site, SGSG linker, F2A site, a TCR alpha variable region, a TCR alpha constant region, a T2A site, and a puromycin resistance gene (FIGs. 3A and 3B).

Example 6: Transfection and transduction

[00401] Lentivirus encoding antigen-specific TCRs was prepared by transient transfection of 293T cells. The cells were seeded on a 10 cm plate at 7×10⁶ cells 16 hours before transfection with 7 µg of lentiviral vector, 7 µg of packaging plasmid mix (pPAX and pMD2.G), 28 µL of Eugene (Promega) and 1 mL of Opti-MEM (Gibco). The culture media was replaced a day after transfection. 72 hours after transfection, the supernatant was harvested concentrated 10-fold.

[00402] Jurkat cells or PBMCs were transduced with concentrated lentivirus encoding TCR sequences. Jurkat cells were washed and resuspended in RPMI-1640 containing polybrene and 10% FBS. 5×10⁵ CD8-Jurkat cells in 100 µL of media were plated per well in 96-well plate and 25 µL of concentrated lentivirus was added. The cells were centrifuged at 2400 rotation per minute (rpm) for 1 hour and incubated in a CO₂ incubator. The cells

were transduced again with fresh media with polybrene and FBS and 25 μ L of concentrated lentivirus. The media was replaced with RPMI-1640 containing 10% FBS and Pen/Strep 24 hours after the second transduction. Puromycin treatment (1 μ g/ml) started at day 4 after transduction.

Example 7: TCR transduced Jurkat binding to HLA-peptide

[00403] To evaluate TCR transduction, transduced Jurkat cells were stained with fluorochrome conjugated multimer (HLA-neoantigen), anti-CD8 antibody, anti-mTCR constant region antibody, and Live/Dead IR dye. mTCR and multimer positive cells were measured by flow cytometry (FIGs. 4B, 6A, 6B, 10A-10F, 11 and 13).

Example 8: Peptide loading of target cells

[00404] For exogenous peptide pulsing, 1×10^6 T2, 293T or A375 cells were incubated at 37 °C and 5% CO₂ for 2 h with 10 pg/mL human β_2 -microglobulin (Calbiochem) and titrating amounts, ranging from 1×10^{-5} M to 1×10^{-12} M of the RAS or GATA3 peptides, T2 cells pulsed with 10^{-5} M influenza peptide GIL (influenza matrix protein₅₈₋₆₆ GILGFVTL, Metabion) served as negative control. After washing, peptide-loaded T2 cells were used in IL-2 release assays (FIGs. 6B, 7, 8, 12E and 14).

Example 9: Neoantigen expressing target cells

[00405] For endogenous antigen expressing target cells, 1×10^6 HEK293 or A375 cells were transduced with lentivirus vectors encoding TMPRSS2::ERG, BTK, GATA3 or KRAS mutated peptides. The transduced target cells were selected by puromycin (1 μ g/ml) in culture media (DMEM with 10% FBS).

Example 10: IL-2 Release Assay

[00406] For investigation of specificity, T cell clones (2.5×10^5 cells in 50 μ L) can be incubated with HEK293T, HLA-A03.01 transduced A375 or HLA-A11.01 transduced A375 cell lines (5×10^4 cells in 50 μ L) and TMPRSS2::ERG, BTK, GATA3 or KRAS mutated peptide neoantigens. The following figures demonstrate IL2 release assay results in case of the respective TCRs as depicted within the figures: FIGs. 6B, 7A, 7B, 8E, 10C, 12A, 12B and 14). Culture supernatants were harvested after 24 h co-culture and assessed IL-2 concentration by a standard MSD using V-PLEX Human IL-2 assays (Meso Scale Discovery).

Example 11: IFN- γ Release Assay

[00407] For investigation of specificity, T cell clones (2×10^3 cells in 100 μ L) were incubated with cell lines expressing TMPRSS2::ERG, BTK, GATA3 or KRAS mutated peptide neoantigens. Culture supernatants were harvested after 24 h co-culture and assessed by a standard ELISA using the OptEIA™ Human IFN- γ Set (BD Biosciences Pharmingen).

Example 12: Cytotoxicity Assay

[00408] Cytotoxic activity of T cell clones can be analyzed in a standard 4 h ⁵¹chromium release assay. Briefly, 1×10^6 target cells can be labeled with 100 μ Ci Na₂ ⁵¹CrO₄ (ICN Biochemicals) for 1-1.5 h. ⁵¹Cr-labeled target cells can be cultured with T cells in RPMI 1640 with 12% FCS. For determination of functional avidity 1×10^4 T cells can be added to 1×10^3 peptide-pulsed T2 cells loaded with titrated amounts of TMPRSS2::ERG, BTK, GATA3 or KRAS mutated peptide neoantigens, giving a constant E:T of 10:1.

[00409] After 4 h co-culture at 37° C, 50 μ L of supernatant can be collected and radioactivity can be measured in a gamma counter. The percentage of specific lysis can be calculated as: $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. Spontaneous release can be assessed by incubating target cells in the absence of effector cells. For the calculation of percent relative lysis, the maximum percent specific lysis can be set to the reference value of 100% and corresponding values can be calculated corresponding to this reference. To determine half-maximum lysis, percent relative lysis can be plotted against peptide concentration. The peptide concentration at which the curve crossed 50% relative lysis can be taken as the value of half-maximum lysis.

Example 13: Cell Killing Assay

[00410] A RAS-neoantigen specific recombinant TCR was transduced into PBMCs and their ability to kill a cancer cell line was analyzed (FIGs. 8A, 8B). The recombinant TCR expressing cells killed showed more than a 30% higher killing of cancer cell lines compared to control. A modified recombinant TCR (rTCR) with mouse constant regions was expressed from a SFFV promoter and a 30% neoantigen specific TCR transduction yield in PBMCs from a healthy donor was achieved. The SW620 cell line was used as target cell which naturally expresses the KRAS G12V mutation. HLA-A11:01 was introduced into the SW620 cell line by lentiviral transductions. The rTCR transduced PBMCs were co-cultured with two different SW620 cell lines with or without expression of HLA-A11:01 for 6 hours. Supernatant and cells were then harvested to analyze cytokine secretion and apoptosis.

[00411] After 6 hour co-culture, significantly higher levels of IFN γ , IL-2, and TNF α were detected for the groups of HLA-A11:01 transduced SW620 cell line (Ras^{mut} cell line + HLA-A11:01) compared to non-transduced SW620 (Ras^{mut} cell line). This shows that the rTCR PBMC can specifically recognize a RAS peptide containing a G12V mutation on HLA-A11:01 of a cell line close to real tumor model. Also, a significantly higher percent of Caspase-3 (apoptosis marker) positive cells was observed in HLA-A11:01 transduced SW620 cell lines compared to control. Thus, the rTCR transduced PBMCs can not only secrete cytokine (IFN γ , IL-2, and TNF α) but also functionally kill target cells specifically.

[00412] In some examples, cytotoxicity activity is assessed by co-culturing T cells expressing a TCR specific to a mutant RAS peptide on a specific HLA, with mutant RAS peptide-transduced target cancer cells expressing the corresponding HLA, and by determining the relative growth of the target cells, along with measuring the apoptotic marker Annexin V in the target cancer cells specifically (FIGs. 8C, 8D, 10D, 10E). Target cancer cells are engineered to express the mutant peptide along with the proper MHC-I allele. Mock-transduced target cells (i.e. not expressing the mutant peptide) are used as a negative control. The cells are also transduced to stably express GFP allowing the tracking of target cell growth. PBMCs from healthy donors, used as effector cells, are transduced to express a TCR specific to a mutant RAS peptide. Mock-transduced cells are used as a negative control. The target cells are cocultured with different amount of effector cells for 72h in media containing Annexin V-detection reagent. The GFP signal and Annexin-V signal are measured over time with an IncuCyte S3 apparatus. Annexin V signal originating from effector cells is filtered out by size exclusion.

Target cell growth and death is expressed as GFP and Annexin-V area (mm²) over time, respectively. FIG. 8C demonstrate high degree of inverse correlation of the TCR levels as determined by the TCR/CD8⁺ target ratio with the growth of the target cells (upper panel). Similarly, higher TCR levels correlated with higher Annexin V positive target cells, indicating higher number of apoptotic target cells. This indicates high degree of specificity and efficiency in target cell destruction with RAS TCR4.

[00413] In some examples, cytotoxic activity is assessed before TCR cloning. T cells induced against a mutant RAS peptide on a specific HLA are co-cultured with mutant target cancer cells expressing the corresponding HLA loaded with a range of concentrations of the RAS mutant peptides (FIGs. 8F, 8G). The relative growth and the apoptotic marker Annexin V in the target cancer cells specifically are both measured. The target cells are also transduced to stably express GFP allowing the tracking of target cell growth. The GFP signal and Annexin-V signal are measured over time with an IncuCyte S3 apparatus. Annexin V signal originating from effector cells is filtered out by size exclusion. Target cell growth and death is expressed as GFP and Annexin-V area (mm²) over time, respectively. For T cells demonstrating cytotoxicity at low peptide concentrations compared to no peptide and/or wild-type peptide, TCR sequencing can be performed as above. Regarding the data shown in experiments shown in FIG. 8F and 8G, (figures on the upper right corner), the cytotoxicity of the T cells showed good dose responsiveness to the peptides as indicated by lower GFP-expressing cells with the higher dose of peptides over the indicated time. The inverse correlation depicts that with higher amounts of peptides for stimulating the TCR on the T cells, higher suppression of target cell growth was observed, as demonstrated by lower GFP-positive cells. This demonstrates that the T cells exhibit high TCR specificity and effectivity in limiting target cell progression.

Example 14: Summary of recombinant TCRs developed

[00414] This example provides the details of the TCRs developed. Table 1 provides a synopsis of the TCRs described herein and Table 2 provides the specific amino acid and coding sequences.

Table 1.

TCR name	Gene	Mutation	Allele	TCRbeta CDR3	TCR binding to peptide-MHC	Method of determining TCR binding to peptide-MHC	
						Multimer Hit	IL-2 by Jurkat and/or PBMC
RAS TCR-1	KRAS	G12V, G12D, G12C	A02:01	SARDRGLVSLPSVEAFF	-	-	-
RAS TCR-2	KRAS	G12V, G12D, G12C	A02:01	ASYLSGSIYNEQFF	-	-	-
RAS TCR-3	KRAS	G12V	A11:01	ASSYSTERGTIY	Yes	Yes	Yes
RAS TCR-4	KRAS	G12V	A11:01	ASSLADIYEQY	Yes	Yes	Yes
RAS TCR-5	KRAS	G12V	A03:01	CASSARNDEAFF	Yes	Yes	Yes
RAS TCR-6	KRAS	G12V	A03:01	CASSLGDSQYF	Yes	Yes	IL-2 by Jurkat

RAS TCR-7	KRAS	G12C	A03:01	CASSQRSNTGELFF	Yes	Yes	Yes
RAS TCR-8	KRAS	G12V	A11:01	CASGGRDSTDTQYF	Yes	Yes	IL-2 by Jurkat
RAS TCR-10	KRAS	G12C	A11:01	ASSTSFWEVNTEAF	Yes	-	IL-2 by Jurkat
RAS TCR-11	KRAS	G12C	A11:01	ASSKRGWPYEQY	Yes	-	IL-2 by Jurkat
RAS TCR-12	KRAS	G12C	A11:01	ASSLADIYEQY	-	-	-
RAS TCR-13	KRAS	G12D	A03:01	ASSSTDRIEAF	-	-	-
RAS TCR-14	KRAS	G12D	A03:01	ASTTFKTGRAIEKLF	-	-	-
RAS TCR-15	KRAS	G12D	A03:01	ASSSRGHSNGTEAF	-	-	-
RAS TCR-16	KRAS	G12D	A03:01	ASSSRGHSNGTEAF	-	-	-
RAS TCR-17	KRAS	G12D	A03:01	ATYKVGDEQF	-	-	-
RAS TCR-18	KRAS	G12D	A11:01	ASSDWLAGAKDEQY	-	-	-
RAS TCR-19	KRAS	G12V	A03:01	ASSLVASNEQF	-	-	-
RAS TCR-20	KRAS	G12V	A11:01	ASSLGLLLYNEQF	Yes	-	IL-2 by Jurkat
RAS TCR-21	KRAS	G12V	A11:01	ASSLGDSYEQYF	-	-	-
RAS TCR-26	KRAS	G12V	A11:01	ASSEWGSGTELF	-	-	-
RAS-TCR-27	KRAS	G12V	A11:01	ASSEWGSGTELF	-	-	-
RAS-TCR-28	KRAS	G12V	A11:01	ASSEYTMGTQY	-	-	-
GATA3 TCR-1	GATA3	neoORF (CSNH)	A02:01	ASSLDFVLAGSYSYNEQF	Yes	Yes	IL-2 by Jurkat
GATA3 TCR-2	GATA3	neoORF (CSNH)	B07:02	ASSQSGQGPYEQY	-	-	-
GATA3 TCR-3	GATA3	neoORF (CSNH)	B08:01	ASSRTAMNTEAF	Yes	-	IL-2 by Jurkat
TMPRSS2::ERG TCR-1	TMPRSS2::ERG	Fusion	A02:01	ASSQADSPLH	Yes	Yes	IL-2 by Jurkat and PBMC
BTK TCR-1	BTK	C481S	A02:01	ASSFGPDEKLFF	Yes	Yes	IL-2 by Jurkat
BTK TCR-2	BTK	C481S	A02:01	ASSPGANEKLF	Yes	Yes	IL-2 by Jurkat
EGFR TCR-1	EGFR	T790M	A02:01	ASGGGLGLFETQY	-	-	-
EGFR TCR-2	EGFR	T790M	A02:01	SARRREGEIEQY	-	-	-
EGFR TCR-3	EGFR	T790M	A02:01	ASSLAYLTGRVEAF	-	-	-
EGFR TCR-4	EGFR	T790M	A02:01	SAQGSSGRIEQF	-	-	-
EGFR TCR-5	EGFR	T790M	A02:01	SALPGFSYEQY	-	-	-

[00415] While preferred embodiments of the present invention have been shown and described herein, it will be apparent to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

[00416] Table 2. SEQUENCES

Name	SEQ ID NO	Sequence
RAS TCR-1 alpha chain CDR1	1	SIFNT
RAS TCR-1 alpha chain CDR2	2	LYKAGEL
RAS TCR-1 alpha chain CDR3	3	CAGRNFNGNEKLTF
RAS TCR-1 beta chain CDR1	4	DFQATT
RAS TCR-1 beta chain CDR2	5	SNEGSKA
RAS TCR-1 beta chain CDR3	6	SARDRGLVSLPSVEAFF
RAS TCR-1 alpha chain variable domain	7	ATGCTCCTTGAACATTTATTAATAATCTTGTGGATGCAGCTGACATGGGTCAGTGGTCAACAGCTGAA TCAGAGTCCTCAATCTATGTTTATCCAGGAAGGAGAAGATGTCTCCATGAACTGCACTTCTTCAAGCA TATTTAACACCTGGCTATGGTACAAGCAGGACCCTGGGGAAGGTCCTGTCTCTTGATAGCCTTATAT AAGGCTGGTGAATTGACCTCAAATGGAAGACTGACTGCTCAGTTTGGTATAACCAGAAAGGACAGCTT CCTGAATATCTCAGCATCCATACCTAGTGATGTAGGCATCTACTTCTGTGCTGGGAGAACTTTGGAA ATGAGAAATTAACCTTTGGGACTGGAACAAGACTCACCATCATACCC
	8	ATGCTCCTTGAACATTTATTAATAATCTTGTGGATGCAGCTGACATGGGTCAGTGGTCAACAGCTGAA TCAGAGTCCTCAATCTATGTTTATCCAGGAAGGAGAAGATGTCTCCATGAACTGCACTTCTTCAAGCA TATTTAACACCTGGCTATGGTACAAGCAGGACCCTGGGGAAGGTCCTGTCTCTTGATAGCCTTATAT AAGGCTGGTGAATTGACCTCAAATGGAAGACTGACTGCTCAGTTTGGTATAACCAGAAAGGACAGCTT CCTGAATATCTCAGCATCCATACCTAGTGATGTAGGCATCTACTTCTGTGCTGGGAGAACTTTGGAA ATGAGAAATTAACCTTTGGGACTGGAACAAGACTCACCATCATACCC
	9	MLLEHLLIILWMQLTWVSGQQLNQSPQSMFIQEGEDVSMNCTSSSIFNTWLWYKQDPGEGPVLIIALY KAGELTSNGRLTAQFGITRKDSFLNISASIPSDVGIYFCAGRNFNGNEKLTFGTGTRLTIIP
RAS TCR-1 beta chain variable domain	10	ATGCTGCTGCTTCTGCTGCTTCTGGGGCCAGGCTCCGGGCTTGGTGTCTGCTCTCTCAACATCCGAG CAGGGTTATCTGTAAGAGTGAACCTCTGTGAAGATCGAGTGCCGTTCCCTGGACTTTTCAGGCCACAA CTATGTTTTGGTATCGTCAGTTCGGAAACAGAGTCTCATGCTGATGGCAACTTCCAATGAGGGCTCC AAGGCCACATACGAGCAAGGCGTCGAGAAGGACAAGTTTCTCATCAACCATGCAAGCCTGACCTTGTC CACTCTGACAGTGACCACTGCCCATCCTGAAGACAGCAGCTTCTACATCTGCAGTGCTCGCGACAGGG GGCTTGTATCGTTGCCGTCGCTAGAAAGCTTTCTTTGGACAAGGCACCACTCAGATTGTACTG
	11	ATGCTGCTGCTTCTGCTGCTTCTGGGGCCAGGCTCCGGGCTTGGTGTCTGCTCTCTCAACATCCGAG CAGGGTTATCTGTAAGAGTGAACCTCTGTGAAGATCGAGTGCCGTTCCCTGGACTTTTCAGGCCACAA CTATGTTTTGGTATCGTCAGTTCGGAAACAGAGTCTCATGCTGATGGCAACTTCCAATGAGGGCTCC AAGGCCACATACGAGCAAGGCGTCGAGAAGGACAAGTTTCTCATCAACCATGCAAGCCTGACCTTGTC CACTCTGACAGTGACCACTGCCCATCCTGAAGACAGCAGCTTCTACATCTGCAGTGCTCGCGACAGGG GGCTTGTATCGTTGCCGTCGCTAGAAAGCTTTCTTTGGACAAGGCACCACTCAGATTGTACTG
	12	MLLLLLLLGPGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNESG KATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICARDRGLVSLPSVEAFFGQGTRLTVV
RAS TCR-1 alpha chain	13	MLLEHLLIILWMQLTWVSGQQLNQSPQSMFIQEGEDVSMNCTSSSIFNTWLWYKQDPGEGPVLIIALY KAGELTSNGRLTAQFGITRKDSFLNISASIPSDVGIYFCAGRNFNGNEKLTFGTGTRLTIIPDIQNPDP AVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFACAN AFNNSIIPEDTFFPSPSSCDVKLVEKSFETDTNLFQNL SVIGFRILLK VAGENLLMTLRLWSS
RAS TCR-1 beta chain	14	MLLLLLLLGPGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNESG KATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICARDRGLVSLPSVEAFFGQGTRLTVVLE DLNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPAL NDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSVS YQQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
RAS TCR-1/2 peptide	15	KLVVVGACGV
RAS TCR-2 alpha chain CDR1	16	VSGNPY

Name	SEQ ID NO	Sequence
RAS TCR-2 alpha chain CDR2	17	YITGDNLV
RAS TCR-2 alpha chain CDR3	18	CAVRDQSGANNLFF
RAS TCR-2 beta chain CDR1	19	SEHNR
RAS TCR-2 beta chain CDR2	20	FQNEAQ
Ras TCR-2 beta chain CDR3	21	ASYLSGSIYNEQFF
RAS TCR-2 alpha chain variable domain	22	ATGGCCTCTGCACCCATCTCGATGCTTGCGATGCTCTTCACATTGAGTGGGCTGAGAGCTCAGTCAGTGGCTCAGCCGGAAGATCAGGTCAACGTTGCTGAAGGGAATCCTCTGACTGTGAAATGCACCTATTTCAGTCTCTGGAAACCCCTTATCTTTTGGTATGTTCAATACCCCAACCGAGGCCCTCCAGTTCCTTCTGAAATACATCACAGGGGATAACCTGGTTAAAGGCAGCTATGGCTTTGAAGCTGAATTTAACAAGAGCCAAACCTCCTTCCACCTGAAGAAACCATCTGCCCTTGAGGCGACTCCGCTTTGTACTTCTGTGCTGTGAGAGACCAAAGTGGGGCAAACAACCTCTTCTTTGGGACTGGAACGAGACTCACCGTTATTCCC
	23	ATGGCTTCTGCGCCTATATCAATGCTTGCCATGCTGTTTACACTGTCCGGTCTGAGGGCTCAAAGCGTGGCCCAACCTGAGGATCAGGTGAATGTAGCGGAGGGCAATCCGTTGACAGTTAAGTGTACATACTCCGTATCAGGCAATCCGTACTTGTGTTTGGTATGTGCGAGTACCCCAATCGGGGGCTTCAATTCTTGCTGAAGTACATTACAGGCGATAATCTGGTAAAAGGTAGTTATGGTTTTGAGGCCGAATCAACAAATCACAAACATCATTTTCATCTTAAAAAGCCAAGCGCACTTGTGAGTACTCAGCGCTTTATTTCTGTGCGAGTCAGAGACCAATCAGGGGCAAATAATCTGTTCTTTGGGACAGGGACTAGATTGACTGTTATACCC
	24	MASAPI SMLAMLF T L SGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLK YITGDNLVKGSYGFEAEFNKSQTSFHLKKP SALVSDSALYFCAVRDQSGANNLFFGTGTRLTVIP
RAS TCR-2 beta chain variable domain	25	ATGGGCACCAAGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGCAGATCACGCAGATACTGGAGTCTCCCAGGACCCAGACACAAGATCACAAAGAGGGGACAGAATGTAACCTTCAGGTGTGATCCAATTTCTGAACACAACCGCCTTTATTTGGTACCGACAGACCCCTGGGGCAGGGCCAGAGTTTCTGACTTACTTCTCAAGATGAAGCTCAACTAGAAAAATCAAGGCTGCTCAGTGATCGGTTCTCTGCAGAGAGGCCCTAAGGGATCTTTCTCCACCTTGAGATCCAGCGCACAGAGCAGGGGGACTCGGCCATGTATCTCTGTGCCAGCTACCTGAGCGGTTCCATTTACAATGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
	26	ATGGGCACCTAGCCTCTTGTGTTGGATGGCACTTTGCCTTCTTGGCGCGGATCACGCCGATACAGGCGTCTCCCAAGATCCCAGACATAAAATCACAAACGGGGCCAGAACGTTACCTTTCGCTGCGATCCGATATCAGAGCATAATCGACTGTATTGGTATAGGCAAACTCTCGGGCAAGGGCCTGAGTTCTCCTACTTATTTCCAAAATGAGGCGCAACTGGAAAAGAGCCGGTTGTTGAGTGATAGGTTTTCCGCAGAGCGACCCAGGGGAGGCTTCTCAACACTGGAGATACAAAGGACCGAACAAGGTGATTCCGCAATGTATCTCTGTGCTAGTTATTTGAGCGGCTCCATATATAACGAACAGTTTTCGGACCGGGCACTCGCCTGACCGTACTA
	27	MGTSLLCWMALCCLLGADHADTGVSQDPRHKITKRQNVTFRCDFI SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFS AERP KGSFSTLEIQRT EQGDSAMYL CASYLSGSIYNEQFFGPGTRLTVL
RAS TCR-2 alpha chain	28	MASAPI SMLAMLF T L SGLRAQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLK YITGDNLVKGSYGFEAEFNKSQTSFHLKKP SALVSDSALYFCAVRDQSGANNLFFGTGTRLTVIPDIQ NPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFACANAFNNSIIPEDTFFPSP ESSCDVKLVEKS FETDTNLNFQNL SVIGFRI LLLKVAGFNLLMTLRLWSS
RAS TCR-2 beta chain	29	MGTSLLCWMALCCLLGADHADTGVSQDPRHKITKRQNVTFRCDFI SEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFS AERP KGSFSTLEIQRT EQGDSAMYL CASYLSGSIYNEQFFGPGTRLTVLED LNKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPV TQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
RAS TCR-1/2 peptide	30	LVVVGACGV
Ras TCR-3 alpha chain CDR1	31	NSMFDY
RAS TCR-3 alpha chain CDR2	32	ISSIKDK
RAS TCR-3 alpha chain CDR3	33	AASGGGGADGLT

Name	SEQ ID NO	Sequence
RAS TCR-3 beta chain CDR1	34	MNHNH
RAS TCR-3 beta chain CDR2	35	SVGAGI
RAS TCR-3 beta chain CDR3	36	ASSYSTERGTIY
RAS TCR-3 alpha chain variable domain	37	ATGGCCATGCTCCTGGGGGCATCAGTGCTGATTCTGTGGCTTCAGCCAGACTGGGTAAACAGTCAACA GAAGAATGATGACCAGCAAGTTAAGCAAAATTCACCATCCCTGAGCGTCCAGGAAGGAAGAATTTCTA TTCTGAACGTGACTATACCAACAGCATGTTTGATTATTTCTATGGTACAAAAATACCCCTGCTGAA GGTCCTACATTCCTGATATCTATAAGTTCCATTAAGGATAAAAAATGAAGATGGAAGATTCACTGTCTT CTTAAACAAAAGTGCCAAGCACCTCTCTCTGCACATTGTGCCCTCCCAGCCTGGAGACTCTGCAGTGT ACTTCTGTGCAGCAAGCGGGGAGGAGGTGCTGACGGACTCACCTTTGGCAAAGGGACTCATCTAATC ATCCAGCCC
	38	ATGGCCATGCTGCTGGGGGCCAGCGTGCTGATTTTATGGCTGCAGCCGACTGGGTGAACAGCCAGCA GAAGAACGACGACCAGCAAGTGAAGCAGAACTCCCTTCTTTAAGCGTGCAAGAAGGTCTGATCAGCA TTTTAACTGCGACTACACCAACAGCATGTTGACTACTTTTATGGTACAAAGAAGTACCCCGCCGAG GGCCCCACCTTTTAAATCAGCATCAGCAGCATCAAGGACAAGAACGAGGACGGTCTGTTTACCCTGTT TTTAAACAAGAGCGCCAAGCATTTATCTTTACACATCGTGCCCTCCCAGCCCGGTGATAGCGCCGTGT ACTTCTGCGCCGCGAGCGGAGGAGGCGCGGATGGACTGACCTTCGGCAAAGGGACCCATTTAATC ATCCAGCCC
	39	MAMLLGASVLILWLQPDWVNSQQKNDDQVQKQNSPSPSLSVQEGRISILNCDYTNMSFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKSARKHLSLHIVPSQPGDSAVYFCAASGGGGADGLTFGKGTHLI IQP
RAS TCR-3 beta chain variable domain	40	ATGAGGTCTCAGAATGACTTCCTTGAGAGTCTGTTCCTTTCATCAATGCACAGATACAGAAGACC CCTCCGTCTGGAGCACCTGCCATGAGCATCAGCCTCCTGTGCTGTGCAGCCTTTCCTCTCCTGTGGG CAGGTCCAGTGAATGCTGGTGTCACTCAGACCCCAAAATCCGCATCCTGAAGATAGGACAGAGCATG ACACTGCAGTGATCCAGGATATGAACCATAACTACATGTACTGGTATCGACAAGACCCAGGCATGGG GCTGAAGCTGATTTATTATTAGTTGGTGTGGTATCACTGATAAAGGAGAAGTCCCGAATGGCTACA ACGTCTCCAGATCAACCACAGAGGATTTCCCGCTCAGGCTGGAGTTGGCTGCTCCCTCCCAGACATCT GTGTACTTCTGTGCCAGCAGTTACTCGACGGAACGCGGGACCATATATTTTGGAGAGGGAAGTTGGCT CACTGTTGTA
	41	ATGAGGAGCCAGAACGACTTTTATAGAGAGCCCGTGCTCTGAGCAGCATGCATAGGTATAGGAGGCC TCTGAGACCCGGTGCCCCGCTATGAGCATCTCTTTACTGTGCTGTGCTGCCCTTTCCTTTACTGTGGG CTGGCCCCGTAAACGCTGGCGTGACCCAGACCCCAAGTTTAGGATTTTAAAGATCGGCCAGTCCATG ACTTTACAGTGACCCCAAGATATGAACCACAACACTACATGTACTGGTATCGTCAAGATCCCGGCATGGG TTTAAAGCTGATTTACTACAGCGTGGGAGCCGGCATCACCGACAAGGGCGAGGTGCCCAACGGCTACA ATGTGTCTCGTAGCACCACGAGGACTTCCCTCTGAGACTGGAGCTGGCCGCCCTAGCCAGACAAGC GTGTACTTCTGCGCCTCCTCTACAGCACCAGAGGGGCACCATCTACTTCGGCGAGGGCAGCTGGCT GACCGTGGTG
	42	MRSQNDFLESFVPLSSMHRYRRLRPGAPAMISILLCCAAFPLLWAGPVNAGVTQTPKFRILKIGQSM TLQCTQDMNHNMYWYRQDPGMGLKLIYYSVGAGITDKGEVPNGYNVSRSTTEDFPLRLELAAPSQTS VYFCASSYSTERGTIYFGEGLWTLV
RAS TCR-3 alpha chain	43	MAMLLGASVLILWLQPDWVNSQQKNDDQVQKQNSPSPSLSVQEGRISILNCDYTNMSFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKSARKHLSLHIVPSQPGDSAVYFCAASGGGGADGLTFGKGTHLI IQPDIQNPDPVYQLRDSKSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAW SNKSDFACANAFNNSIIPEDTFFPSPESPSCDVKLVEKSFETDTNLNLFQNLVIGFRILLKLVAGENLL MTLRLWSS
RAS TCR-3 beta chain	44	MRSQNDFLESFVPLSSMHRYRRLRPGAPAMISILLCCAAFPLLWAGPVNAGVTQTPKFRILKIGQSM TLQCTQDMNHNMYWYRQDPGMGLKLIYYSVGAGITDKGEVPNGYNVSRSTTEDFPLRLELAAPSQTS VYFCASSYSTERGTIYFGEGLWTLVVEDLNKVFPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVE LSWWVNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFWQNPNRNHFRCQVQFYGLSENDEWT QDRAKPVTQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLVSAVLVLMAMVKRKDF
RAS TCR-3 peptide	45	VVGAVGVGK
	46	VVGAVGVGK
RAS TCR-4 alpha chain CDR1	47	TSINN

Name	SEQ ID NO	Sequence
RAS TCR-4 alpha chain CDR2	48	IRSNERE
RAS TCR-4 alpha chain CDR3	49	ATDRQSSGDKLT
RAS TCR-4 beta chain CDR1	50	SGHAT
RAS TCR-4 beta chain CDR2	51	FQNNGV
RAS TCR-4 beta chain CDR3	52	ASSLADIYEQY
RAS TCR-4 alpha chain variable domain	53	ATGGAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAATGCCACCATGAACTGCAGTTACA AAACTAGTATAAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTGTCCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAACACAGTGAAGATTAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTGTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTACGGACCGTC AAAGCAGCGGAGACAAGCTGACTTTTGGGACCGGGACTCGTTAGCAGTTAGGCCC
	54	ATGGAGACTTTACTGGGCGTGTCTTTAGTGATTTTATGGCTGCAGCTGGCTCGTGTGAATAGCCAGCA AGGTGAAGAGGACCCCCAAGCTTTAAGCATCCAAGAAGGCGAGAACGCCACCATGAACTGCTCCTACA AGACCAGCATCAACAATTTACAGTGGTATCGTCAGAACAGCGGTCGTGGTTTGTGTCATTTAATTTTA ATTCTGTAGCAACGAGAGGGGAGAAGCACAGCGGTCGTCTGAGGGTGACTTTAGACACCAGCAAGAAGAG CAGCTCTTTACTGATCACAGCCTCTAGGGCCGCTGACACCGCTAGTACTTCTGCGCCACCGACAGAC AGAGCAGCGGCGACAAGCTGACCTTCGGCACCGGCACAAGACTGGCCGTGAGACCC
	55	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEGENATMNC SYKTS INNLQWYRQNSGRGLVHLIL IRSNEREKHSGRLRVTLDTSKSS SLLITASRAADTASYFCATDRQSSGDKLTFGTGTRLAVRP
RAS TCR-4 beta chain variable domain	56	ATGGGCACCAGGCTCCTCTGCTGGGCGGCCCTCTGTCTCCTGGGAGCAGAACTCACAGAAGCTGGAGT TGCCAGTCTCCAGATATAAGATTATAGAGAAAAGGCAGAGTGTGGCTTTTTGGTGCAATCCTATAT CTGGCCATGCTACCCTTTACTGGTACCAGCAGATCCTGGGACAGGGGCCAAAGCTTCTGATTCAGTTT CAGAATAACGGGTGTAGTGGATGATTACAGTTGCCTAAGGATCGATTTTCTGCAGAGAGGCTCAAAGG AGTAGACTCCACTCTCAAGATCCAGCCTGCAAAGCTTGAGGACTCGGCCGTGTATCTCTGTGCCAGCA GCTTAGCCGACATCTACGAGCAGTACTTCGGCCCGGCACCGGCTCACGGTCACA
	57	ATGGGCACCAGACTGCTGTGCTGGGCGCTCTGTGTCTGCTGGGCGCTGAGCTGACAGAAGCTGGCGT GGCCCAGAGCCCTCGTTACAAGATCATCGAGAAGAGGCAGAGCGTGGCCTTCTGGTGCAACCCCATCA GCGGCCACGCCACTTTATACTGGTACCAGCAGATTTTAGGCCAAGGTCCCAAGCTGCTGATCCAGTTC CAGAACAACGGCGTGGTGGACGACAGCCAGCTGCCCAAGGATCGTTTCAGCGCCGAGAGGCTGAAGGG CGTGGACAGCACTTTAAAAATCCAGCCCGCTAAGCTGGAGGACAGCGCCGTGTATTTATGCGCTAGCT CTTTAGCCGACATCTACGAGCAGTACTTCGGCCCGGCACTCGTCTGACCGTGACC
	58	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLADIYEQYFGPGTRLTVT
RAS TCR-4 alpha chain	59	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEGENATMNC SYKTS INNLQWYRQNSGRGLVHLIL IRSNEREKHSGRLRVTLDTSKSS SLLITASRAADTASYFCATDRQSSGDKLTFGTGTRLAVRPDIQN PDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFA CANAFNNSIIPEDTFFPSPRESSCDVKLVEKSFETDTNLFQNL SVIGFRILLK VAGFNLLMTLRLWS S
RAS TCR-4 beta chain	60	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLADIYEQYFGPGTRLTVTEDLN KVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDS RYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPVTTQIVSAEAWGRADCGFTSVSYQQ GVL SATILYEILLGKATLYAVLV SALVLMAMVKRKDF
RAS TCR-4 peptide	61	VVGAVGVGK
	62	VVVGAVGVGK
RAS TCR-5 alpha chain CDR1	63	TSGFNG
RAS TCR-5 alpha chain CDR2	64	NVLDGL

Name	SEQ ID NO	Sequence
RAS TCR-5 alpha chain CDR3	65	CAPGDNFNKFYF
RAS TCR-5 beta chain CDR1	66	SGHRS
RAS TCR-5 beta chain CDR2	67	YFSETQ
RAS TCR-5 beta chain CDR3	68	CASSARNDEAFF
RAS TCR-5 alpha chain variable domain	69	ATGTGGGGAGTTTTCCTTCTTTATGTTTCCATGAAGATGGGAGGCACTACAGGACAAAACATTGACCA GCCCAGTACAGATGACAGCTACGGAAGGTGCCATTGTCCAGATCAACTGCACGTACCAGACATCTGGGT TCAACGGGCTGTTCTGGTACCAGCAACATGCTGGCGAAGCACCCACATTTCTGTCTTACAATGTCTG GATGGTTTGGAGGAGAAAGGTCGTTTTTCTTCATTCTTAGTCGGTCTAAAGGGTACAGTTACCTCCT TTTGAAGGAGCTCCAGATGAAAGACTCTGCCTCTTACCTCTGTGCTCCCGGGGACAACTTCAACAAAT TTTACTTTGGATCTGGGACCAACTCAATGTAAAACCA
	70	ATGTGGGGCGTGTCTGTGCTGTACGTGTCCATGAAGATGGGCGGCACCACAGGCCAGAACATCGACCA GCCAACCGAGATGACCGCCACAGAGGGCGCCATCGTGCAGATCAACTGCACCTACCAGACATCTGGCT TCAATGGCCTGTTTTTGGTATCAGCAGCACGAGGAGAGGCACCCACATTCTGAGCTATAATGTGCTG GATGGCCTGGAGGAGAAGGGCAGGTTCTCTCTTTTCTGTCTCGCAGCAAGGGCTACTCCTATCTGCT GCTGAAGGAGCTGCAGATGAAGGACTCCGCCTCTTACCTGTGCGCCCCCTGGCGATAACTTTAATAAGT TCTATTTTCGGCTCTGGCACCAGCTGAATGTGAAGCCA
	71	MWGVFLLYVSMKMGTTGQNIQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRSKGYSYLLKELQMKDSASYLCAPGDNFNKFYFGSGTKLNVKP
RAS TCR-5 beta chain variable domain	72	ATGGGCTCCAGGCTGCTCTGTTGGGTGCTGCTTTGTCTCCTGGGAGCAGGCCAGTAAAGGCTGGAGT CACTCAAACCTCAAGATATCTGATCAAACGAGAGGACAGCAAGTACACTGAGCTGCTCCCTATCTCT CTGGGCATAGGAGTGTATCCTGGTACCAACAGACCCAGGACAGGGCCTTCAGTTCTCTTTTGAATAC TTCAGTGAGACACAGAGAAACAAAGGAACTTCCCTGGTTCGATTCTCAGGGCGCCAGTTCTCTAACTC TCGCTCTGAGATGAATGTGAGCACCTTGGAGCTGGGGGACTCGGCCCTTTATCTTTGCGCCAGCAGCG CGAGAAATGATGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
	73	ATGGGCAGCCGGCTGCTGTGCTGGGTGCTGCTGTGCCTGCTGGGAGCAGGACCAGTGAAGGCAGGCGT GACCCAGACACCTCGGTACCTGATCAAGACCAGAGGCCAGCAGGTGACACTGAGCTGCTCCCCAATCT CCGGCCACAGATCTGTGAGCTGGTACCAGCAGACCCAGGACAGGGACTGCAGTTCTCTGTTTGAGTAT TTCTCCGAGACACAGAGGAACAAGGGCAATTTCCCTGGCCGGTTTTCTGGCAGACAGTTTTTCCAACTC TCGCAGCGAGATGAATGTGAGCACCTTGGAGCTGGGCGACTCCGCCCTGTACCTGTGCGCCAGCTCCG CCAGGAACGATGAGGCCTTCTTTGGCCAGGGCACCCGGCTGACAGTGGTG
	74	MGRLLCWVLLCLLGAGPVKAGVTQTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEY FSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGDSALYLCASSARNDEAFFGQGTRLTVV
RAS TCR-5 alpha chain	75	MWGVFLLYVSMKMGTTGQNIQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRSKGYSYLLKELQMKDSASYLCAPGDNFNKFYFGSGTKLNVKPDINPDPFVY QLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFN NSIIPEDTFFPSPPESSCDVKLVEKSFETDTNLFQNLVIGFRILLKLVAGFNLLMTLRLWSS
RAS TCR-5 beta chain	76	MGRLLCWVLLCLLGAGPVKAGVTQTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEY FSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGDSALYLCASSARNDEAFFGQGTRLTVVVDLNV FPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAPVTQIVSAEAWGRADCGFTSVSYQQGV LSATILYEILLGKATLYAVLVLSALVLMAMVKRKDF
RAS TCR-5 peptide	77	VVGAVGVGK
	78	VVGAVGVGK
RAS TCR-6 alpha chain CDR1	79	DRGSQS
RAS TCR-6 alpha chain CDR2	80	IYSNGD
RAS TCR-6 alpha chain CDR3	81	CAVKSRAGSYQLTF
RAS TCR-6 beta chain CDR1	82	SGHNS

Name	SEQ ID NO	Sequence
RAS TCR-6 beta chain CDR2	83	FNNNVF
RAS TCR-6 beta chain CDR3	84	CASSLGDSEQYF
RAS TCR-6 alpha chain variable domain	85	ATGAAATCCTTGAGAGTTTTACTAGTGATCCTGTGGCTTCAGTTGAGCTGGGTTTGGAGCCAACAGAA GGAGGTGGAGCAGAATTCTGGACCCCTCAGTGTTCCAGAGGGAGCCATTGCCTCTCTCAACTGCACTT ACAGTGACCGAGGTTCCAGTCTCTTCTGTTACAGACAATATTCTGGGAAAAGCCCTGAGTTGATA ATGTTTCATATACTCCAATGGTGACAAAGAAGATGGAAGGTTTACAGCACAGCTCAATAAAGCCAGCCA GTATGTTTCTCTGCTCATCAGAGACTCCCAGCCCAGTGATTTCAGCCACCTACCTCTGTGCCGTGAAGT CAAGGGCTGGGAGTTACCAACTCACTTTTCGGGAAGGGGACCAAACCTCTCGGTCATACCA
	86	ATGAAGAGCCTGCGGGTGCTGCTGGTCATCCTGTGGCTGCAGCTGTCTGGGTGTTGGTCTCAGCAGAA GGAGGTGGAGCAGAATAGCGGACCACTGTCCGTGCCAGAGGGAGCCATCGCTCCCTGAAGTGCACAT ACTCTGACAGGGGCTCCAGTCTTTCTTTTGGTACCGCCAGTATAGCGGCAAGTCCCCGAGCTGATC ATGTTTCATCTACTCTAATGGCGACAAGGAGGATGGCAGGTTTACCGCCCAGCTGAACAAGGCCTCTCA GTATGTGAGCCTGCTGATCCGCGACAGCCAGCCTAGCGATTCCGCCACATACCTGTGCGCAGTGAAGT CCCGGGCAGGCTCTTATCAGCTGACCTTTGGCAAGGGCACAAAGCTGAGCGTGATCCCA
	87	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELI MFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVAVKSRAGSYQLTFGKGTCLSVIP
RAS TCR-6 beta chain variable domain	88	ATGGACTCCTGGACCTTCTGCTGTGTGTCCCTTTCATCCTGGTAGCGAAGCATAACAGATGCTGGAGT TATCCAGTCACCCCGCCATGAGGTGACAGAGATGGGACAAGAAGTGACTCTGAGATGTAAACCAATTT CAGGCCACAACCTCCCTTTTCTGGTACAGACAGACCATGATGCGGGGACTGGAGTTGCTCATTTACTTT AACAACAACGTTCCGATAGATGATTCAGGGATGCCCCGAGGATCGATTCTCAGCTAAGATGCCTAATGC ATCATTCTCCACTCTGAAGATCCAGCCCTCAGAACCAGGGACTCAGCTGTGTACTTCTGTGCCAGCA GTCTCGGGGACAGCGAGCAGTACTTCGGGCCGGGCACCAGGCTCACGGTCACA
	89	ATGGACAGCTGGACCTTCTGCTGCGTGAGCCTGTGCATCCTGGTGGCCAAGCACACAGATGCAGGCGT GATCCAGTCCCCAAGGCACGAGGTGACCGAGATGGGACAGGAGGTGACACTGAGGTGTAAGCCTATCT CTGGCCACAATAGCCTGTTCTGGTACAGGCAGACCATGATGCGCGGCCTGGAGCTGCTGATCTACTTC AACAATAACGTGCCTATCGACGATTCGGGCATGCCAGAGGACAGATTCTCTGCCAAGATGCCCAACGC CTCCTTTTCTACACTGAAGATCCAGCCAAGCGAGCCTAGGGACTCCGCCGTGTACTTCTGCGCCAGCT CCCTGGGCGATAGCGAGCAGTATTTTGGCCCTGGCACCCGGCTGACCGTGACA
	90	MDSWTFCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHNSLFWYRQTMRRGLELLIYF NNNVPIDDSGMPEDRFSKMPNASFSTLKIQPSRDSAVYFCASSLGDSEQYFPGTRTLTVT
RAS TCR-6 alpha chain	91	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELI MFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVAVKSRAGSYQLTFGKGTCLSVIPDIQ NPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVVSQKSDSVYITDKTVLDMRSMDFKSNSAVAWSNKSDF ACANAFNNSIIPEDTFFPSPSSCDVKLVEKSFETDTNLFQNLVIGFRIILLKVAGFNLLMTLRLW SS
RAS TCR-6 beta chain	92	MDSWTFCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHNSLFWYRQTMRRGLELLIYF NNNVPIDDSGMPEDRFSKMPNASFSTLKIQPSRDSAVYFCASSLGDSEQYFPGTRTLTVTEDLNK VFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSR YCLSSRLRVSATFWQNPNRNHFRCQVQFYGLSENDEWTQDRAKPVTVQIVSAEAWGRADCGFTSVSYQQG VLSATILYEILLGKATLYAVLVLSALVLMAMVVRKDF
RAS TCR-6 peptide	93	VVGAVGVGK
	94	VVVGAVGVGK
RAS TCR-7 alpha chain CDR1	95	SSYSPS
RAS TCR-7 alpha chain CDR2	96	YTSATLV
RAS TCR-7 alpha chain CDR3	97	CVVSGGGSSNTGKLIF
RAS TCR-7 beta chain CDR1	98	SGHAT
RAS TCR-7 beta chain CDR2	99	FQNNGV
RAS TCR-7 beta chain CDR3	100	CASSQRSNTGELFF

Name	SEQ ID NO	Sequence
RAS TCR-7 alpha chain variable domain	101	ATGCTCCTGCTGCTCGTCCCAGTGCTCGAGGTGATTTTTACTCTGGGAGGAACCAAGAGCCAGTCGGT GACCCAGCTTGACAGCCACGTCTCTGTCTCTGAAGGAACCCCGGTGCTGCTGAGGTGCAACTACTCAT CTTCTTATTCACCATCTCTCTTCTGGTATGTGCAACACCCCAACAAAGGACTCCAGCTTCTCCTGAAG TACACATCAGCGGCCACCCCTGGTTAAAGGCATCAACGGTTTTGAGGCTGAATTTAAGAAGAGTGAAAC CTCCTTCCACCTGACGAAACCTCAGCCCATATGAGCGACGCGGCTGAGTACTTCTGTGTTGTGAGTG GGGGAGGCTCTAGCAACACAGGCAAACTAATCTTTGGGCAAGGGACAACCTTTACAAGTAAACCA
	102	ATGCTGCTGCTGCTGGTGCCCGTGCTGGAAGTGATCTTCACCTGGGAGGAACAAGGGCACAGAGCGT GACCCAGCTGGACTCCCACGTGTCCGTGTCTGAGGGCACACCCGTGCTGCTGAGATGCAACTACTCCT CTAGCTATAGCCCCCTCCCTGTTCTGGTACGTGCAGCACCCTAATAAGGGCCTGCAGCTGCTGCTGAAG TATACCTCCGCCGCCACACTGGTGAAGGGCATCAACGGCTTCGAGGCCGAGTTTAAGAAGAGCGAGAC CTCCTTCCACCTGACAAAGCCTTCTGCCCACATGAGCGATGCCGCCGAGTACTTTTGCGTGGTGAGCG GCGGCGGCTCCTCTAATACCGGCAAGCTGATCTTCGGCCAGGGCACCACTGCAGGTGAAGCCA
	103	MLLLLVPVLEVI FTLLGGTRAQSVTLQDLSHVSVEGTPVLLRCNYSSSYSPSLFWYVQHPNKGQLQLLK YTSATLVKINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCVVS GGGSSNTGKLI FGQGTTLQVKP
RAS TCR-7 beta chain variable domain	104	ATGGGCACCAAGGCTCCTCTGCTGGGCGGCCCTCTGTCTCCTGGGAGCAGAATCACAAGAGCTGGAGT TGCCAGCTCTCCAGATATAAGATTATAGAGAAAAGGCAGAGTGTGGCTTTTTGGTGCAATCCTATAT CTGGCCATGCTACCTTTTACTGGTACCAGCAGATCCTGGGACAGGGCCCAAAGCTTCTGATTCAGTTT CAGAATAACGGTGTAGTGGATGATTACAGTTGCCTAAGGATCGATTTTCTGCAGAGAGGCTCAAAGG AGTAGACTCCACTCTCAAGATCCAACCTGCAAAGCTTGAGGACTCGGCCGTGTATCTCTGTGCCAGCA GCCAGAGGTGCAACACCGGGGAGCTGTTTTTGGAGAAGGCTCTAGGCTGACCGTACTG
	105	ATGGGCACCCGGCTGCTGTGCTGGGCGGCCCTGTGCCTGCTGGGAGCAGAGCTGACAGAGGCAGGAGT GGCCAGTCCCCACGGTACAAGATCATCGAGAAGAGACAGTCCGTGGCCTTTTGGTGCAACCCCATCT CTGGCCACGCCACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATCCAGTTC CAGAACAATGGCGTGGTGGACGATTCTCAGCTGCCAAAGGACAGGTTTAGCGCCGAGCGCCTGAAGGG CGTGGATAGCACCTGAAGATCCAGCCTGCCAAGCTGGAGGACAGCGCCGTGTATCTGTGCGCCAGCT CCCAGCGGTCCAATACAGGCGAGCTGTTCTTTGGCGAGGGCTCTAGGCTGACCGTGCTG
	106	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSQRSNTGELFFGEGSRLTVL
RAS TCR-7 alpha chain	107	MLLLLVPVLEVI FTLLGGTRAQSVTLQDLSHVSVEGTPVLLRCNYSSSYSPSLFWYVQHPNKGQLQLLK YTSATLVKINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCVVS GGGSSNTGKLI FGQGTTLQVKPD IQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNKS DFACANAFNNSIIPEDTFFPSPSSCDVKLVEKS FETDTNLNFQNL SVIGFRI LLLKVAGFNLLMTLR LWSS
RAS TCR-7 beta chain	108	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSQRSNTGELFFGEGSRLTVLEDL NKVFPPEVAVFEPSEAEI SHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALND SRYCLSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPVTVQIVSAEAWGRADCGFTSVSYQ QGVLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
RAS TCR-7 peptide	109	VVGACGVGK
	110	VVVGACGVGK
RAS TCR-8 alpha chain CDR1	111	TSINN
RAS TCR-8 alpha chain CDR2	112	IRSNERE
RAS TCR-8 alpha chain CDR3	113	CATDAGGGADGLTF
RAS TCR-8 beta chain CDR1	114	SGDLS
RAS TCR-8 beta chain CDR2	115	YYNGEE
RAS TCR-8 beta chain CDR3	116	CASGGRDSTDTQYF

Name	SEQ ID NO	Sequence
RAS TCR-8 alpha chain variable domain	117	ATGGAAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAAATGCCACCATGAACTGCAGTTACA AACTAGTATAAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTGTCCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAACACAGTGGAAAGATTAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTACGGACGCCG GAGGAGGTGCTGACGGACTCACCTTTGGCAAAGGGGACTCATCTAATCATCCAGCCC
	118	ATGGAGACACTGCTGGGCGTGTCCCTGGTCATCCTGTGGCTGCAGCTGGCCAGGGTGAACAGCCAGCA GGGAGAGGAGGAGCCCCAGGCCCTGTCTATCCAGGAGGGCGAGAACGCCACCATGAATTGCTCTTACA AGACAAGCATCAACAATCTGCAGTGGTATAGACAGAACTCCGGCAGGGGCCCTGGTGCACCTGATCCTG ATCCGCTCCAATGAGCGGGAGAAGCACTCTGGCCGGCTGAGAGTGACCCTGGATACATCTAAGAAGTC CTCTAGCCTGCTGATCACCGCCAGCCGGGCAGCAGACACAGCCTCCTACTTTTGTGCCACCGATGCCG GGGGCGGAGCAGACGGACTGACATTTCGGGAAGGGGACTCACCTGATTATCCAGCCA
	119	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEENATMNC SYKTS INN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDAGGGADGLTFGKGTHLI IQP
RAS TCR-8 beta chain variable domain	120	ATGGGCTTCAGGCTCCTCTGCTGTGTGGCCTTTTGTCTCCTGGGAGCAGGCCAGTGGATTCTGGAGT CACACAAACCCCAAAGCACCTGATCACAGCAACTGGACAGCGAGTGACGCTGAGATGCTCCCTAGGT CTGGAGACCTCTCTGTGTACTGGTACCAACAGAGCCTGGACCAGGGCCTCCAGTTCCTCATTACAGTAT TATAATGGAGAAGAGAGAGCAAAAGGAACATTCTTGAACGATTCTCCGCACACAGTTCCCTGACTT GCACTCTGAACTAAACCTGAGCTCTCTGGAGCTGGGGGACTCAGCTTTGTATTTCTGTGCCAGCGGGG GACGGGATTCCACAGATACGAGTATTTTGGCCCAGGCACCCGGCTGACAGTGCTC
	121	ATGGGCTTTCGGCTGCTGTGTGCTGCGTGGCTTTTGCCTGCTGGGGGCTGGGCCCTGTGGATAGCGGGT CACTCAGACACCTAAACATCTGATCACCGCAACAGGACAGAGGGTGACCTGAGGTGCTCTCCTCGGA GCGGCGACCTGAGCGTGTACTGGTATCAGCAGAGCCTGGATCAGGGCCTGCAGTTCTGATCCAGTAC TATAACGGCGAGGAGCGCGCAAGGGCAATATCCTGGAGCGGTTCTCTGCCAGCAGTTTCCAGACCT GCACAGCGAGCTGAACCTGAGCTCCCTGGAGCTGGGCGATAGCGCCCTGTACTTCTGCGCCTCCGGCG GCAGAGACTCTACCGATACACAGTATTTTGGCCCCGGCACCCAGACTGACAGTGCTG
	122	MGRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQY YNGEERAKGNILERFSAQQFPDLHSELNLS SLELGDSALYFCASGGRDSTDQYFGPGTRLTVL
RAS TCR-8 alpha chain	123	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEENATMNC SYKTS INN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDAGGGADGLTFGKGTHLI IQPDIQN PDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSVYITDKTVLDMRSMDFKSN SAVAWSNKSDFA CANAFNNSI IPEDTFFPSPSSCDVKLVEKSFETDTNLFQNL SVIGFRILLKLVAGFNLLMTLRLWS S
RAS TCR-8 beta chain	124	MGRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQY YNGEERAKGNILERFSAQQFPDLHSELNLS SLELGDSALYFCASGGRDSTDQYFGPGTRLTVLLEDLN KVFPPEVAVFEPSEAEI SHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDS RYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSVSYQQ GVLSATILYEILLGKATLYAVLV SALVLMAMVVRKDF
RAS TCR-8 peptide	125	VVGAVGVGK
	126	VVVGAVGVGK
Ras TCR-1/2 peptide	219	KLVVVGADGV
Ras TCR-1/2 peptide	220	LVVVGADGV
Ras TCR-1/2 peptide	221	KLVVVGAVGV
Ras TCR-1/2 peptide	222	LVVVGAVGV
RAS TCR-10 alpha chain CDR1	239	SVFSS
RAS TCR-10 alpha chain CDR2	240	VVTGGEV
RAS TCR-10 alpha chain CDR3	241	AGGPNTGNQFY

Name	SEQ ID NO	Sequence
RAS TCR-10 beta chain CDR1	242	SGHNT
RAS TCR-10 beta chain CDR2	243	YYREEE
RAS TCR-10 beta chain CDR3	244	ASSTSFWEVNTEAF
RAS TCR-10 alpha chain variable domains	245	ATGGTCCTGAAATTCTCCGTGTCCATTCTTTGGATTAGTTGGCATGGGTGAGCACCCAGCTGCTGGA GCAGAGCCCTCAGTTTCTAAGCATCCAAGAGGGAGAAAATCTCACTGTGTACTGCAACTCCTCAAGTG TTTTTCCAGCTTACAATGGTACAGACAGGAGCCTGGGGAAGGTCTGTCCCTCTGGTGACAGTAGTT ACGGGTGGAGAAGTGAAGAAGCTGAAGAGACTAACCTTTCAGTTTGGTGATGCAAGAAAGGACAGTTC TCTCCACATCACTGCGGCCAGCCTGGTGATACAGGCCTCTACCTCTGTGCAGGAGGGCCGAACACCG GTAACCAGTTCTATTTTGGGACAGGGACAAGTTTGACGGTCATTCCAAAT
	246	ATGGTGCTGAAGTTTTCCGTGTCTATCCTGTGGATTAGCTGGCCTGGGTGTCTACCCAGCTGCTGGA GCAGAGCCCCAGTTTCTGTCCATCCAGGAGGGCGAGAACCCTGACAGTGTACTGCAATTCTAGCTCCG TGTTTTCTAGCCTGCAGTGGTATAGGCAGGAGCCAGGAGAGGGACCCGTGCTGCTGGTGACCGTGGTG ACAGGCGGCGAGGTGAAGAAGCTGAAGAGACTGACCTTCCAGTTTGGCGACGCCAGGAAGGATTCCTC TCTGCACATCACCGCAGCACAGCCTGGCGATACAGGACTGTACCTGTGCGCAGGAGGACCAAAACACCG GCAATCAGTTCTATTTTGGCACCGGCACATCCCTGACAGTGATCCCTAAT
	247	MVLKFSVILWQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLVTVV TGGEVKKLRLTFQFGDARKDSSLHITAAQPGDTGLYLCAAGPNTGNQFYFGTGTSLTVIPN
RAS TCR-10 beta chain variable domain	248	ATGGGCCCTGGGCTCCTCTGCTGGGTGCTGCTTTGTCTCCTGGGAGCAGGCTCAGTGGAGACTGGAGT CACCCAAAGTCCACACACCTGATCAAAACGAGAGGACAGCAAGTGACTCTGAGATGCTCTTCTCAGT CTGGGCACAACACTGTGTCTGGTACCAACAGGCCCTGGGTGAGGGGCCAGTTTATCTTTTCAGTAT TATAGGGAGGAAGAGAATGGCAGAGGAACTTCCCTCCTAGATTCTCAGGTCTCCAGTTCCCTAATTA TAGCTCTGAGCTGAATGTGAACGCCTTGGAGCTGGACGACTCGGCCCTGTATCTCTGTGCCAGCAGCA CATCTTTTGGGAGGTGAACACTGAAGCTTTCTTTGGACAAGGCACACAGACTCACAGTTGTA
	249	ATGGGACCAGGACTGCTGTGCTGGGTGCTGCTGTGCCTGCTGGGAGCAGGCTCCGTGGAGACCGGCGT GACACAGTCTCCACCCACCTGATCAAGACAAGAGGCCAGCAGGTGACCCTGAGGTGCAGCTCCAGT CTGGCCACAACACAGTGAGCTGGTACCAGCAGGCCCTGGGACAGGGACCTCAGTTCATCTTTTCAGTAC TATAGGGAGGAGGAGAACGGCCGCGGAATTTCCCCCTCGGTTTAGCGGCTGCAGTTCCCAAATA CTCTAGCGAGCTGAACGTGAATGCCCTGGAGCTGGACGATAGCGCCCTGTATCTGTGCGCCTCCTCTA CCTCTTTTGGGAAGTGAATACAGAGGCCCTTCTTTGGCCAGGGCACCCGCCCTGACAGTGGTG
	250	MGPGLLCWVLLCCLLGAGSVETGVTQSPHLLIKTRGQQTTLRCSSQSGHNTVSWYQQALGQGPQFIQY YREEENGRGNFPPRFSGLQFPNYSSELNVNALELDDLSALYLCASSTSFWEVNTEAFFGQGTRLTVV
RAS TCR-10 alpha chain	251	MVLKFSVILWQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLVTVV TGGEVKKLRLTFQFGDARKDSSLHITAAQPGDTGLYLCAAGPNTGNQFYFGTGTSLTVIPNDIQNPE PAVYQLKDRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFTCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVSMGLRILLLKVAGFNLLMTLRLWSS
RAS TCR-10 beta chain	252	MGPGLLCWVLLCCLLGAGSVETGVTQSPHLLIKTRGQQTTLRCSSQSGHNTVSWYQQALGQGPQFIQY YREEENGRGNFPPRFSGLQFPNYSSELNVNALELDDLSALYLCASSTSFWEVNTEAFFGQGTRLTVVKD LRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSY CLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGV LSATILYEILLGKATLYAVLVSLVLMAMVKKKNS
TCR peptide	253	VVGACGVGK
	254	VVVGACGVGK
RAS TCR-11 alpha chain CDR1	255	TSGFNG
RAS TCR-11 alpha chain CDR2	256	NVLDGL
RAS TCR-11 alpha chain CDR3	257	AVREEVLYNQGGKLI
RAS TCR-11 beta chain CDR1	258	LNHDA

Name	SEQ ID NO	Sequence
RAS TCR-11 beta chain CDR2	259	SQIVND
RAS TCR-11 beta chain CDR3	260	ASSKRGWPYEQY
RAS TCR-11 alpha chain variable domain	261	ATGTGGGGAGTTTTCCTTCTTTATGTTTCCATGAAGATGGGAGGCACTACAGGACAAAACATTGACCA GCCCCTGAGATGACAGCTACGGAAGGTGCCATTGTCCAGATCAACTGCACGTACCAGACATCTGGGT TCAACGGGCTGTTCTGGTACCAGCAACATGCTGGCGAAGCACCCACATTTCTGTCTTACAATGTTCTG GATGGTTTGGAGGAGAAAGGTCGTTTTTCTTCATTCTTAGTCGGTCTAAAGGGTACAGTTACCTCCT TTTGAAGGAGCTCCAGATGAAAGACTCTGCCTCTTACCTCTGTGCTGTGAGAGAGGAGGTCTTTATA ACCAGGGAGGAAAAGCTTATCTTCGGACAGGGAACGGAGTTATCTGTGAAACCC
	262	ATGTGGGGCGTGTCTGCTGTACGTGAGCATGAAGATGGGCGGCACCACAGGCCAGAACATCGACCA GCCAACCGAGATGACCGCCACAGAGGGCGCCATCGTGCAGATCAACTGCACCTACCAGACAAGCGGCT TCAATGGCCTGTTTTGGTATCAGCAGCACGAGGAGAGGACCCACATTCTGTCTTATAATGTGCTG GACGGCCTGGAGGAGAAGGGCAGGTTCTCCTCTTTTCTGAGCCGCTCCAAGGGCTACTCCTATCTGCT GCTGAAGGAGCTGCAGATGAAGGATTCTGCCAGCTACCTGTGCGCCGTGCGGGAGGAGGTGCTGTATA ATCAGGGCGGCAAGCTGATCTTTGGCCAGGACCGAGCTGAGCGTGAAGCCT
	263	MWGVFLLYVSMKMGTTGQNIQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRKSGYSYLLKELQMKDSASYLCAVREEVLYNQGGKLIFGQGTLSVKP
RAS TCR-11 beta chain variable domain	264	ATGAGCAACCAGGTGCTCTGCTGTGTGGTCTTTGTCTCTCTGGGAGCAAACACCGTGGATGGTGGAA CACTCAGTCCCCGAAGTACCTGTTTCAAGAAAGGAGGACAGAATGTGACCCTGAGTTGTGAACAGAATT TGAACCACGATGCCATGTACTGGTACCGACAGGACCCAGGGCAAGGGCTGAGATTGATCTACTACTCA CAGATAGTAAATGACTTTTCAAGAAAGGAGATATAGCTGAAGGGTACAGCGTCTCTCGGGAGAAGAAGGA ATCCTTTCTCTCACTGTGACATCGGCCAAAAGAACCCGACAGCTTTCTATCTCTGTGCCAGTAGTA AAAGGGGATGGCCCTACGAGCAGTACTTCGGGCCGGGCACCAGGCTCACGGTCACA
	265	ATGTCCAACCAGGTGCTGTGCTGCGTGGTGTGTGCCTGCTGGGAGCAAATACCGTGGACGGAGGCAT CACACAGTCCCCCAAGTACCTGTTCCGGAAGGAGGGCCAGAACGTGACCCTGTCTTGTGAGCAGAACC TGAATCACGACGCCATGTACTGGTATAGGCAGGACCCCGGACAGGGACTGAGACTGATCTACTATAGC CAGATCGTGAACGACTTTTCAAGGGGCGACATCGCCGAGGGCTACAGCGTGTCCCGGGAGAAGAAGGA GTCCTTCCCACTGACCGTGACATCTGCCCAAGAAGATCCCACCGCCTTTTATCTGTGCGCCAGCTCCA AGAGAGGCTGGCCCTACGAGCAGTATTTTCGGCCCTGGCACCAGGCTGACCGTGACA
	266	MSNQVLCCVVLCLLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYS QIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSKRGWPYEQYFPGPTRLTVT
RAS TCR-11 alpha chain	267	MWGVFLLYVSMKMGTTGQNIQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRKSGYSYLLKELQMKDSASYLCAVREEVLYNQGGKLIFGQGTLSVKPDIQNP EPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSFTC QDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVSMGLRILLKLVAGFNLLMTLRLWSS
RAS TCR-11 beta chain	268	MSNQVLCCVVLCLLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYS QIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSKRGWPYEQYFPGPTRLTVTKDLR NVTPPKVSLFEPSCAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCL SSRLRVSATFWHNPARNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGVLS ATILYEILLGKATLYAVLVSGVLMLAMVKKKNS
TCR peptide	269	VVGACGVGK
	270	VVVGACGVGK
RAS TCR-12 alpha chain CDR1	271	TSINN
RAS TCR-12 alpha chain CDR2	272	IRSNERE
RAS TCR-12 alpha chain CDR3	273	ATDRQSSGDKLT
RAS TCR-12 beta chain CDR1	274	SGHAT
RAS TCR-12 beta chain CDR2	275	FQNNGV

Name	SEQ ID NO	Sequence
RAS TCR-12 beta chain CDR3	276	ASSLADIYEQY
RAS TCR-12 alpha chain variable domain	277	ATGGAAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAAATGCCACCATGAACTGCAGTTACA AACTAGTATAAAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTGTCCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAAACACAGTGAAGATTAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTACGGACCGTC AAAGCAGCGGAGACAAGCTGACTTTTGGGACCGGGACTCGTTTAGCAGTTAGGCCC
	278	ATGGAGACCCTGCTGGGCGTGTCCCTGGTCATCCTGTGGCTGCAGCTGGCCAGGGTGAACAGCCAGCA GGGAGAGGAGGACCCCCAGGCCTTGAGCATCCAGGAGGGCGAGAACGCCACCATGAATTGCTCTTACA AGACAAGCATCAACAATCTGCAGTGGTATAGGCAGAACTCCGGCCGCGGACTGGTGCACCTGATCCTG ATCCGGAGCAATGAGAGAGAGAAGCACTCCGGCCGGCTGAGAGTGACCCTGGACACATCTAAGAAGTC CTCTAGCCTGCTGATCACCGCTCTCGGGCAGCAGATACAGCCAGCTACTTCTGTGCCACCGACAGAC AGTCCTCTGGCGATAAGCTGACCTTTGGCACCGGCACAAGGCTGGCCGTGCGCCCC
	279	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEENATMNC SYKTS INNLOWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSS SLLITASRAADTASYFCATDRQSSGDKLTFGTGTRLAVRP
RAS TCR-12 beta chain variable domain	280	ATGGGCACCAGGCTCCTCTGCTGGGCGGCCCTCTGTCTCCTGGGAGCAGAACTCACAGAAGCTGGAGT TGCCCACTCTCCAGATATAAGATTATAGAGAAAAGCAGAGTGTGGCTTTTGGTGCAATCCTATAT CTGGCCATGCTACCCTTTACTGGTACCAGCAGATCCTGGGACAGGGCCCAAAGCTTCTGATTAGTTT CAGAATAACGGTGTAGTGGATGATTACAGTTGCCTAAGGATCGATTTTCTGCAGAGAGGCTCAAAGG AGTAGACTCCACTCTCAAGATCCAGCCTGCAAAGCTTGAGGACTCGGCCGTGTATCTCTGTGCCAGCA GCTTAGCCGACATCTACGAGCAGTACTTCGGGCCGGGCACCAAGGCTCACGGTGACA
	281	ATGGGAACAAGGCTGCTGTGCTGGGCGGCCCTGTGCCTGCTGGGAGCAGAGCTGACCGAGGCCGGCGT GGCCCAGAGCCCCCGGTACAAGATCATCGAGAAGAGACAGAGCGTGGCCTTCTGGTGCAACCTATCT CCGGCCACGCCACACTGTACTGGTATCAGCAGATCCTGGGCCAGGGCCCAAAGCTGCTGATCCAGTTC CAGAACAATGGCGTGGTGGACGATTCAGCTGCCCAAGGACCGGTTTCTGCCGAGAGACTGAAGGG CGTGGATTCCACCCTGAAGATCCAGCCCGCCAAGCTGGAGGACTCTGCCGTGTATCTGTGCCCGAGCT CCCTGGCCGACATCTACGAGCAGTATTTCCGGCCTGGCACAAAGGCTGACCGTGACA
	282	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLADIYEQYFGPGTRLTVT
RAS TCR-12 alpha chain	283	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEENATMNC SYKTS INNLOWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSS SLLITASRAADTASYFCATDRQSSGDKLTFGTGTRLAVRPDIQN PEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILLK VAGFNLLMTLRLWSS
RAS TCR-12 beta chain	284	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLADIYEQYFGPGTRLTVT KD LR NVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCL SSRLRVSATFWHNPRNHFRCVQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGVLS ATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
TCR peptide	285	VVGACGVGK
	286	VVVGACGVGK
RAS TCR-13 alpha chain CDR1	287	TSESDYY
RAS TCR-13 alpha chain CDR2	288	QEAYKQQN
RAS TCR-13 alpha chain CDR3	289	ALYIYGGSQGNLI
RAS TCR-13 beta chain CDR1	290	SEHNR
RAS TCR-13 beta chain CDR2	291	FQNEAQ
RAS TCR-13 beta chain CDR3	292	ASSSTDRIEAF

Name	SEQ ID NO	Sequence
RAS TCR-13 alpha chain variable domain	293	ATGGCATGCCCTGGCTTCCTGTGGGCACCTTGATCTCCACCTGTCTTGAATTTAGCATGGCTCAGAC AGTCACTCAGTCTCAACCAGAGATGTCTGTGCAGGAGGCAGAGACCGTGACCCTGAGCTGCACATATG ACACCAAGTGAGAGTGATTATTATTTATTCTGGTACAAGCAGCCTCCCAGCAGGCAGATGATTCTCGTT ATTCGCCAAGAAGCTTATAAGCAACAGAATGCAACAGAGAATCGTTTCTCTGTGAACCTCCAGAAAGC AGCCAAATCCTTCAGTCTCAAGATCTCAGACTCACAGCTGGGGGATGCCGCGATGTATTTCTGTGCTC TCTATATTTATGGAGGAAGCCAAGGAAATCTCATCTTTGGAAAAGGCACTAAACTCTCTGTAAACCA
	294	ATGGCATGCCAGGCTTCCTGTGGGCACCTGGTCATCAGCACATGTCTGGAGTTTCTATGGCCCAGAC CGTGACACAGTCTCAGCCTGAGATGAGCGTGCAGGAGGCCGAGACCGTGACACTGAGCTGCACCTACG ACACATCTGAGAGCGATTACTATCTGTTCTGGTATAAGCAGCCACCCTCCAGACAGATGATCCTGGTC ATCAGGCAGGAGGCCTACAAGCAGCAGAACGCCACCGAGAATCGGTTCTCCGTGAACTTTCAGAAAGGC CGCCAAGTCCTTTTCTCTGAAGATCAGCGACTCCCAGCTGGGCGATGCCCGCATGTATTTCTGTGCCC TGTACATCTATGGCGGCTCTCAGGGCAATCTGATCTTTGGCAAGGGCACCAAGCTGAGCGTGAAGCCT
	295	MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCYDTSSESDYYLFWYKQPPSRQMILV IRQEAQKQONATENRFSVNFQKAASKSFLKISDSQLGDAAMYFCALYIYGGSQGNLIFGKGTKLSVKP
RAS TCR-13 beta chain variable domain	296	ATGGGCACCGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGAGATCAGCGAGATACTGGAGT CTCCCAGGACCCAGACACAAGATCACAAAGAGGGGACAGAAATGTAACCTTCAGGTGTGATCCAATTT CTGAACACAACCGCCTTTATTGGTACCGACAGACCCTGGGGCAGGGGCCAGAGTTTCTGACTTACTTC CAGAATGAAGCTCAACTAGAAAAATCAAGGCTGCTCAGTGATCGGTTCTCTGCAGAGAGGCCAAGGG ATCTTTCTCCACCTTGGAGATCCAGCGCACAGAGCAGGGGGACTCGGCCATGTATCTCTGTGCCAGCA GCTCCACCGACAGGATTGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
	297	ATGGGCACCTCCCTGCTGTGCTGGATGGCACTGTGCCTGCTGGGAGCAGACCACGCAGATACAGGCGT GTCTCAGGACCCACGCCACAAGATCACCAAGCGGGGCCAGAACGTGACATTCAGATGCGATCCCATCT CCGAGCACAAATAGGCTGTACTGGTATAGGCAGACCCTGGGACAGGGACCAGAGTTCTGACATACTTT CAGAACGAGGGCCAGCTGGAGAAGAGCCGGCTGCTGTCCGACAGATTCTCTGCCGAGAGGCCCAAGGG CTCTTTTAGCACCTTGGAGATCCAGAGAACAGAGCAGGGCGACAGCGCCATGTATCTGTGCGCCAGCT CCTCTACCGATAGGATCGAGGCCTTCTTTGGCCAGGGCACCCGCTGACAGTGGTG
	298	MGTSLLCWMALCLLGADHADTGVSQDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYF QNEAQLEKSRLLSDRFSAERPKGFSSTLEIQRTQGD SAMYLCASSSTDRIEAFQGGTRLTVV
RAS TCR-13 alpha chain	299	MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCYDTSSESDYYLFWYKQPPSRQMILV IRQEAQKQONATENRFSVNFQKAASKSFLKISDSQLGDAAMYFCALYIYGGSQGNLIFGKGTKLSVKP DIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQ TSFTCQDIFKETNATYPSSDVPFCDATLTEKSFETDMNLNFQNL SVMGLRIILLKVAGFNLLMTLRLWS S
RAS TCR-13 beta chain	300	MGTSLLCWMALCLLGADHADTGVSQDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYF QNEAQLEKSRLLSDRFSAERPKGFSSTLEIQRTQGD SAMYLCASSSTDRIEAFQGGTRLTVVKDLR NVTPPKVSLFEPKAEIANQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCL SSRLRVSAFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQVLS ATILYEILLGKATLYAVLVSLGLVLMAMVKKNS
	301	VVGADGVGK
TCR Peptides	302	VVGADGVGK
RAS TCR-14 alpha chain CDR1	303	VSNAYN
RAS TCR-14 alpha chain CDR2	304	GSKP
RAS TCR-14 alpha chain CDR3	305	ATYNFNKFY
RAS TCR-14 beta chain CDR1	306	SGHTS
RAS TCR-14 beta chain CDR2	307	YDEGEE
RAS TCR-14 beta chain CDR3	308	ASTTFKTKGRAIEKLF

Name	SEQ ID NO	Sequence
RAS TCR-14 alpha chain variable domain	309	ATGGCTTTGCAGAGCACTCTGGGGGCGGTGTGGCTAGGGCTTCTCCTCAACTCTCTCTGGAAGGTTGC AGAAAGCAAGGACCAAGTGTTCAGCCTTCCACAGTGGCATCTTCAGAGGGAGCTGTGGTGGAAATCT TCTGTAATCACTCTGTGTCCAATGCTTACAACCTTCTTCTGGTACCTTCACTTCCCGGGATGTGCACCA AGACTCCTTGTAAAGGCTCAAAGCCTTCTCAGCAGGGACGATACAACATGACCTATGAACGGTTCTC TTCATCGCTGCTCATCCTCCAGGTGCGGGAGGCAGATGCTGCTGTTTACTACTGTGCTACGTACAACCT TCAACAAATTTTACTTTGGATCTGGGACCAAACCTCAATGTAAAACCA
	310	ATGGCCCTGCAGTCTACACTGGGAGCCGTGTGGCTGGGACTGCTGCTGAACCTCTCTGTGGAAGGTGGC CGAGAGCAAGGACCAGGTGTCCAGCCTAGCACCGTGGCCTCCTCTGAGGGAGCAGTGGTGGAGATCT TTTGCAATCACTCCGTGTCTAACGCCTACAATTTCTTTTGGTATCTGCACCTTCCAGGATGTGCACCA AGGCTGCTGGTGAAGGGCAGCAAGCCATCCAGCAGGGCCGGTACAACATGACCTATGAGAGATTGAG CTCCTCTGCTGATCCTGCAGGTGAGAGAGGCCGATGCCGCCGTGTACTATTGTGCCACCTACAACCT TTAATAAGTTCTATTTTGGCTCCGGCACAAGCTGAATGTGAAGCCT
	311	MALQSTLGAVWLGLLLNSLWKVAESKDQVFQPSSTVASSEGAVVEIFCNHVSNSAYNFFWYLHFPGCAP RLLVKGSKPSQQGRYNMTYERFSSLLILQVREADAAVYYCATYNFNKFYFGSGTKLNVKP
RAS TCR-14 beta chain variable domain	312	ATGGGACCCAGGCTCCTCTTCTGGGCACCTGCTTTGTCTCCTCGGAACAGGCCAGTGGAGGCTGGAGT CACACAAAGTCCACACACCTGATCAAAACGAGAGGACAGCAAGCGACTCTGAGATGCTCTCCTATCT CTGGGCACACCAGTGTGTACTGGTACCAACAGGCCCTGGGTCTGGGCCTCCAGTTCTCTCTTTGGTAT GACGAGGGTGAAGAGAGAAACAGAGGAACTTCCCTCCTAGATTTTCAGGTCGCGCAGTTCCCTAATTA TAGCTCTGAGCTGAATGTGAACGCCTTGGAGCTGGAGGACTCGGCCCTGTATCTCTGTGCCAGCACCA CTTTTAAGACGGGACGGGCAATTGAAAACTGTTTTTGGCAGTGGAACCCAGCTCTCTGTCTTG
	313	ATGGGACCAAGGCTGCTGTTCTGGGCACCTGCTGTGCCTGCTGGGAACCGGACCTGTGGAGGCCGGCGT GACCCAGTCTCCAACACACCTGATCAAGACCAGGGGACAGCAGGCCACACTGAGGTGTAGCCCCATCT CCGGCCACACAAGCGTGTACTGGTATCAGCAGGCCCTGGGACTGGGACTGCAGTTCTCTGCTGTGGTAC GACGAGGGCGAGGAGAGGAACCGCGGCAATTTCCACCTCGGTTACGCGGCCGGCAGTTTCCCAACTA CAGCTCCGAGCTGAACGTGAATGCCCTGGAGCTGGAGGACAGCGCCCTGTATCTGTGCGCCTCCACCA CATTCAAGACCGGCAGGGCCATCGAGAAGCTGTTCTTTGGCTCTGGCACCCAGCTGAGCGTGCTG
	314	MGPRLFWALLCLLGTGPVEAGVTQSPHLLIKTRGQATLRCSPISGHTSVYWYQQALGLGLQFLWY DEGEERNRGNFPPRFSGRQFPNYSSELNVNALELEDSALYLCASTTFKTGRAIEKLFFGSGTQLSVL
RAS TCR-14 alpha chain	315	MALQSTLGAVWLGLLLNSLWKVAESKDQVFQPSSTVASSEGAVVEIFCNHVSNSAYNFFWYLHFPGCAP RLLVKGSKPSQQGRYNMTYERFSSLLILQVREADAAVYYCATYNFNKFYFGSGTKLNVKPDQNP AVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSDDVPCDALTLEKSFETDMNLNFQNLVSMGLRILLLKLVAGFNLLMTLRLWSS
RAS TCR-14 beta chain	316	MGPRLFWALLCLLGTGPVEAGVTQSPHLLIKTRGQATLRCSPISGHTSVYWYQQALGLGLQFLWY DEGEERNRGNFPPRFSGRQFPNYSSELNVNALELEDSALYLCASTTFKTGRAIEKLFFGSGTQLSVLK DLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYS YCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYHQG VLSATILYEILLGKATLYAVLVSGVLVLMAMVKKNS
TCR peptide	317	VVGADGVGK
	318	VVVGADGVGK
RAS TCR-15 alpha chain CDR1	319	TSGFNG
RAS TCR-15 alpha chain CDR2	320	NVLDGL
RAS TCR-15 alpha chain CDR3	321	AVRDRGGSYIPT
RAS TCR-15 beta chain CDR1	322	MNHEY
RAS TCR-15 beta chain CDR2	323	SMNVEV
RAS TCR-15 beta chain CDR3	324	ASSSRGHSGTEAF

Name	SEQ ID NO	Sequence
RAS TCR-15 alpha chain variable domain	325	ATGTGGGGAGTTTTCCTTCTTTATGTTTCCATGAAGATGGGAGGCACTACAGGACAAAACATTGACCA GCCCACTGAGATGACAGCTACGGAAGGTGCCATTGTCCAGATCAACTGCACGTACCAGACATCTGGGT TCAACGGGCTGTTCTGGTACCAGCAACATGCTGGCGAAGCACCCACATTTCTGTCTTACAATGTTCTG GATGGTTTGGAGGAGAAAGGTCGTTTTTCTTCATTCTTAGTCGGTCTAAAGGGTACAGTTACCTCCT TTTGAAGGAGCTCCAGATGAAAGACTCTGCCTCTTACCTCTGTGCTGTGAGAGATCGAGGAGGAAGCT ACATACCTACATTTGGAAGAGGAACAGCCTTATTGTTTCATCCG
	326	ATGTGGGGCGTGTTCCTGCTGTACGTGTCTATGAAGATGGGCGGCACCACAGGCCAGAACATCGACCA GCCTACCGAGATGACCGCCACAGAGGGCGCCATCGTGCAGATCAACTGCACCTACCAGACATCTGGCT TCAATGGCCTGTTTTGGTATCAGCAGCAGCCGGCGAGGCCCAACATTCCTGTCTATAATGTGCTG GATGGCCTGGAGGAGAAGGGCAGGTTCTCTAGCTTTCTGTCCCGCTCTAAGGGCTACAGCTATCTGCT GCTGAAGGAGCTGCAGATGAAGGACAGCGCCTCTACCTGTGCGCCGTGCGGGATAGAGGAGGCTCCT ATATCCCTACCTTTGGCCGGGCACATCTCTGATCGTGACCCCA
	327	MWGVFLLYVSMKMGTTGQNIQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRKGYSYLLKELQMKDSASYLCAVRDRGGSYIPTFGRGTS LIVHP
RAS TCR-15 beta chain variable domain	328	ATGGGCCCCAGCTCCTTGGCTATGTGGTCTTTGCCTTCTAGGAGCAGGCCCTTGAAGCCCAAGT GACCCAGAACCCAAAGATACCTCATCACAGTGACTGGAAAGAGTTAACAGTGACTTGTTCTCAGAATA TGAACCATGAGTATATGTCCTGGTATCGACAAGACCCAGGGCTGGGCTTAAGGCAGATCTACTATTCA ATGAATGTTGAGGTGACTGATAAGGGAGATGTTCTGAAGGGTACAAAGTCTCTCGAAAAGAGAAGAG GAATTTCCCTGATCCTGGAGTCGCCAGCCCCAACAGACCTCTCTGTACTTCTGTGCCAGCAGTT CCAGGGGGCATTGCGGCACTGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
	329	ATGGGACCACAGCTGCTGGGATACGTGGTGTCTGCCTGCTGGGAGCAGGACCACTGGAGGCACAGGT GACCCAGAACCCACGGTATCTGATCACCGTGACAGGCAAGAAGCTGACCGTGACATGTTCTCAGAACA TGAATCACGAGTACATGAGCTGGTATAGGCAGGACCCTGGACTGGGACTGAGACAGATCTACTATAGC ATGAATGTGGAGGTGACCGACAAGGGCGATGTGCCCCGAGGGCTACAAGGTGTCCAGGAAGGAGAAGCG CAACTTCCCTCTGATCCTGGAGTCCCCATCTCCAATCAGACCAGCCTGTATTTTTCGCGCCAGCTCCT CTAGGGGACACTCCGGAACAGAGGCCTTCTTTGGCCAGGGCACCAGGCTGACAGTGGTG
	330	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTSLYFCASSSRGHS GTEAFFGQGT RLTVV
RAS TCR-15 alpha chain	331	MWGVFLLYVSMKMGTTGQNIQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVL DGLEEKGRFSSFLSRKGYSYLLKELQMKDSASYLCAVRDRGGSYIPTFGRGTS LIVHPDIQNPEPA VYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMTLRLWSS
RAS TCR-15 beta chain	332	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTSLYFCASSSRGHS GTEAFFGQGT RLTVVKDL RNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYC LSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGV SATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS
TCR Peptides	333	VVGADGVGK
	334	VVVGADGVGK
RAS TCR-16 alpha chain CDR1	335	TSINN
RAS TCR-16 alpha chain CDR2	336	IRSNERE
RAS TCR-16 alpha chain CDR3	337	AGLYSSASKII
RAS TCR-16 beta chain CDR1	338	MNHEY
RAS TCR-16 beta chain CDR2	339	SMNVEV
RAS TCR-16 beta chain CDR3	340	ASSSRGHS GTEAF

Name	SEQ ID NO	Sequence
RAS TCR-16 alpha chain variable domain	341	ATGGAAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAATGCCACCATGAAGTGCAGTTACA AACTAGTATATAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTTGTCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAACACAGTGAAGATTAAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTGGGCTGTACA GCAGTGCTTCCAAGATAATCTTTGGATCAGGGACCAGACTCAGCATCCGGCCA
	342	ATGGAGACACTGCTGGGCGTGTCCCTGGTCATCCTGTGGCTGCAGCTGGCCAGAGTGAACAGCCAGCA GGGAGAGGAGGACCCTCAGGCCTTGAGCATCCAGGAGGGCGAGAACGCCACCATGAATTGCTCTTACA AGACAAGCATCAACAATCTGCAGTGGTATAGGCAGAACTCCGGCCGCGGACTGGTGCACCTGATCCTG ATCAGGTCTAATGAGCGCGAGAAGCACAGCGGGCCGGCTGAGAGTGACCCTGGACACAAGCAAGAAGTC TAGTCCCTGCTGATCACGCCTCCAGAGCAGCAGATACAGCCTCTTACTTCTGTGCTGGGCTGTATT CTAGCGCTCCAAGATCATCTTTGGCAGCGGCACCCGGCTGTCCATCAGACCC
	343	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSSSLITASRAADTASYFCAGLYSSASKIIFGSGTRLISIRP
RAS TCR-16 beta chain variable domain	344	ATGGGCCCCAGCTCCTTGGCTATGTGGTCTTTGCCTTCTAGGAGCAGGCCCCCTGGAAGCCCAAGT GACCCAGAACCCAGATACCTCATCACAGTGACTGGAAAGAGTTAACAGTGACTTGTTCTCAGAATA TGAACCATGAGTATATGTCTTGGTATCGACAAGACCCAGGGCTGGGCTTAAGGCAGATCTACTATTCA ATGAATGTTGAGGTGACTGATAAGGGAGATGTTCTGAAGGGTACAAAGTCTCTCGAAAAGAGAAGAG GAATTTCCCTGATCCTGGAGTCGCCAGCCCCAACAGACCTCTCTGTACTTCTGTGCCAGCAGTT CCAGGGGGCATTCGGGCACTGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
	345	ATGGGCCCCAGCTGCTGGGCTACGTGGTGCTGTGCCTGCTGGGAGCAGGACCCTGGAGGCACAGGT GACCCAGAACCCAGGTATCTGATCACCGTGACAGGCAAGAAGCTGACCGTGACATGTAGCCAGAACA TGAATCACGAGTACATGTCTTGGTATAGGCAGGACCCCGGACTGGGACTGAGACAGATCTACTATTCC ATGAATGTGGAGGTGACCGACAAGGGCGATGTGCCTGAGGGCTACAAGGTGTCTAGGAAGGAGAAGCG CAACTTCCCACTGATCCTGGAGTCCCCATCTCCAATCAGACCTCCCTGTATTTTGCGCCAGCTCCT CTAGGGGCCACTCTGGCACAGAGGCCTTCTTTGGCCAGGGCACCAGGCTGACAGTGGTG
	346	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTS L YFCASSSRGHSGTEAFFGQGT RLTVV
RAS TCR-16 alpha chain	347	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSSSLITASRAADTASYFCAGLYSSASKIIFGSGTRLISIRPD IQNP EPAVYQLKDP RSQDSTLCLFDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSN GAIAWSNQTSFTC QDIFKETNATY P SSDVPCDALTLEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMTLRLWSS
RAS TCR-16 beta chain	348	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTS L YFCASSSRGHSGTEAFFGQGT RLTVVKDL RNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYC LSSRLRSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGITSASYHQGV L SATILYEILLGKATLYAVLVSGVLVLMAMVKKNS
TCR Peptides	349	VVGADGVGK
	350	VVVGADGVGK
RAS TCR-17 alpha chain CDR1	351	NIATNDY
RAS TCR-17 alpha chain CDR2	352	GYKTK
RAS TCR-17 alpha chain CDR3	353	LANTGGFKTI
RAS TCR-17 beta chain CDR1	354	SGHVS
RAS TCR-17 beta chain CDR2	355	FQNEAQ
RAS TCR-17 beta chain CDR3	356	ATYKVGDEQF

Name	SEQ ID NO	Sequence
RAS TCR-17 alpha chain variable domains	357	ATGAGGCAAGTGGCGAGAGTGATCGTGTTCCTGACCCTGAGTACTTTGAGCCTTGCTAAGACCACCCA GCCCATCTCCATGGACTCATATGAAGGACAGAAGTGAACATAACCTGTAGCCACAACAACATTGCTA CAAATGATTATATCACGTGGTACCAACAGTTTCCCAGCCAAGGACCACGATTTATTATTCAAGGATAC AAGACAAAAGTTACAAACGAAGTGGCCTCCCTGTTTATCCCTGCCGACAGAAAGTCCAGCACTCTGAG CCTGCCCCGGGTTTCCCTGAGCGACACTGCTGTGTACTACTGCCTCGCTAATACTGGAGGCTTCAAAA CTATCTTTGGAGCAGGAACAAGACTATTTGTTAAAGCA
	358	ATGAGGCAGGTGGCACGCGTGATCGTGTTCCTGACCCTGAGCACACTGTCCCTGGCCAAGACCACACA GCCTATCTCTATGGACAGCTACGAGGGCCAGGAGGTGAACATCACCTGCTCTACAACAATATCGCCA CCAATGATTACATCACATGGTATCAGCAGTTCCCCAGCCAGGGCCCTCGGTTTATCATCCAGGGCTAT AAGACCAAGGTGACAAACGAGGTGGCCAGCCTGTTTCATCCCTGCCGACAGGAAGTCTAGCACCCCTGTC CCTGCCACGCGTGAGCCTGTCCGATACAGCGTGTACTATTGTCTGGCCAATACCGGCGGGCTTCAAGA CAATCTTTGGCGCCGGCACAGACTGTTTGTGAAGGCC
	359	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGY KTKVTNEVASLFI PADRKSSLSLPRVSLSDTAVYYCLANTGGFKTIFGAGTRLFVKA
RAS TCR-17 beta chain variable domains	360	ATGGGCACCAGGCTCCTCTGCTGGGTGGTCTGGGTTTCTTAGGGACAGATCACACAGGTGCTGGAGT CTCCAGTCCCCTAGGTACAAAGTCGAAAGAGAGGACAGGATGTAGCTCTCAGGTGTGATCCAATTT CGGGTCATGTATCCCTTTTTTGGTACCAACAGGCCCTGGGGCAGGGGCCAGAGTTTCTGACTTATTTT CAGAATGAAGCTCAACTAGACAAATCGGGGCTGCCAGTGATCGCTTCTTTGCAGAAAGGCCTGAGGG ATCCGTCTCCACTCTGAAGATCCAGCGCACACAGCAGGAGGACTCCGCCGTGTATCTCTGTGCCACCT ATAAGGTCGGGGATGAGCAGTTCTTCGGGGCCAGGGACACGGCTCACCGTGCTA
	361	ATGGGAACCAGGCTGCTGTGCTGGGTGGTGTGGGCTTCTGGGAACCGACCACACAGGAGCAGGCGT GTCCCAGTCTCCAAGGTACAGGTGGCAAAGAGGGGACAGGACGTGGCCCTGAGATGTGATCCTATCT CCGGCCACGTGTCTCTGTTTGGTACCAGCAGGCCCTGGGACAGGGACCTGAGTTCTGACCTATTTT CAGAACGAGGCACAGCTGGACAAGAGCGGACTGCCATCCGATCGGTTCTTTGCAGAGAGACCAGAGGG CAGCGTGTCCACCCTGAAGATCCAGAGGACACAGCAGGAGGACTCCGCCGTGTACCTGTGCCACAT ATAAAGTGGGCGATGAGCAGTTCTTTGGCCAGGCACCCGGCTGACAGTGCTG
	362	MGTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPI SGHVSFLWYQQALQGQPEFLTYF QNEAQLDKSGLPSDRFFAERPEGSVSTLKIQRTOQEDSAVYLCATYKVGDEQFFGPGTRLTVL
RAS TCR-17 alpha chain	363	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGY KTKVTNEVASLFI PADRKSSLSLPRVSLSDTAVYYCLANTGGFKTIFGAGTRLFVKADIQNEPAVY QLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATALTEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMTLRLWSS
RAS TCR-17 beta chain	364	MGTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPI SGHVSFLWYQQALQGQPEFLTYF QNEAQLDKSGLPSDRFFAERPEGSVSTLKIQRTOQEDSAVYLCATYKVGDEQFFGPGTRLTVLKDRLN VTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGVLSA TILYEILLGKATLYAVLVSLVLMAMVKKKNS
TCR Peptides	365	VVGADGVGK
	366	VVVGADGVGK
RAS TCR-18 alpha chain CDR1	367	DSASNY
RAS TCR-18 alpha chain CDR2	368	IRSNVGE
RAS TCR-18 alpha chain CDR3	369	AETGFQKLIV
RAS TCR-18 beta chain CDR1	370	MDHEN
RAS TCR-18 beta chain CDR2	371	SYDVKM
RAS TCR-18 beta chain CDR3	372	ASSDWLAGAKDEQY

Name	SEQ ID NO	Sequence
RAS TCR-18 alpha chain variable domains	373	ATGACATCCATTTCGAGCTGTATTTATATTCCTGTGGCTGCAGCTGGACTTGGTGAATGGAGAGAATGT GGAGCAGCATCCTTCAACCTGAGTGTCCAGGAGGGAGACAGCGCTGTTATCAAGTGTACTTTATTCAG ACAGTGCCTCAAACCTACTTCCCTTGGTATAAGCAAGAACTTGGAAAAAGACCTCAGCTTATTATAGAC ATTCGTTCAAATGTGGGCGAAAAGAAAGACCAACGAATTGCTGTTACATTGAACAAGACAGCCAAACA TTTCTCCCTGCACATCACAGAGACCAACCTGAAGACTCGGCTGTCTACTTCTGTGCAGAAACAGGCT TTCAGAACTTGTATTTGGAAGTGGCACCCGACTTCTGGTCAGTCCA
	374	ATGACATCTATCCGCGCCGTGTTTCATCTTTCTGTGGCTGCAGCTGGACCTGGTGAACGGCGAGAATGT GGAGCAGCACCCCAAGCACCTGTCCGTGCAGGAGGGCGACAGCGCCGTGATCAAGTGCACATACTCTG ATAGCGCCTCCAACCTACTTTCCCTGGTATAAGCAGGAGCTGGGCAAGCGGCCTCAGCTGATCATCGAC ATCAGATCCAACGTGGGCGAGAAGAAGGATCAGCGGATCGCCGTGACCCTGAATAAGACAGCCAAGCA CTTCAGCCTGCACATCACGAGACACAGCCGAGGATTCCGCCGTGTATTTTGTGCCGAGACCGGCT TCCAGAAGCTGGTGTGTTGGCACCGGCACAAGACTGCTGGTGTCCCCCT
	375	MTSIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKRPQLIID IRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAETGFQKL VFGTGRLLVSP
RAS TCR-18 beta chain variable domains	376	ATGGGAATCAGGCTCCTCTGTCGTGTGGCCTTTTGTTCCTGGCTGTAGGCCTCGTAGATGTGAAAGT AACCAGAGCTCGAGATATCTAGTCAAAAGGACGGGAGAGAAAGTTTTTCTGGAATGTGTCCAGGATA TGGACCATGAAAATATGTTCTGGTATCGACAAGACCCAGGTCTGGGGCTACGGCTGATCTATTCTCA TATGATGTTAAAATGAAAGAAAAAGGAGATATTCCTGAGGGGTACAGTGTCTCTAGAGAGAAGAAGGA GCGCTTCTCCCTGATTCTGGAGTCCGCCAGCACAACAGACATCTATGTACCTCTGTGCCAGCAGTG ACTGGCTAGCGGGAGCGAAGGACGAGCAGTACTTCGGGCCGGGCACCAGGCTCACGGTCACA
	377	ATGGGCATCCGGCTGCTGTGCAGAGTGGCCTTCTGTTTTCTGGCCGTGGGCCTGGTGGACGTGAAGGT GACCCAGAGCTCCCGGTACCTGGTGAAGAGAACAGGCGAGAAAGTGTTCCTGGAGTGCCTGCAGGACA TGGATCACGAGAACATGTTTTGGTATAGGCAGGACCCCGGACTGGGACTGAGACTGATCTACTTCAGC TATGACGTGAAGATGAAGGAGAAGGGCGACATCCCAGAGGGCTACAGCGTGTCCAGGGAGAAGAAGGA GCGGTTTCAAGCTGATCCTGGAGTCTGCCAGCACAATCAGACAAGCATGTACCTGTGCGCCTCTAGCG ACTGGCTGGCCGGAGCAAAGGATGAGCAGTATTTTCGGCCCAGGCACCAGGCTGACCGTGACA
	378	MGIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWRQDPGLGLRLIYFS YDVKMKEKGDIP EGYSVSREKKERFSLI LESASTNQTSMYLCASSDWLAGAKDEQYFGPGTRRLTVT
RAS TCR-18 alpha chain	379	MTSIRAVFIFLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKRPQLIID IRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAETGFQKL VFGTGRLLVSPDIQNPEP AVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSDDVPCDALTLEKSFETDMNLNFQNL SVMGLRILLKLVAGFNLLMTLRLWSS
RAS TCR-18 beta chain	380	MGIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWRQDPGLGLRLIYFS YDVKMKEKGDIP EGYSVSREKKERFSLI LESASTNQTSMYLCASSDWLAGAKDEQYFGPGTRRLTVTKD LRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSY CLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGV LSATILYEILLGKATLYAVLVSGLVLMAMVKKNS
TCR peptides	381	VVGADGVGK
	382	VVVGADGVGK
RAS TCR-19 alpha chain CDR1	383	TSINN
RAS TCR-19 alpha chain CDR2	384	IRSNERE
RAS TCR-19 alpha chain CDR3	385	ATDPLDYKLS
RAS TCR-19 beta chain CDR1	386	MNHEY
RAS TCR-19 beta chain CDR2	387	SMNVEV
RAS TCR-19 beta chain CDR3	388	ASSLVASNEQF

Name	SEQ ID NO	Sequence
RAS TCR-19 alpha chain variable domains	389	ATGGAAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAAATGCCACCATGAACTGCAGTTACA AACTAGTATATAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTTGTCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAACACAGTGAAGATTAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTACGGACCCCT TAGACTACAAGCTCAGCTTTGGAGCCGGAACACAGTAACGTGAAGAGCA
	390	ATGGAGACCCTGCTGGGCGTGTCTCTGGTCATCCTGTGGCTGCAGCTGGCCAGAGTGAACCTCTCAGCA GGGAGAGGAGGACCCTCAGGCCTTGAGCATCCAGGAGGGCGAGAACGCCACCATGAATTGCTCTTACA AGACAAGCATCAACAATCTGCAGTGGTATCGGCAGAACTCCGGCAGAGGCCCTGGTGCACCTGATCCTG ATCAGGAGCAATGAGCGCGAGAAGCACTCCGGCCGGCTGAGAGTGACCCTGGACACATCTAAGAAGTC CTCTAGCCTGCTGATCACCGCCTCTAGGGCAGCAGATACAGCCAGCTACTTCTGTGCCACCGACCCAC TGGATTATAAGCTGTCCTTTGGCGCCGGCACCACAGTGACCGTGCGCGCC
	391	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSS SLLITASRAADTASYFCATDPLDYKLSFGAGTTVTVRA
RAS TCR-19 beta chain variable domains	392	ATGGGCCCCAGCTCCTTGCTATGTGGTCTTTGCCTTCTAGGAGCAGGCCCCCTGGAAGCCCAAGT GACCCAGAACCCAAGATACCTCATCACAGTGACTGGAAAGAGTTAACAGTGACTTGTTCTCAGAATA TGAACCATGAGTATATGTCTTGGTATCGACAAGACCCAGGGCTGGGCTTAAGGCAGATCTACTATTCA ATGAATGTTGAGGTGACTGATAAGGGAGATGTTCTGAAGGGTACAAAGTCTCTCGAAAAGAGAAGAG GAATTTCCCGCTGATCCTGGAGTCGCCAGCCCCAACCCAGACCTCTCTGTACTTCTGTGCCAGCAGTT TGGTGGCTAGCAATGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
	393	ATGGGCCCCAGCTGCTGGGCTACGTGGTGTGTGCCTGCTGGGAGCAGGACCACTGGAGGCACAGGT GACCCAGAAATCCCGGTATCTGATCACCGTGACAGGCAAGAAGCTGACCGTGACATGTTCCCAAGACA TGAATCACAGTACATGTCTTGGTATAGGCAGGACCCCGGACTGGGACTGAGGCAGATCTACTATTCT ATGAACGTGGAGGTGACAGACAAGGGCGATGTGCCTGAGGGCTACAAGGTGAGCAGGAAGGAGAAGCG CAACTTCCCACTGATCCTGGAGTCCCCATCTCCAATCAGACCAGCCTGTATTTTTCGCCAGCTCCC TGGTGGCCTCCAACGAGCAGTTCTTTGGCCCTGGCACCCGGCTGACAGTGCTG
	394	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTS L YFCASSLVASNEQFFGPGTRLTVL
RAS TCR-19 alpha chain	395	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSS SLLITASRAADTASYFCATDPLDYKLSFGAGTTVTVRADIQNPE PAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNSGAIASWNSQTSFTCQ DIFKETNATYPS SDVPCDALT EKS FETDMNLNFQNL SVMGLRILL LK VAGFNLLMTLRLWSS
RAS TCR-19 beta chain	396	MGPQLLGYVVLCLLGAGPLEAQVTQNPRLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYS MNVEVTDKGDVPEGYKVS RKEKRNFLI LESPSPNQTS L YFCASSLVASNEQFFGPGTRLTVLKD L RN VTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLS SRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQVLSA TILYEI LLGKATLYAVLVSGVLVLMAMVKKKNS
TCR Peptides	397	VVGAVGVGK
	398	VVGAVGVGK
RAS TCR-20 alpha chain CDR1	399	TSESDYY
RAS TCR-20 alpha chain CDR2	400	QEAYKQQN
RAS TCR-20 alpha chain CDR3	401	ACQGGSEKLV
RAS TCR-20 beta chain CDR1	402	SGHNT
RAS TCR-20 beta chain CDR2	403	YYREEE
RAS TCR-20 beta chain CDR3	404	ASSLGLLLYNEQF

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RAS TCR-20 alpha chain variable domains	405	ATGGCATGCCCTGGCTTCCTGTGGGCACCTTGATCTCCACCTGTCTTGAATTTAGCATGGCTCAGAC AGTCACTCAGTCTCAACCAGAGATGTCTGTGCAGGAGGCAGAGACCGTGACCTGTAGCTGCACATATG ACACCAAGTGAGAGTGATTATTTATTCTGGTACAAGCAGCCTCCCAGCAGGCAGATGATTCTCGTT ATTCGCCAAGAAGCTTATAAGCAACAGAATGCAACAGAGAATCGTTTCTCTGTGAACCTCCAGAAAGC AGCCAAATCCTTCAGTCTCAAGATCTCAGACTCACAGCTGGGGGATGCCGCGATGTATTTCTGTGCTT GTCAGGGCGGATCTGAAAAGCTGGTCTTTGGAAAGGGAACGAACTGACAGTAAACCCA
	406	ATGGCATGCCAGGCTTCCTGTGGGCACCTGGTCATCAGCACCTGTCTGGAGTTTCTATGGCCCAGAC CGTGACACAGAGCCAGCCAGAGATGTCCGTGCAGGAGGCAGAGACCGTGACACTGTCTGTACCTACG ACACAAGCGAGTCCGATTACTATCTGTTCTGGTATAAGCAGCCTCCATCTCGCCAGATGATCCTGGTC ATCCGGCAGGAGGCCTACAAGCAGCAGAACGCCACCGAGAATCGGTTCTCTGTGAATTTTCAGAAAGGC CGCCAAAGTCTTTAGCCTGAAGATCTCCGACTCTCAGCTGGGCGATGCCGCCATGTATTTCTGCGCAT GTCAGGGAGGCAGCAGAGAAGCTGGTGTGTTGGCAAGGGCACCAAGCTGACAGTGAACCTT
	407	MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCYDTSSESDYYLFWYKQPPSRQMILV IRQEAAYKQONATENRFSVNFQKAASFSFLKISDSQLGDAAMYFCACQGGSEKLVFGKGTCLTVNP
RAS TCR-20 beta chain variable domains	408	ATGGGCCCTGGGCTCCTCTGCTGGGTGCTGCTTTGTCTCCTGGGAGCAGGCTCAGTGGAGACTGGAGT CACCCAAAGTCCACACACCTGATCAAAACGAGAGGACAGCAAGTGACTCTGAGATGCTCTTCTCAGT CTGGGCACAACACTGTGTCTGGTACCAACAGGCCCTGGGTGAGGGGCCCCAGTTTATCTTTTCAGTAT TATAGGGAGGAAGAGAATGGCAGAGGAACTTCCCTCCTAGATTCTCAGGTCTCCAGTTCCCTAATTA TAGCTCTGAGCTGAATGTGAACGCCTTGGAGCTGGACGACTCGGCCCTGTATCTCTGTGCCAGCAGCT TGGGACTCCTCCTCTACAATGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
	409	ATGGGACCAGGACTGCTGTGCTGGGTGCTGCTGTGCCTGCTGGGAGCAGGCAGCGTGGAGACCGGCGT GACACAGTCCCTACCCACCTGATCAAGACAAGAGGCCAGCAGGTGACCTGAGGTGCAGCTCCCAGT CTGGCCACAATACAGTGAGCTGGTACCAGCAGGCCCTGGGACAGGGACCTCAGTTCATCTTTTCAGTAC TATAGGGAGGAGGAGAACGGCCGCGGCAATTTCCCCCTCGGTTTAGCGGCCTGCAGTTCCTCAACTA TTCTAGCGAGCTGAACGTGAATGCCCTGGAGCTGGACGATTCCGCCCTGTACCTGTGCGCCTCCTCTC TGGGCCTGCTGCTGTATAACGAGCAGTTCTTTGGCCCCGGCACCAAGCTGACAGTGCTG
	410	MGPGLLCWVLLCLLGAGSVETGVTQSPHLLIKTRGQQVTLRCSSQSGHNTVSWYQQALGQGPQFIQY YREEENGRGNFPPRFSGLQFPNYSSELNVNALELDDSSALYLCASSLGLLLYNEQFFGPGTRLTVL
RAS TCR-20 alpha chain	411	MACPGFLWALVISTCLEFSMAQTVTQSQPEMSVQEAETVTLSCYDTSSESDYYLFWYKQPPSRQMILV IRQEAAYKQONATENRFSVNFQKAASFSFLKISDSQLGDAAMYFCACQGGSEKLVFGKGTCLTVNPDIQ NPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSSKNGAIAWSNQTSF TCQDIFKETNATYPSDDVPCDATLTEKSFETDMNLNFQNLVSMGLRILLKLVAGFNLLMTLRLWSS
RAS TCR-20 beta chain	412	MGPGLLCWVLLCLLGAGSVETGVTQSPHLLIKTRGQQVTLRCSSQSGHNTVSWYQQALGQGPQFIQY YREEENGRGNFPPRFSGLQFPNYSSELNVNALELDDSSALYLCASSLGLLLYNEQFFGPGTRLTVLKD LNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYC LSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSAHYHQGV SATILYEILGKATLYAVLVSGVLVLMAMVKKNS
TCR Peptides	413	VVGAVGVGK
	414	VVVGAVGVGK
RAS TCR-21 alpha chain CDR1	415	TSINN
RAS TCR-21 alpha chain CDR2	416	IRSNERE
RAS TCR-21 alpha chain CDR3	417	ATDAQTGANNLF
RAS TCR-21 beta chain CDR1	418	SGHAT
RAS TCR-21 beta chain CDR2	419	FQNNGV
RAS TCR-21 beta chain CDR3	420	ASSLGDSYEQYF

Name	SEQ ID NO	Sequence
RAS TCR-21 alpha chain variable domains	421	ATGGAAACTCTCCTGGGAGTGTCTTTGGTGATTCTATGGCTTCAACTGGCTAGGGTGAACAGTCAACA GGGAGAAGAGGATCCTCAGGCCTTGAGCATCCAGGAGGGTGAAAATGCCACCATGAAGTGCAGTTACA AACTAGTATAAACAATTTACAGTGGTATAGACAAAATTCAGGTAGAGGCCCTTGTCACCTAATTTTA ATACGTTCAAATGAAAGAGAGAAAACACAGTGAAGATTAAAGAGTCACGCTTGACACTTCCAAGAAAAG CAGTTCCTTGTTGATCACGGCTTCCCGGGCAGCAGACACTGCTTCTTACTTCTGTGCTACGGACGCTC AACTGGGGCAAACAACCTCTTCTTTGGGACTGGAACGAGACTCACCGTTATTCCC
	422	ATGGAGACACTGCTGGGCGTGTCTCTGGTCATCCTGTGGCTGCAGCTGGCCAGAGTGAATAGCCAGCA GGGAGAGGAGGACCCCCAGGCCTGTCCATCCAGGAGGGCGAGAACGCCACCATGAATTGCAGTACA AGACATCCATCAACAATCTGCAGTGGTATCGGCAGAACTCTGGCAGAGGCCCTGGTGCACCTGATCCTG ATCCGGTCCAATGAGAGAGAGAAGCACTCTGGCCGGCTGAGAGTGACCCTGGATACATCAAGAAGTC CTCTAGCCTGCTGATCACGCCAGCCGGGCAGACACAGCCTCCTATTTTGTGCCACCGATGCCC AGACAGGCCCAACAATCTGTTCTTTGGCACCGGCACAAGACTGACCGTGATCCCT
	423	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSSSLITASRAADTASYFCATDAQTGANNLFFGTGTRLTVIP
RAS TCR-21 beta chain variable domains	424	ATGGGCACCAGGCTCCTCTGCTGGGCGGCCCTCTGTCTCCTGGGAGCAGAACTCACAGAAGCTGGAGT TGCCCACTCTCCAGATATAAGATTATAGAGAAAAGGCAGAGTGTGGCTTTTGGTGCAATCCTATAT CTGGCCATGCTACCTTTACTGGTACCAGCAGATCCTGGGACAGGGCCCCAAAGCTTCTGATTCACTTT CAGAATAACGGTGTAGTGGATGATTACAGTTGCCTAAGGATCGATTTTCTGCAGAGAGGCTCAAAGG AGTAGACTCCACTCTCAAGATCCAGCCTGCAAAGCTTGAGGACTCGGCCGTGTATCTCTGTGCCAGCA GCTTA
	425	ATGGGCACCAGGCTGCTGTGCTGGGCGGCCCTGTGCCTGCTGGGAGCAGAGCTGACAGAGGCAGGAGT GGCCCAGAGCCCCAGGTACAGATCATCGAGAAGCGCCAGTCCGTGGCCTTCTGGTGCAACCTATCT CTGGCCACGCCACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGCCCCAAAGCTGCTGATCCAGTTC CAGAACAATGGCGTGGTGGACGATTCTCAGCTGCCCAAGGACAGGTTTAGCGCCGAGCGCCTGAAGGG CGTGGATTCTACCCTGAAGATCCAGCCAGCAAAGCTGGAGGACAGCGCCGTGTACCTGTGCCAGCT CCCTG
	426	MGTRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSL
RAS TCR-21 alpha chain	427	METLLGVSLVILWLQRLARVNSQQGEEDPQALS IQEENATMNC SYKTSINN LQWYRQNSGRGLVHLIL IRSNEREKHSGRRLRVTLDTSKSSSLITASRAADTASYFCATDAQTGANNLFFGTGTRLTVIPDIQN PEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSFT QDIFKETNATYPSSDVPCDALTLEKSFETDMNLNFQNL SVMGLRILLKLVAGFNLLMTLRWSS
RAS TCR-21 beta chain	428	MGTRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQF QNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLKDRLNVTPPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNP RNH FRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYHQGVLSATILYEILLGKATLYAV LVSGLVLMAMVKKKNS
TCR Peptides	429	VVGAVGVGK
	430	VVVGAVGVGK
RAS TCR-26 alpha chain CDR1	532	NSMFDY
RAS TCR-26 alpha chain CDR2	533	ISSIKDK
RAS TCR-26 alpha chain CDR3	534	AANAGGTSYGKLT
RAS TCR-26 beta chain CDR1	535	SNHLY
RAS TCR-26 beta chain CDR2	536	FYNNEI
RAS TCR-26 beta chain CDR3	537	ASSEWGSTGELF

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RAS TCR-26 alpha chain variable domain	538	atggccatgctcctgggggcatcagtgctgattctgtggcttcagccagactgggtaaacagtcaaca gaagaatgatgaccagcaagtttaagcaaaattccaccatccctgagcgtccaggaaggaagaatttcta ttctgaactgtgactatactaacagcatgtttgattatttccatggtacaaaaataccctgctgaa ggctctacattcctgatatctataagttccattaaggataaaaaatgaagatggaagattcactgtctt cttaacaaaagtgccaagcacctctctctgcacattgtgccctcccagcctggagactctgcagtg acttctgtgcagcaaatgctggtggtactagctatggaaagctgacatttggacaaggaccatcttg actgtccatccaa
	539	MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTN SMFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAANAGGTSYGKLTFGQGTL TVHP
RAS TCR-26 beta chain variable domain	540	atggatacctggctcgtatgctgggcaatttttagtctcttgaagcaggactcacagaacctgaagt caccagactcccagccatcaggtcacacagatgggacaggaagtgatcttgcgctgtgtcccatct ctaatacattatacttctatttggtacagacaaatcttggggcagaaagtcgagtttctggttctctt tataataatgaaatctcagagaagctctgaaatattcgatgatcaattctcagttgaaaggcctgatgg atcaaatttcactctgaagatccggtccacaaagctggaggactcagccatgtacttctgtgccagca gtgaatggggaagcaccggggagctgttttttggagaaggctctaggtgacctgactgg
	541	MDTWLVCWAI FSLKAGLTEPEVTQT PSHQVTQMGEVILRCVPI SNHLYFYWYRQILGQKVEFLVSF YNNEISEKSEIFDDQFSVERPDGSNFTLKI RSTKLEDSAMYFCASSEWGSGTGELFFGEGSRLTVL
RAS TCR-26 alpha chain	542	MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTN SMFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAANAGGTSYGKLTFGQGTL TVHPDIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIA WSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMTL RLWSS
RAS TCR-26 beta chain	543	MDTWLVCWAI FSLKAGLTEPEVTQT PSHQVTQMGEVILRCVPI SNHLYFYWYRQILGQKVEFLVSF YNNEISEKSEIFDDQFSVERPDGSNFTLKI RSTKLEDSAMYFCASSEWGSGTGELFFGEGSRLTVLKD LNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSY LS SRLRV SATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGITSASYHQGVL SATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
RAS TCR-26 peptide	544	VVGAVGVGK
RAS TCR-27 alpha chain CDR1	545	TTSDR
RAS TCR-27 alpha chain CDR2	546	LLSNGAV
RAS TCR-27 alpha chain CDR3	547	AVDIIGGKST
RAS TCR-27 beta chain CDR1	548	SNHLY
RAS TCR-27 beta chain CDR2	549	FYNNEI
RAS TCR-27 beta chain CDR3	550	ASSEWGSGTGELF
RAS TCR-27 alpha chain variable domain	551	atgaagaagctactagcaatgattctgtggcttcaactagaccggttaagtggagagctgaaagtgga acaaaaccctctgttctgagcatgcaggaggggaaaaactataccatctactgcaattattcaacca cttcagacagactgtattggtacaggcaggatcctgggaaaagtctggaatctctgtttgtgtgcta tcaaattggagcagtgaagcaggaggagacgattaatggcctcacttgataccaaagccgctctcagcac cctccacatcacagctgccgtgcatgacctctctgccacctacttctgtgccgtggacatcatcgagag gcaaatcaacccttggggatgggactacgctcactgtgaagccaa
	552	MKKLLAMI LWLQDLRLSGELKVEQNPLF LMSQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLES LFLVLL SNGAVKQEGRLMASLDTKARLSTLHITA AVHDL SATYFCAVDIIGGKSTFGDGTTLTVKP
RAS TCR-27 beta chain variable domain	553	atggatacctggctcgtatgctgggcaatttttagtctcttgaagcaggactcacagaacctgaagt caccagactcccagccatcaggtcacacagatgggacaggaagtgatcttgcgctgtgtcccatct ctaatacattatacttctatttggtacagacaaatcttggggcagaaagtcgagtttctggttctctt tataataatgaaatctcagagaagctctgaaatattcgatgatcaattctcagttgaaaggcctgatgg atcaaatttcactctgaagatccggtccacaaagctggaggactcagccatgtacttctgtgccagca gtgaatggggaagcaccggggagctgttttttggagaaggctctaggtgacctgactgg

Name	SEQ ID NO	Sequence
	554	MDTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGEVILRCVPI SNHLYFYWYRQILGQKVEFLVSF YNNEISEKSEIFDDQFSVERPDGSNFTLKI RSTKLEDSAMYFCASSEWGSGELFFGEGSRLTVL
RAS TCR-27 alpha chain	555	MKKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYWYRQDPGKSLESLEFVLL SNGAVKQEGRLMASLDTKARLSTLHITAAVHDL SATYFCAVDI IGGKSTFGDGTTLTVKPDIQNPEPA VYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMTLRLWSS
RAS TCR-27 beta chain	556	MDTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGEVILRCVPI SNHLYFYWYRQILGQKVEFLVSF YNNEISEKSEIFDDQFSVERPDGSNFTLKI RSTKLEDSAMYFCASSEWGSGELFFGEGSRLTVLKD L RNVTTPKVSLEFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSYC LSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGVL SATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
RAS TCR-27 peptide	557	VVGAVGVGK
RAS TCR-28 alpha chain CDR1	558	NSMFDY
RAS TCR-28 alpha chain CDR2	559	ISSIKDK
RAS TCR-28 alpha chain CDR3	560	AASAVGQEYGNKLV
RAS TCR-28 beta chain CDR1	561	SEHNR
RAS TCR-28 beta chain CDR2	562	FQNEAQ
RAS TCR-28 beta chain CDR3	563	ASSEYTMGTQY
RAS TCR-28 alpha chain variable domain	564	atggccatgctcctgggggcatcagtgctgattctgtggcttcagccagactgggtaaacagtcaca gaagaatgatgaccagcaagttaagcaaaattcaccatccctgagcgctccaggaaggaagaatttcta ttctgaactgtgactataactaacagcatgtttgattatttcctatggtacaaaaataccctgctgaa ggctctacattcctgatatactataagttccattaaggataaaaaatgaagatggaagattcactgtctt cttaaacaaaagtgcccaagcacctctctctgcacattgtgcctcccagcctggagactctgcagtg t acttctgtgcagcaagcgcagtaggtcaggaatatggaaacaagctggctctttggcgccaggaaccatt ctgagagtcgaagtcct
	565	MAMLLGASVLILWLQPDWVNSQQKNDDQVKQNSPSLSVQEGRISILNCDYTNMFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKS AKHLS LHIVPSQPGDSAVYFCAASAVGQEYGNKLVFGAGTI LRVKS
RAS TCR-28 beta chain variable domain	566	atggggcaccagcctcctctgctggatggcctgtgtctcctgggggcagatcacgcagatactggagt ctcccagaacccagacacaaagatcacaaagaggggacagaatgtaactttcaggtgtgatccaattt ctgaacacaaccgcctttattggtaccgacagaccctggggcagggcccagagtttctgacttacttc cagaatgaagctcaactagaaaaatcaaggctgctcagtgatcggttctctgcagagaggcctaaggg atctttctccaccttgagatccagcgcacagagcagggggactcgccatgtatctctgtgccagca gtgaatatactatgggggaccagctacttcggggccaggcacgcggctcctgggtgctcg
	567	MGTSLLCWMALCLLGADHADTGVSNPRHKITKRGQNVTFRCDFI SEHNRLYWYRQTLGQGPEFLTYF QNEAQLEKSRLSDRFS AERP KGSFSTLEIQ RTEQ GDSAMYLCASSEYTMGTQYFGPGTRLLVL
RAS TCR-28 alpha chain	568	MAMLLGASVLILWLQPDWVNSQQKNDDQVKQNSPSLSVQEGRISILNCDYTNMFDYFLWYKKYPAE GPTFLISISSIKDKNEDGRFTVFLNKS AKHLS LHIVPSQPGDSAVYFCAASAVGQEYGNKLVFGAGTI LRVKSDIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKSNGA I AWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRI LLLKVAGFNLLMT LRLWSS
RAS TCR-28 beta chain	569	MGTSLLCWMALCLLGADHADTGVSNPRHKITKRGQNVTFRCDFI SEHNRLYWYRQTLGQGPEFLTYF QNEAQLEKSRLSDRFS AERP KGSFSTLEIQ RTEQ GDSAMYLCASSEYTMGTQYFGPGTRLLVLKDLR NVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSYC LSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYHQGVL S ATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
RAS TCR-28 peptide	600	VVGAVGVGK

Name	SEQ ID NO	Sequence
GATA3 TCR-1 alpha chain CDR1	127	NYSPAY
GATA3 TCR-1 alpha chain CDR2	128	IRENEKE
GATA3 TCR-1 alpha chain CDR3	129	ALDIYGNRLA
GATA3 TCR-1 beta chain CDR1	130	MDHEN
GATA3 TCR-1 beta chain CDR2	131	SYDVKM
GATA3 TCR-1 beta chain CDR3	132	ASSLDFVLAGSYSYNEQF
GATA3 TCR-1 alpha chain variable domain	133	ATGGCTTTTGGCTGAGAAGGCTGGGTCTACATTTTCAGGCCACATTTGGGGGAGACGAATGGAGTCATTCCTGGGAGGTGTTTTGCTGATTTTGTGGCTTCAAGTGGACTGGGTGAAGAGCCAAAAGATAGAACAGAATTCGGAGGCCCTGAACATTCAGGAGGGTAAAACGGCCACCCTGACCTGCAACTATACAACTATTCTCCAGCATACTTACAGTGGTACCGACAAGATCCAGGAAGAGGCCCTGTTTTCTTGCTACTCATACGTGAAAATGAGAAAAGAAAAAGGAAAGAAAGACTGAAGGTACCTTTGATACCACCCTTAAACAGAGTTTGTTCATATCACAGCCTCCCAGCTGCAGACTCAGCTACCTACCTCTGTGCTCTAGACATTTATGGGAACAACAGACTCGCTTTTGGGAAGGGGAACCAAGTGGTGGTCATACCA
	134	ATGGCCTTCTGGCTGAGGAGACTGGGTTTACACTTCAGACCCCATTAGGCAGAAGAATGGAGAGCTTTTAGGCGGCGTGCTGCTGATTTTATGGCTGCAAGTTGACTGGGTGAAGAGCCAGAAGATCGAGCAGAACAGCGAGGCTTTAAACATTCAGAAGGCAAGACAGCCACTTTAACTTGTAACTATACCACTACTCCCCGCTTATTTACAGTGGTACAGACAAGATCCCGGCAGAGGCCCGTGTTTTACTGCTGATTCGTGAGAACGAGAAGGAGAAGAGGAAGGAGAGACTGAAGGTGACCTTCGACACCCTTAAAGCAGTCTTTATTCCACATCACCGCCAGCCAGCCGCTGATAGCGCCACCTATTATGCGCTTTAGACATCTACGGCAACAATCGTCTGGCCTTCGGCAAGGGCAACCAAGTTGTGGTGATCCCC
	135	MAFWLRRRLGLHFRPHLGRRMESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTLTKQSLFHITASQPADSATYLCALDIYGNRLAFGKGNQVVVI P
GATA3 TCR-1 beta chain variable domain	136	ATGGGAATCAGGCTCCTCTGTCGTGTGGCCTTTTGTTCCTGGCTGTAGGCCTCGTAGATGTGAAAGTAACCCAGAGCTCGAGATATCTAGTCAAAAGGACGGGAGAGAAAGTTTTCTGGAATGTGTCCAGGATATGACCATGAAAATATGTTCTGGTATCGACAAGACCCAGGTCTGGGGCTACGGCTGATCTATTTCTCATATGATGTTAAATGAAAGAAAAAGGAGATATTCCTGAGGGGTACAGTGTCTCTAGAGAGAAGAAGGAGCGCTTCTCCCTGATTCTGGAGTCCGCCAGCACCAACCAGACATCTATGTACCTCTGTGCCAGCAGTTTAGATTTTGTGCTAGCGGGTCTACTCTTACAATGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
	137	ATGGGCATTCTGCTGCTGTGTCGTGTGGCCTTCTGCTTTTATAGCCGTGGGTTTAGTGGACGTGAAGGTGACCCAGTCTCTCGTTATTTAGTGAAGAGGACCGGCAGAGAAGGTGTTTTAGAAATGCGTGCAAGATATGACCCAGTCAAGATGTTCTGGTACAGACAAGATCCCGGACTGGGTTTAAAGGTGATCTACTTCAGCTACGACGTGAAGATGAAGGAGAAGGGCGACATCCCCGAGGGCTACTCCGTGTCTCGTGAGAAGAAGGAGAGGTTCTCTTTAATTTTAGAGTCCGCCAGCACCAACCAGACCAGCATGTATTTATGCGCCAGCTCTTTAGACTTTGTGCTGGCCGGCAGCTACAGCTACAACGAGCAGTTCTTCGGCCCCGGCACCAGACTGACCGTGCTG
	138	MGIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLFECVQDMDHENMFWRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQTSMYLCASSLDFVLAGSYSYNEQFFGPGTRLTIVL
GATA3 TCR-1 alpha chain	139	MAFWLRRRLGLHFRPHLGRRMESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTLTKQSLFHITASQPADSATYLCALDIYGNRLAFGKGNQVVVI PDIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVVSQKSDSVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSIIPEDTFFPSPSSCDVKLVKESFETDTNLFQNLVIGFRILLKVAGFNLLMTLRLWSS
GATA3 TCR-1 beta chain	140	MGIRLLCRVAFCFILAVGLVDVKVTQSSRYLVKRTGEKVFLFECVQDMDHENMFWRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQTSMYLCASSLDFVLAGSYSYNEQFFGPGTRLTIVLEDLNKVFPPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWVWNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSAFQWQNPVHFRQVQFYGLSENDEWTQDRAKPVTVQIVSAEAWGRADCGFTSVSYQQGVLSATILYEILLGKATLYAVLVSAVLVLMAMVKRKDF
GATA3 TCR-1 peptide	141	MLTGPPARV

Name	SEQ ID NO	Sequence
GATA3 neoORF mutant protein	157	MRRLSAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLHNINRPLTMKKEGIQTRNRKMSSKS KKCKKVHDSLEDFFPKNSSFPGRPLQTHVLPEPHLALQPLQPHADHAHADAPAIQPVLTWTPPLQHGHRH GLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH
GATA3 neoORF sequence	158	PGRPLQTHVLPEPHLALQPLQPHADHAHADAPAIQPVLTWTPPLQHGHRHGLEPCSMLTGPPARVPAVP FDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH
GATA3 TCR-2 alpha chain CDR1	189	NSMFDY
GATA3 TCR-2 alpha chain CDR2	190	ISSIKDK
GATA3 TCR-2 alpha chain CDR3	191	AASASNNDMR
GATA3 TCR-2 beta chain CDR1	192	SEHNR
GATA3 TCR-2 beta chain CDR2	193	FQNEAQ
GATA3 TCR-2 beta chain CDR3	194	ASSQSGQGPYEQY
GATA3 TCR-2 alpha chain variable domain	195	ATGGCCATGCTCCTGGGGGCATCAGTGCTGATTCTGTGGCTTCAGCCAGACTGGGTAAACAGTCAACAG AAGAATGATGACCAGCAAGTTAAGCAAAATTCACCATCCCTGAGCGTCCAGGAAGGAAGAATTTCTATT CTGAACGTGTACTATACTAAGCATGTTTGATTATTTCTATGGTACAAAAATACCTGTCTGAAGGT CCTACATTCTCTGATATCTATAAGTTCCATTAAGGATAAAAAATGAAGATGGAAGATTCAGTGTCTTCTTA AACAAAAGTGCCAAGCACCTCTCTCTGCACATTGTGCCCTCCCAGCCTGGAGACTCTGCAGTGTACTTC TGTGCAGCAAGCGCGTCAAACAATGACATGCGCTTTGGAGCAGGGACCAGACTGACAGTAAACCA
	196	ATGGCAATGCTGCTGGGAGCCTCTGTGCTGATCCTGTGGCTGCAGCCAGATTGGGTGAACCTCCAGCAG AAGAATGACGATCAGCAGGTGAAGCAGAATAGCCCCCTCCCTGTCTGTGCAGGAGGGCAGAATCAGCATC CTGAACGTGCGACTACACCAATTCCATGTTTCGATTATTTCTGTGGTACAAGAAGTATCCAGCCGAGGGC CCACCTTTCTGATCAGCATCTCCTCTATCAAGGACAAGAACGAGGATGGCAGGTTACAGTGTCTTCTG AATAAGTCTGCCAAGCACCTGAGCCTGCACATCGTGCCATCCAGCCTGGCGACTCTGCCGTGTACTTC TGTGCCGCCAGCGCCTCCAACAATGATATGAGATTTGGCGCCGGCACCAGGCTGACAGTGAAGCCC
	197	MAMLLGASVLILWLQPDWVNSQQKNDDQVQKQNSPSLSVQEGRISILNCDYTNMFDYFLWYKKYPAEG PTFLISISSIKDKNEDGRFTVFLNLSAKHLSLHIVPSQPGDSAVYFCAASASNNDMRFGAGTRLTVKP
GATA3 TCR-2 beta chain variable domain	198	ATGGGCACCGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGCAGATCACGCAGATACTGGAGTC TCCCAGGACCCAGACACAAGATCACAAAGAGGGGACAGAATGTAACCTTCAGGTGTGATCCAATTTCT GAACACAACCGCCTTTATTGGTACCGACAGACCCTGGGGCAGGGCCCAGAGTTTCTGACTTACTTCCAG AATGAAGCTCAACTAGAAAAATCAAGGCTGCTCAGTGATCGGTTCTCTGCAGAGAGGCCAAGGGATCT TTCTCCACCTTGGAGATCCAGCGCACAGAGCAGGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCCAA TCGGGACAGGGGCCCTACGAGCAGTACTTCGGGCCGGGCACCAGGCTCACGGTCACAGAG
	199	ATGGGCACCTCTCTGCTGTGCTGGATGGCACTGTGCCTGCTGGGAGCAGACCACGCAGATACAGGCGTG AGCCAGGACCCCCGCCACAAGATCACCAAGCGGGGCCAGAACGTGACATTGAGATGCGATCCTATCTCC GAGCACAATAGGCTGTACTGGTATAGGCAGACCCTGGGACAGGGACCAGAGTTCCTGACATACTTTTCAG AACGAGGGCCAGCTGGAGAAGAGCCGGCTGCTGTCCGACAGATTCTCTGCCGAGAGGCCAAGGGCAGC TTTTCCACCCTGGAGATCCAGAGGACAGAGCAGGGCGATTCTGCCATGTATCTGTGCCAGCAGCTCCAG AGCGGACAGGGACCTTACGAGCAGTATTTTCGGACCAGGAACCAGGCTGACCGTGACAGAG
	200	MGTSLLCWMALCLLGADHADTGVSDPRHKITKRQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQ NEAQLEKSRLLSDRFSAPERPKGSFSTLEIQRTREQGDSAMYLCASSQSGQGPYEQYFPGPTRLTVTE
GATA3 TCR-2 alpha chain	201	MAMLLGASVLILWLQPDWVNSQQKNDDQVQKQNSPSLSVQEGRISILNCDYTNMFDYFLWYKKYPAEG PTFLISISSIKDKNEDGRFTVFLNLSAKHLSLHIVPSQPGDSAVYFCAASASNNDMRFGAGTRLTVKPD IQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKNSAVAWSNKSD FACANAFNNSIIPEDTFFPSPSSCDVKLVEKSFETDTNLFQNLVIGFRILLKLVAGFNLLMTLRLW SS

Name	SEQ ID NO	Sequence
GATA3 TCR-2 beta chain	202	MGTSLLCWMALCLLGADHDTGVSQDPRHKITKRQNVTFRCDPIS EHNRLYWYRQTLGQGPEFLTYFQ NEAQLEKSRLLSDRFSAERP KGSFSTLEIQRT EQGDSAMYL CASSQS GQGPEYEQYFGPGTRLT VTEEDL NKVFPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDS RYCLSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPV TQIVSAEAWGRADCGFTSVSYQQG VLSATILYEILLGKATLYAVLV SALVLMAMVKRKDF
GATA3 TCR-2 peptide	203	KPKRDGYMF
GATA3 TCR-3 alpha chain CDR1	204	YGGTVN
GATA3 TCR-3 alpha chain CDR2	205	YFSGDPLV
GATA3 TCR-3 alpha chain CDR3	206	AVISVTGNRRKLI
GATA3 TCR-3 beta chain CDR1	207	LNHDA
GATA3 TCR-3 beta chain CDR2	208	SQIVND
GATA3 TCR-3 beta chain CDR3	209	ASSRTAMNTEAF
GATA3 TCR-3 alpha chain variable domain	210	ATGCTCCTGTTGCTCATACCA GTGCTGGGGATGATTTT TGCCCTGAGAGATGCCAGAGCCCAGTCTGTG AGCCAGCAT AACCACCACGTAATCTCTCTGAAGCAGCCTCACTGGAGTTGGGATGCAACTATTCCCTAT GGTGGAAC TGTTAATCTCTTCTGGTATGTCCAGTACCCTGGTCAACACCTTCAGCTTCTCCTCAAGTAC TTTTCAGGGGATCCACTGGTTAAAGGCATCAAGGGCTT TGAGGCTGAATTTATAAAGAGTAAATTCTCC TTTAATCTGAGGAAACCTCTGTGCAGTGGAGTGACACAGCTGAGTACTTCTGTGCCGTGATCTCCGTG ACTGGCAACAACCGTAAGCTGATTTGGGGATTGGGAACAAGCCTGGCAGTAAATCCG
	211	ATGCTGCTGCTGCTGATCCCTGTGCTGGGCATGATCTTTGCACTGAGGGACGCAAGAGCACAGTCCGTG TCTCAGCACAACCACCACGTGATCCTGAGCGAGGCAGCCTCCCTGGAGCTGGGCTGCAACTACTCTTAT GGCGGCACAGTGAATCTGTTCTGGTACGTGCAGTATCCAGGCCAGCACCTGCAGCTGCTGCTGAAGTAC TTTAGCGGGCAGCCCTGGTGAAGGGCATCAAGGGCTTCGAGGCCGAGTTTATCAAGTCCAAGTTCTCT TTTAACCTGCGGAAGCCATCTGTGCAGTGGAGCGATACCGCCGAGTATTTCTGTGCCGTGATCAGCGTG ACAGGCAACAATAGAAAGCTGATCTGGGGACTGGGCACCTCCCTGGCCGTGAATCCC
	212	MLLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKY FSGDPLVKGIKGFEAEFIKSKFSFNL RKPVSQWSDTA EYFCAVISVTGNRRKLIWGLGTS LAVNP
GATA3 TCR-3 beta chain variable domain	213	ATGAGCAACCAGGTGCTCTGCTGTGTGGTCTTTGTCTCCTGGGAGCAAACACCGTGGATGGTGGAATC ACTCAGTCCCCGAAGTACCTGTT CAGAAAGGAAGGACAGAATGTGACCCTGAGTTGTGAACAGAATTTG AACCACGATGCCATGTACTGGTACCGACAGGACCCAGGGCAAGGGCTGAGATTGATCTACTACTCACAG ATAGTAAATGACTTTTCAGAAAGGAGATATAGCTGAAGGGTACAGCGTCTCTCGGGAGAAGAAGGAATCC TTTCCTCTCACTGTGACATCGGCCAAAAGAACCCGACAGCTTTCTATCTCTGTGCCAGTAGTCGGACT GCAATGAACACTGAAGCTTTCTTTGGACAAGGCACCACTCACAGTTGTA
	214	ATGTCCAACCAGGTGCTGTGCTGCGTGGTGTCTGTGCCTGCTGGGAGCAAATACCGTGGACGGAGGCATC ACACAGTCCCCCAAGTACCTGTT CAGGAAGGAGGGCCAGAACGTGACCCTGTCTTGTGAGCAGAACCTG AATCACGACGCCATGTACTGGTATAGGCAGGACCCCGACAGGGACTGAGACTGATCTACTATAGCCAG ATCGTGAATGACTTTTCAGAAAGGGCGACATCGCCGAGGGCTACTCCGTGTCTAGGGAGAAGAAGGAGAGC TTCCCCCTGACCGTGACATCGGCCAGAAGAACCCTACAGCCTTTTATCTGTGCGCCAGCTCCCGCACC GCCATGAATACAGAGGCCTTCTTTGGCCAGGGCACCAGGCTGACAGTGGTG
	215	MSNQVLCCVVLCLLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQ IVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCASSRTAMNTEAFFGQGT RLTVV
GATA3 TCR-3 alpha chain	216	MLLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKY FSGDPLVKGIKGFEAEFIKSKFSFNL RKPVSQWSDTA EYFCAVISVTGNRRKLIWGLGTS LAVNPDIQN PDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSVYITDKTVLDMRSMDFKSN SAVAWSNKSDFAC ANAFNNSIIPEDTFFPSP ESSCDVLVEKS FETDTNLN FQNL SVIGFRILLKLVAGFNLLMTLRLWSS
GATA3 TCR-3 beta chain	217	MSNQVLCCVVLCLLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQ IVNDFQKGDIAEGYSVSREKKESFPLTV TSAQKNPTAFYLCASSRTAMNTEAFFGQGT RLTVV EDLNKV FPPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYC LSSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPV TQIVSAEAWGRADCGFTSVSYQQGVLS ATILYEILLGKATLYAVLV SALVLMAMVKRKDF

Name	SEQ ID NO	Sequence
GATA3 TCR-3 peptide	218	ESKIMFATL
TMPRSS2:ERG TCR-1 alpha chain CDR1	142	TRDTTY
TMPRSS2:ERG TCR-1 alpha chain CDR2	143	RNSFDEQN
TMPRSS2:ERG TCR-1 alpha chain CDR3	144	ALSEARVFNGANSKLT
TMPRSS2:ERG TCR-1 beta chain CDR1	145	SGHDN
TMPRSS2:ERG TCR-1 beta chain CDR2	146	FVKESK
TMPRSS2:ERG TCR-1 beta chain CDR3	147	ASSQADSPLH
TMPRSS2:ERG TCR-1 alpha chain variable domain	148	ATGCTGACTGCCAGCCTGTTGAGGGCAGTCATAGCCTCCATCTGTGTTGTATCCAGCATGGCTCAGAAG GTAACTCAAGCGCAGACTGAAATTTCTGTGGTGGAGAAGGAGGATGTGACCTTGGACTGTGTGTATGAA ACCCGTGATACTACTTATTACTTATTCTGGTACAAGCAACCACCAAGTGAGAAATTGGTTTTCCTTATT CGTCGGAACCTCTTTTGATGAGCAAAATGAAATAAGTGGTCGGTATTCTTGGAACCTCCAGAAATCCACC AGTTCCTTCAACTTCACCATCACAGCCTCACAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAGT GAGGCCCGCGTTTTCAATGGAGCCAAATAGTAAGCTGACATTTGGAAAAGGAATAACTCTGAGTGTTAGA CCA
	149	ATGCTGACCGCCAGCCTGCTGAGGGCTGTGATCGCCAGCATCTGCGTCGTGTCCAGCATGGCTCAAAAG GTCACACAGGCCCAGACAGAGATCTCCGTCGTGAGAAAGAGGACGTGACCTCAGCTGCGTGTATGAG ACCAGGGACACCACATACTACCTGTTTTGGTACAAGCAGCCCCCAGCGGAGAGCTCGTGTCTGATC AGAAGGAACAGCTTTGATGAACAGAATGAGATCTCCGGCAGGTACTCCTGGAACCTCCAGAAGAGCACC TCCAGCTTCAACTTCACAATTACAGCTTCCCAGGTGGTGGATAGCGCCGTGTATTTCTGCGCTCTCAGC GAGGCCAGGTGTTCAACGGCGCCAATTCCAACTGACCTTCGGCAAAGGCATCACACTGTCCGTGAGA CCC
	150	MLTASLLRAVIASICVVSSMAQKVTAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLI RRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEARVFNGANSKLTFGKGITLSVR P
TMPRSS2:ERG TCR-1 beta chain variable domain	151	ATGGTTTCCAGGCTTCTCAGTTTAGTGTCCTTTGTCTCCTGGGAGCAAAGCACATAGAAGCTGGAGTT ACTCAGTTCCCCAGCCACAGCGTAATAGAGAAGGGCCAGACTGTGACTCTGAGATGTGACCAATTTCT GGACATGATAATCTTTATTGGTATCGACGTGTTATGGGAAAAGAAATAAAATTTCTGTTACATTTTGTG AAAGAGTCTAAACAGGATGAATCCGGTATGCCCAACAATCGATTCTTAGCTGAAAGGACTGGAGGGACG TATTCTACTCTGAAGGTGCAGCCTGCAGAACTGGAGGATTCTGGAGTTATTTCTGTGCCAGCAGCCAA GCGGATTACCCCTCCACTTTGGGAATGGGACCAGGCTCACTGTGACA
	152	ATGGTCTCCAGGCTGCTCTCCCTCGTGAGCCTGTGTCTCCTGGGAGCCAAGCACATTGAGGCCGGCGTG ACCCAATTCCCCAGCCACAGCGTGATTGAGAAGGGACAGACCGTCACCTTGAGGTGTGATCCTATCAGC GGCCACGACAACCTCTACTGGTATAGGAGAGTCATGGGCAAGGAAATTAATTTCTGCTGCATTTCTGTG AAAGAGTCCAAACAGGACGAAAGCGGCATGCCAATAATAGGTTCTCCTCGCCGAGAGGACCGGCGGCACA TATTCCACCTGAAGGTCCAGCCCGCTGAGCTCGAAGACTCCGGCGTCTATTTCTGTGCCTCCAGCCAG GCTGACTCCCCTCTCCATTTCCGAAACGGCACAGGCTCACCCTGACC
	153	MVSRLLSLVSLCLLGAHIEAGVTQFPSSHVIEKGQTVTLRCDPISGHDNLYWYRRVMGKEIKFLLHFV KESKQDESGMPNNRFLAERTGGTYSTLKVQPAELEDSSGVYFCASSQADSPLHFGNGTRTLTVT
TMPRSS2:ERG TCR-1 alpha chain	154	MLTASLLRAVIASICVVSSMAQKVTAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLI RRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDSSAVYFCALSEARVFNGANSKLTFGKGITLSVR PDIQNPDPFVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNK SDFACANAFNNSIIPEDTFFPSPSSCDVKLVEKSFETDTNLFQNL SVIGFRI LLLKVAGFNLLMTLR LWSS
TMPRSS2:ERG TCR-1 beta chain	155	MVSRLLSLVSLCLLGAHIEAGVTQFPSSHVIEKGQTVTLRCDPISGHDNLYWYRRVMGKEIKFLLHFV KESKQDESGMPNNRFLAERTGGTYSTLKVQPAELEDSSGVYFCASSQADSPLHFGNGTRTLTVTEDLNKVF PPEVAVFEPSEAEISHTQKATLVCLATGFFPDHVELSWWVNGKEVHSGVSTDPQPLKEQFALNDSRYCL SSRLRVSATFWQNPNNHFRQVQFYGLSENDEWTDQRAKPVTDIVSAEAWGRADCGFTSVSYQQGVLSA TILYEILLGKATLYAVLVSAVLMLAMVKRKDF

Name	SEQ ID NO	Sequence
TMPRSS2:ERG TCR-1 peptide	156	ALNSEALSV
BTK TCR-1 alpha chain CDR1	159	DRGSQS
BTK TCR-1 alpha chain CDR2	160	IYSNGD
BTK TCR-1 alpha chain CDR3	161	AVNDYGGSQGNLIF
BTK TCR-1 beta chain CDR1	162	SEHNR
BTK TCR-1 beta chain CDR2	163	FQNEAQ
BTK TCR-1 beta chain CDR3	164	ASSFGPDEKLFF
BTK TCR-1 alpha chain variable domain	165	ATGATGAAATCCTTGAGAGTTTTACTAGTGATCCTGTGGCTTCAGTTGAGCTGGGTTTGAGGCCAACAG AAGGAGGTGGAGCAGAATTCTGGACCCCTCAGTGTTCCAGAGGGAGCCATTGCCTCTCTCAACTGCAC TACAGTGACCGAGGTCCCAGTCTTCTTCTGGTACAGACAATATTCTGGGAAAAGCCCTGAGTTGATA ATGTTTCATATACTCCAATGGTGACAAAGAAGATGGAAGGTTTACAGCACAGCTCAATAAAGCCAGCCAG TATGTTTCTCTGCTCATCAGAGACTCCCAGCCAGTGATTGAGCCACCTACCTCTGTGCCGTGAACGAT TATGGAGGAAGCCAAGGAAATCTCATCTTTGAAAAGGCACTAACTCTCTGTAAACCA
	166	ATGATGAAGAGCCTGCGGGTGCTGCTGGTCATCCTGTGGCTGCAGCTGCTTTGGGTGTGGAGCCAGCAG AAGGAGGTGGAGCAGAATCCGGACCACTGTCTGTGCCTGAGGGAGCCATCGCCAGCCTGAATTGCACC TACTCCGACAGAGGCTCCCAGTCTTTCTTTGGTACAGGCAGTATAGCGCAAGTCCCCGAGCTGATC ATGTTTCATCTACTCCAACGGCGACAAGGAGGATGGCCGCTTTACAGCCCAGCTGAATAAGGCCAGCCAG TACGTGAGCCTGCTGATCCGGGACTCTCAGCCAAGCGATTCCGCCACCTACCTGTGCGCGTGAACGAT TATGGCGGCAGCCAGGGCAATCTGATCTTTGGCAAGGGCACAAAGCTGTCCTGTAAGCCC
	167	MMKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELI MFIYNSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNDYGGSQGNLIFGKGTKL SVKP
BTK TCR-1 beta chain variable domain	168	ATGGGCACCAGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGCAGATCACGCAGATACTGGAGTC TCCCAGAACCCAGACACAAGATCACAAAGAGGGGACAGAATGTAACCTTCAGGTGTGATCCAATTTCT GAACACAACCGCCTTTATTGGTACCGACAGACCTGGGGCAGGGCCAGAGTTTCTGACTTACTTCCAG AATGAAGCTCAACTAGAAAAATCAAGGCTGCTCAGTGATCGGTTCTCTGCAGAGAGGCCAAGGGATCT TTCTCCACCTTGGAGATCCAGCGCACAGAGCAGGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCTTC GGACCTGATGAAAAACTGTTTTTTGGCAGTGGAACCCAGCTCTCTGTCTTG
	169	ATGGGCACCTCTCTGCTGTGCTGGATGGCACTGTGCCTGCTGGGAGCAGACCACGCAGATACAGGCGTG AGCCAGAACCCACGCCACAAGATCACCAAGCGGGGCCAGAATGTGACATTGAGATGCGACCCCATCAGC GAGCACAACAGGCTGTACTGGTATAGGCAGACCCTGGGACAGGGACCAGAGTTCTTGACATACTTTTCCAG AATGAGGCCCAGCTGGAGAAGTCTCGGCTGCTGAGCGATAGATTCTCCGCCGAGAGGCCAAGGGCTCC TTTTCTACCTTGGAGATCCAGAGGACAGAGCAGGGGCGACTCCGCCATGTATCTGTGCGCCAGCTCCTTC GGCCCTGATGAGAAGCTGTTCTTTGGCTCTGGCACCAGCTGAGCGTGCTG
	170	MGTSLLCWMALCLLGADHADTGVSQNP RHKITKRGQNVTFRCDP ISEHNRLYWYRQTLGQGPEFLTYFQ NEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CASSFGPDEKLFFGSGTQLSVL
BTK TCR-1 alpha chain	171	MMKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELI MFIYNSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNDYGGSQGNLIFGKGTKL SVKPD IQ NPDPVYQLRDSKSSDKSVCLTFDFDSQTNVSQKSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFA CANAFNNSIIPEDTFFPSPSSCDVKLVEKSFETDTNLNFQNL SVIGFRI LLLKVAGFNLLMTLRLWSS
BTK TCR-1 beta chain	172	MGTSLLCWMALCLLGADHADTGVSQNP RHKITKRGQNVTFRCDP ISEHNRLYWYRQTLGQGPEFLTYFQ NEAQLEKSRLLSDRFSAERP KGSFSTLEIQ RTEQGD SAMYL CASSFGPDEKLFFGSGTQLSVLEDLNKV FPPEVAVFEPSEAEI SHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQLKEQPALNDSRYC LSSRLRV SATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPV TQIVSAEAWGRADCGFTSVSYQQGVLS ATILYEILLGKATLYAVLV SALVLMAMVKRKDF
BTK TCR-1 peptide	173	SLNLYLREM
BTK TCR-2 alpha chain CDR1	174	DRGSQS
BTK TCR-2 alpha chain CDR2	175	IYSNGD

Name	SEQ ID NO	Sequence
BTK TCR-2 alpha chain CDR3	176	AVNEGDSSYKLI
BTK TCR-2 beta chain CDR1	177	SGDLS
BTK TCR-2 beta chain CDR2	178	YYNGEE
BTK TCR-2 beta chain CDR3	179	ASSPGANEKLF
BTK TCR-2 alpha chain variable domain	180	ATGATGAAATCCTTGAGAGTTTTACTAGTGATCCTGTGGCTTCAGTTGAGCTGGGTTTGGAGCCAACAG AAGGAGGTGGAGCAGAATTCTGGACCCCTCAGTGTTCCAGAGGGAGCCATTGCCTCTCTCAACTGCACCT TACAGTGACCGAGGTTCAGTCCCTTCTTCTGGTACAGACAATATTCTGGGAAAAGCCCTGAGTTGATA ATGTTTCATATACTCCAATGGTGACAAAGAAGATGGAAGGTTTACAGCACAGCTCAATAAAGCCAGCCAG TATGTTTCTCTGCTCATCAGAGACTCCCAGCCCAGTGATTACGCCACCTACCTCTGTGCCGTGAACGAG GGGGATAGCAGCTATAAATTGATCTTCGGGAGTGGGACCAGACTGCTGGTCAGGCCCT
	181	ATGATGAAGAGCCTGCGGGTGCTGCTGGTCATCCTGTGGCTGCAGCTGAGCTGGGTGTGGTCCCAGCAG AAGGAGGTGGAGCAGAATCTGGACCACTGAGCGTGCCTGAGGGAGCCATCGCCTCCCTGAATTGCACC TACTCTGACAGAGGCAGCCAGTCCCTTTTGGTACAGGCAGTATTCGGCAAGTCTCCCGAGCTGATC ATGTTTCATCTACAGCAACGCGCACAAGGAGGATGGCCGCTTTACAGCCCAGCTGAATAAGGCCCTCCCAG TACGTGAGCCTGCTGATCCGGGACTCTCAGCCATCTGATAGCGCCACCTACCTGTGCCGTGAACGAG GCGGATAGCTCCTATAAGCTGATCTTTGGCAGCGGCACAAGACTGCTGGTGAGGCCCT
	182	MMKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSP ELI MFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNEGDSSYKLI FGSGTRLLVRP
BTK TCR-2 beta chain variable domain	183	ATGGGCTTCAGGCTCCTCTGCTGTGTGGCCTTTTGTCTCCTGGGAGCAGGCCAGTGGATTCTGGAGTC ACACAAACCCCAAAGCACCTGATCACAGCAACTGGACAGCGAGTGACGCTGAGATGCTCCCTAGGTCT GGAGACCTCTCTGTGTACTGGTACCAACAGAGCCTGGACCAGGGCCTCCAGTTCCCTCATTCAGTATTAT AATGGAGAAGAGAGAGACAAAGGAACATTCTGAACGATTCTCCGCACAACAGTTCCTTGACTTGCAC TCTGAATAAACCTGAGCTCTCTGGAGCTGGGGGACTCAGCTTTGTATTCTGTGCCAGCAGCCCCGGG GCTAATGAAAACTGTTTTTGGCAGTGAACCCAGCTCTCTGTCTTG
	184	ATGGGCTTCGGGCTGCTGTGCTGCGTGGCATTTCCTGCTGGGAGCAGGACCAGTGGACTCCGGCGTG ACCCAGACACCCAAAGCACCTGATCACCGCAACAGGACAGAGGGTGACCCTGAGATGTTCCCTAGGTCT GGCGACCTGAGCGTGTACTGGTATCAGCAGTCCCTGGATCAGGGCCTGCAGTTCTCTGATCCAGTACTAT AACGGCGAGGAGCGCGCCAAGGGCAATATCCTGGAGCGGTTCTCCGCCAGCAGTTTCCCGACCTGCAC TCTGAGCTGAACCTGAGCTCCCTGGAGCTGGGCGATAGCGCCCTGTACTTCTGCGCCTCTAGCCCTGGC GCCAATGAGAAGCTGTTCTTTGGCAGCGGCACCCAGCTGTCCGTGCTG
	185	MGFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYY NGEERAKGNILERFSAQQFPDLHSELNLSSLELGDSALYFCASSPGANEKLFFGSGTQLSVL
BTK TCR-2 alpha chain	186	MMKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSP ELI MFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCVNEGDSSYKLI FGSGTRLLVRPDIQN PDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDVYITDKTVLDMRSMDFKSN SAVAWSNKSDFAC ANAFNNSIIPEDTFFPSPESSCDVKLVEKS FETDTNLFQNL SVIGFRILLK VAGFNLLMTLRLWSS
BTK TCR-2 beta chain	187	MGFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYY NGEERAKGNILERFSAQQFPDLHSELNLSSLELGDSALYFCASSPGANEKLFFGSGTQLSVLEDLNKVF PPEVAVFEPSEAEI SHTQKATLVCLATGFFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCL SSRLRVSATFWQNP RNHFRCQVQFYGLSENDEWTQDRAKPV TQIVSAEAWGRADCGFTSVSYQQGVLSA TILYEILLGKATLYAVLV SALVLMAMV KRKDF
BTK TCR-2 peptide	188	SLNLYREM
EGFR TCR-1 alpha chain CDR1	447	TRDTTYY
EGFR TCR-1 alpha chain CDR2	448	RNSFDEQN
EGFR TCR-1 alpha chain CDR3	449	ALKGANTGFQKLV
EGFR TCR-1 beta chain CDR1	450	SGHDY

Name	SEQ ID NO	Sequence
EGFR TCR-1 beta chain CDR2	451	FNNNVP
EGFR TCR-1 beta chain CDR3	452	ASGGGLGLFETQY
EGFR TCR-1 alpha chain variable domains	453	ATGCTGACTGCCAGCCTGTTGAGGGCAGTCATAGCCTCCATCTGTGTTGTATCCAGCATGGCTCAGAAG GTAACCTCAAGCGCAGACTGAAATTTCTGTGGTGGAGAAGGAGGATGTGACCTTGGACTGTGTGTATGAA ACCCGTGATACTACTTATTACTTATCTGGTACAAGCAACCACCAAGTGGAGAATTGGTTTTCTTATT CGTCGGAACCTCTTTTGATGAGCAAAATGAAATAAGTGGTCGGTATTCTTGGAACTTCCAGAAATCCACC AGTTCCTTCAACTTCACCATCACAGCCTCACAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAAA GGGCGAACACAGGCTTTCAGAAACTTGTATTTGGAACTGGCACCCGACTTCTGGTCAGTCCA
	454	ATGCTGACAGCCTCCCTGCTGAGGGCCGTGATCGCCTCTATCTGCGTGGTGTCTAGCATGGCCAGAAG GTGACCCAGGCCCAGACAGAGATCAGCGTGGTGGAGAAGGAGGACGTGACCTGGATTGCGTGTACGAG ACACGGGACACCACATACTATCTGTTTTGGTATAAGCAGCCACCCAGCGCGAGCTGGTGTTCCTGATC AGGCGCAATTCTTTTGATGAGCAGAACGAGATCTCCGGCAGATACTCTTGGAAATTTCCAGAAGTCCACC TCCTCTTTCAACTTTACCATCACAGCCTCCCAGTGGTGGACTCTGCCGTGTATTTTGTGCCCTGAAG GGCGCAACACAGGCTTCCAGAAGCTGGTGGTGGCACCCGACAGACTGCTGGTGAGCCCT
	455	MLTASLLRAVIASICVVS SMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLI RRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALKGANTGFQKL VFGTGRLLVSP
EGFR TCR-1 beta chain variable domains	456	ATGGACTCCTGGACCCTCTGCTGTGTGTCCCTTTGCATCCTGGTAGCAAAGCACACAGATGCTGGAGTT ATCCAGTCACCCCGGCACGAGGTGACAGAGATGGGACAAGAAGTGA CTCTGAGATGTAAACCAATTTCA GGACAGACTACCTTTTCTGGTACAGACAGACCATGATGCGGGGACTGGAGTTGCTCATTTACTTTAAC AACAACGTTCCGATAGATGATTACAGGATGCCCGAGGATCGATTCTCAGCTAAGATGCCAATGCATCA TTCTCCACTCTGAAGATCCAGCCCTCAGAACCCAGGGACTCAGCTGTGTACTTCTGTGCCAGCGGAGGG GGACTAGGTCTATTTGAGACCCAGTACTTCCGGGCCAGGCACGCGGCTCCTGGTGCTC
	457	ATGGACAGCTGGACCCTGTGCTGCGTGAGCCTGTGCATCCTGGTGGCCAAGCACACAGATGCAGGCGTG ATCCAGTCCCCAAGGCACGAGGTGACCGAGATGGGACAGGAGGTGACACTGAGGTGTAAGCCTATCTCT GGCCACGACTACCTGTTCTGGTATCGGCAGACCATGATGAGAGGCCTGGAGCTGCTGATCTACTTTAAC AATAACGTGCCTATCGACGATTCTGGCATGCCAGAGGACAGGTTACAGCCCAAGATGCCAATGCCAGC TTTTCCACCCTGAAGATCCAGCCAAGCGAGCCAAGGGATTCCGCCGTGTACTTCTGCGCCTCCGGAGGA GGACTGGGACTGTTTCGAGACCCAGTATTTGGCCAGGCACAAGGCTGCTGGTGCTG
	458	MDSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTM MRGLELLIYFN NNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDS AVYFCASGGGLGLFETQYFGPGTRLLVL
EGFR TCR-1 alpha chain	459	MLTASLLRAVIASICVVS SMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPS GELVFLIRRN SFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALKGANTGFQKL VFGTGRLLVSPDIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVL DMKAMDSKSNIAIWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLS VMGLRILLLLKVAGFNLLMTLRLWSS
EGFR TCR-1 beta chain	460	MDSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTM MRGL ELLIYFN NNVPIDDSGMPEDRFS AKMPNASFSTLKI QPSEPRDS AVYFCASGGGLGLFETQY FGPGTRLLVLKDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGF FPDHVELSWWVNGKEV HSGVSTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCGITSASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
Peptides	461	QLIMQLMPF
	462	LIMQLMPFGC
	463	MQLMPFGCLL
EGFR TCR2 alpha chain CDR1	464	DSSSTY
EGFR TCR2 alpha chain CDR2	465	IFSNMDM
EGFR TCR2 alpha chain CDR3	466	AEWANTDKLI
EGFR TCR2 beta chain CDR1	467	DFQATT
EGFR TCR2 beta chain CDR2	468	SNEGSKA

Name	SEQ ID NO	Sequence
EGFR TCR2 beta chain CDR3	469	SARRREGEIEQY
EGFR TCR2 alpha chain variable domains	470	ATGAAGACATTTGCTGGATTTTCGTTCTGTTTTGTGGCTGCAGCTGGACTGTATGAGTAGAGGAGAG GATGTGGAGCAGAGTCTTTTCTGAGTGTCCGAGAGGGAGACAGCTCCGTTATAAACTGCACCTTACACA GACAGCTCCTCCACCTACTTATACTGGTATAAGCAAGAACCTGGAGCAGGTCTCCAGTTGCTGACGTAT ATTTTTTCAAATATGGACATGAAACAAGACCAAAGACTCACTGTTCTATTGAATAAAAAGGATAAACAT CTGTCTCTGCGCATTGCAGACACCCAGACTGGGGACTCAGCTATCTACTTCTGTGCAGAGTGGGCTAAC ACCGACAAGCTCATCTTTGGGACTGGGACCAGATTACAAGTCTTTCCA
	471	ATGAAGACCTTCGCCGCTTCTCCTTCTGTTCTGTTCTGCTGCAGCTGGACTGCATGAGCCGGGGAGAG GATGTGGAGCAGTCCCTGTTCTGTCTGTGAGGGAGGGCGACTCCTCTGTGATCAACTGTACATATACC GATAGCTCCTCTACCTACCTGTATTGGTACAAGCAGGAGCCAGGAGCAGGACTGCAGCTGCTGACATAC ATCTTTAGCAACATGGACATGAAGCAGGATCAGCGCCTGACCGTGTCTGCTGAATAAGAAGGACAAGCAC CTGTCTCTGCGGATCGCCGACACACAGACCGGCGATAGCGCCATCTACTTCTGTGCCGAGTGGGCCAAT ACCGATAAGCTGATCTTTGGCACAGGCACCCGGCTGCAGGTGTTCCCT
	472	MKTFAGFSFLFLWLQLDCMSRGEDEVQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTY IFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEWANTDKLIFGTGTRLQVFP
EGFR TCR2 beta chain variable domains	473	ATGCTGCTGCTTCTGCTGCTTCTGGGGCCAGGCTCCGGGCTTGGTGTCTGCTGCTCTCTCAACATCCGAGC TGGGTTATCTGTAAGAGTGAACCTCTGTGAAGATCGAGTGCCGTTCCCTGGACTTTTCAAGGCCACAAC ATGTTTTGGTATCGTCAGTTCGGAAGCAGAGTCTCATGCTGATGGCACTTCCAATGAGGGCTCCAAG GCCACATACGAGCAAGGCGTCGAGAAGGACAAGTTTCTCATCAACCATGCAAGCCTGACCTTGTCCACT CTGACAGTGACCACTGCCCATCTGAAGACAGCAGCTTCTACATCTGCAGTGCTAGAAGGCGGGAGGGG GAGATCGAGCAGTACTTCGGGCGGGGACCAGGCTCACGGTCACA
	474	ATGTTATTACTGCTGCTGCTGCTGGGACCAGGCTCCGGACTGGGAGCCGTGGTGTCCCAGCACCTTCT TGGGTCATCTGCAAGTCCGGCACATCTGTGAAGATCGAGTGTCGCTCTCTGGACTTTTCAAGGCCACCACA ATGTTTTGGTATCGGCAGTTCGGAAGCAGAGCCTGATGCTGATGGCCACAAGCAACGAGGGCTCCAAG GCCACCTACGAGCAGGCGGTGGAGAAGGACAAGTTCTGATCAATCACGCTCTCTGACCTGAGCACC CTGACAGTGACCTCCGCCACCCTGAGGATAGCTCCTTTTATATCTGCTCTGCCCGGAGAAGGGAGGGC GAGATCGAGCAGTACTTCGGGCCAGGCACAAGACTGACAGTGACC
	475	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSK ATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAARRREGEIEQYFGPGTRLTVT
EGFR TCR2 alpha chain	476	MKTFAGFSFLFLWLQLDCMSRGEDEVQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGA GLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEWANTDKLIFGTG TRLQVFPDIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAM DSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNL SVMGLR I LLLKVAGFNLLMTLRLWSS
EGFR TCR2 beta chain	477	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAARRREGEIEQYFGPG TRLTVTKDLRNVTTPKVSLEFSPKAEIANKQKATLVCLARGFFPDHVELSWWWNGKEVHSGV STD PQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONIS AEAWGRADCGITSASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS
Peptides	478	QLIMQLMPF
	479	LIMQLMPFGC
	480	MQLMPFGCLL
EGFR TCR3 alpha chain CDR1	481	TRDTTYY
EGFR TCR3 alpha chain CDR2	482	RNSFDEQN
EGFR TCR3 alpha chain CDR3	483	ALTPFPNAGGTSYGKLT
EGFR TCR3 beta chain CDR1	484	SGHNS
EGFR TCR3 beta chain CDR2	485	FNNNVP
EGFR TCR3 beta chain CDR3	486	ASSLAYLTGRVEAF

Name	SEQ ID NO	Sequence
EGFR TCR3 alpha chain variable domains	487	ATGCTGACTGCCAGCCTGTTGAGGGCAGTCATAGCCTCCATCTGTGTTGTATCCAGCATGGCTCAGAAG GTAACCTCAAGCGCAGACTGAAATTTCTGTGGTGGAGAAGGAGGATGTGACCTTGGACTGTGTGTATGAA ACCCGTGATACTACTTATTACTTATTCTGGTACAAGCAACCACCAAGTGGAGAATTGGTTTTCTTATT CGTCGGAACCTCTTTTGATGAGCAAAATGAAATAAGTGGTCCGTATTCTTGGAACCTCCAGAAATCCACC AGTTCCTTCAACTTACCACATCACAGCCTCACAGTGGTGGACTCAGCAGTATACTTCTGTGCTCTGACT CCCTTCCCAATGCTGGTGGTACTAGCTATGGAAAGCTGACATTTGGACAAGGGACCACCTTGACTGTC CATCCA
	488	ATGCTGACAGCCTCTCTGCTGAGGGCCGTGATCGCCAGCATCTGCGTGGTGTCTCTATGGCCAGAAG GTGACCCAGGCCCAGACAGAGATCAGCGTGGTGGAGAAGGAGGACGTGACCTTGGATTGCGTGTACGAG ACACGGGACACCACATACTATCTGTTCTGGTATAAGCAGCCACCCTCCGGCGAGCTGGTGTTCCTGATC AGGCGCAATTCTTTTGATGAGCAGAACGAGATCTCTGGCAGATACAGCTGGAATTTTCAGAAGTCTACC AGTTCCTTCAACTTACCACATCACAGCCTCTCAGTGGTGGATAGCGCCGTGTACTTCTGTGCCCTGACA CCATTTCCCAATGCCGGCGGCACCAGCTATGGCAAGCTGACATTCGGCCAGGGCACCACCTGACAGTG CACCT
	489	MLTASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVYETRDTTYLFWYKQPPSGELVFLI RRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDASVYFCALTPFPNAGGTSYKGLTFGQGTILTV HP
EGFR TCR3 beta chain variable domains	490	ATGGACTCCTGGACCTTCTGCTGTGTGTCCCTTTGCATCCTGGTAGCGAAGCATAACAGATGCTGGAGTT ATCCAGTCACCCCGCCATGAGGTGACAGAGATGGGACAAGAAGTGAAGTCTGAGATGTAAACCAATTTCA GGCCACAACCTCCCTTTTCTGGTACAGACAGACCATGATGCGGGGACTGGAGTTGCTCATTTACTTTAAC AACAACGTTCCGATAGATGATTCAAGGATGCCCGAGGATCGATTCTCAGCTAAGATGCCTAATGCATCA TTCTCCACTCTGAAGATCCAGCCCTCAGAACCAGGGACTCAGCTGTGTACTTCTGTGCCAGCAGTTTA GCCTACCTGACAGGGAGGGTTGAAGCTTTCTTTGGACAAGGCACCAGACTCACAGTTGTA
	491	ATGGACTCCTGGACCTTCTGCTGCGTGAGCCTGTGCATCCTGGTGGCCAAGCACACAGATGCAGGCGTG ATCCAGTCCCCAAGGCACGAGGTGACCGAGATGGGACAGGAGGTGACACTGAGGTGTAAGCCCATCAGC GGCCACAATTCCCTGTTCTGGTACCGGCAGACCATGATGAGAGGCCTGGAGCTGCTGATCTACTTCAAC AATAACGTGCCCATCGACGATAGCGGCATGCCTGAGGACCGGTTCTCCGCCAAGATGCCCAACGCCTCT TTTAGCACCTGAAGATCCAGCCTTCCGAGCCAAGGATTCTGCCGTGTACTTCTGCGCCAGCTCCCTG GCCTATCTGACCGGAAGGGTGGAGGCCTTCTTTGGACAGGGCACCAGGCTGACAGTGGTG
	492	MDSWTFCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHNSLFWYRQTMRLGLELLIYFN NNVPIDDSGMPEDRFSKMPNASFSTLKIQPSERDSAVYFCASSLAYLTGRVEAFFGQGTRLTVV
EGFR TCR3 alpha chain	493	MLTASLLRAVIASICVVSSMAQKVTQAQTEISVVEKEDVTLDVYETRDTTYLFWYKQPPS GELVFLIRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDASVYFCALTPFPNAGGTS YKGLTFGQGTILTVHPDIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITD KTVLDMKAMDSSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNF QNL SVMGLRILLLKVAGFNLLMTLRLWSS
EGFR TCR3 beta chain	494	MDSWTFCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHNSLFWYRQTMRLGL ELLIYFN NNVPIDDSGMPEDRFSKMPNASFSTLKIQPSERDSAVYFCASSLAYLTGRVEA FFGQGTRLTVVKDLRNVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKE VHSGVSTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCGITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS
Peptides	495	QLIMQLMPF
	496	LIMQLMPFGC
	497	MQLMPFGCLL
EGFR TCR4 alpha chain CDR1	498	TRDTTY
EGFR TCR4 alpha chain CDR2	499	RNSFDEQN
EGFR TCR4 alpha chain CDR3	500	ALIRGSYQLI
EGFR TCR4 beta chain CDR1	501	DFQATT
EGFR TCR4 beta chain CDR2	502	SNEGSKA
EGFR TCR4 beta chain CDR3	503	SAQGSSGRIEQF

Name	SEQ ID NO	Sequence
EGFR TCR4 alpha chain variable domains	504	ATGCTGACTGCCAGCCTGTTGAGGGCAGTCATAGCCTCCATCTGTGTTGTATCCAGCATGGCTCAGAAG GTAACCTCAAGCGCAGACTGAAATTTCTGTGGTGGAGAAGGAGGATGTGACCTTGGACTGTGTGTATGAA ACCCGTGATACTACTTATTACTTATTCTGGTACAAGCAACCACCAAGTGGAGAATTGGTTTTCTTATT CGTCGGAACCTCTTTTGATGAGCAAAATGAAATAAGTGGTGGTATTCTTGGAACCTCCAGAAATCCACC AGTTCCCTTCAACTTCACCATCACAGCCTCACAAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGATT CGAGGGAGCTATCAGTTAATCTGGGGCGCTGGGACCAAGCTAATTATAAAGCCA
	505	ATGCTGACCGCCTCTCTGCTGAGGGCCGTGATCGCCAGCATCTGCGTGGTGGAGTCCATGGCCCAGAAG GTGACACAGGCCCAGACCGAGATCAGCGTGGTGGAGAAGGAGGACGTGACACTGGATTGCGTGTACGAG ACCCGCGACACCACATACTATCTGTTTTGGTATAAGCAGCCACCCTCCGGCGAGCTGGTGTTCCTGATC AGGCGCAACTCTTTTGATGAGCAGAAATGAGATCTCTGGCCGGTACAGCTGGAACCTCCAGAAGAGCACA TCTAGCTTCAACTTCACCATCAGCGCCAGCCAGGTGGTGGACTCCGCGGTGTACTTTTGTGCCCTGATC AGAGGCTCCTATCAGCTGATCTGGGGCGCCGGCACCAGCTGATCATCAAGCCC
	506	MLTASLLRAVIASICVVSSMAQKVTAQTEISVVEKEDVTLDVYETRDTTYLFWYKQPPSGELVFLI RRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDASVYFCALIRGSYQLIWGAGTKLI IKP
EGFR TCR4 beta chain variable domains	507	ATGCTGCTGCTTCTGCTGCTTCTGGGGCCAGGCTCCGGGCTTGGTGTCTCGTCTCTCAACATCCGAGC AGGGTTATCTGTAAGAGTGGAACTCTGTGAAGATCGAGTGCCGTTCCCTGGACTTTTCAAGCCACA ATGTTTTGGTATCGTCAGTTCCCGAAACAGAGTCTCATGCTGATGGCAACTTCCAATGAGGGCTCCAAG GCCACATACGAGCAAGGCGTCGAGAAGGACAAGTTTCTCATCAACCATGCAAGCCTGACCTTGTCCACT CTGACAGTGACCAGTGCCCATCCTGAAGACAGCAGCTTCTACATCTGCAGCGCCAGGGGAGTAGCGGG AGGATTGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTGCTA
	508	ATGTTATTACTGCTGCTGCTGCTGGGACCAGGCTCCGGACTGGGAGCAGTGGTGTCTCAGCACCCAAGC AGAGTGATCTGCAAGTCTGGCACCAGCGTGAAGATCGAGTGTAGGTCCCTGGACTTCCAGGCCACCACA ATGTTCTGGTACCGCCAGTTTCCAAAGCAGTCTCTGATGCTGATGGCCACATCCAACGAGGGCTCTAAG GCCACCTATGAGCAGGGCGTGGAGAAGGACAAGTTCTGATCAATCACGCCAGCCTGACCCTGTCCACC CTGACAGTGACCAGCGCCACCCAGAGGATAGCTCCTTTTACATCTGCTCCGCCCAGGGCTCTAGCGGC CGGATCGAGCAGTTCTTTGGCCCTGGCACACGGCTGACCGTGCTG
	509	MLLLLLLLGPGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSK ATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICSAQGS SGRIEQFFGPGTRLTVL
EGFR TCR4 alpha chain	510	MLTASLLRAVIASICVVSSMAQKVTAQTEISVVEKEDVTLDVYETRDTTYLFWYKQPPS GELVFLIRRNSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVDASVYFCALIRGSYQLIWG AGTKLI IKPDIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMK AMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTLEKSFETDMNLNFQNL SVMG LRLLLLKVAGFNLLMTLRLWSS
EGFR TCR4 beta chain	511	MLLLLLLLGPGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICSAQGS SGRIEQFFGPG TRLTVLKDRLNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGV STD PQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONIS AEAWGRADCGITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKKNS
Peptides	512	QLIMQLMPF
	513	LIMQLMPFGC
	514	MQLMPFGCLL
EGFR TCR5 alpha chain CDR1	515	DSVNN
EGFR TCR5 alpha chain CDR2	516	IPSGT
EGFR TCR5 alpha chain CDR3	517	AVMDSSYKLI
EGFR TCR5 beta chain CDR1	518	DFQATT
EGFR TCR5 beta chain CDR2	519	SNEGSKA
EGFR TCR5 beta chain CDR3	520	SALPGFSYEQY

Name	SEQ ID NO	Sequence
EGFR TCR5 alpha chain variable domains	521	ATGAAGAGGATATTGGGAGCTCTGCTGGGGCTCTTGAGTGCCAGGTTTGCTGTGTGAGAGGAATACAA GTGGAGCAGAGTCCCTCCAGACCTGATTCTCCAGGAGGGAGCCAATTCCACGCTGCGGTGCAATTTTTCT GACTCTGTGAACAATTTGCAGTGGTTTCATCAAAACCCCTGGGGACAGCTCATCAACCTGTTTTACATT CCTCAGGGACAAAACAGAATGGAAGATTAAGCGCCACGACTGTCGCTACGGAACGCTACAGCTTATTG TACATTTCTCTCTCCAGACCACAGACTCAGGCGTTTATTTCTGTGCTGTGATGGATAGCAGCTATAAA TTGATCTTCGGGAGTGGGACCAGACTGCTGGTCAGGCCT
	522	ATGAAGAGAATCCTGGGCGCCCTGCTGGGACTGCTGTCCGCCCAGGTGTGCTGCGTGCGGGGCATCCAG GTGGAGCAGAGCCCACCAGACCTGATCCTGCAGGAGGGAGCCAACCTCCACCTGAGATGCAATTTCTCC GATTCTGTGAACAATCTGCAGTGGTTTCACCAGAACCCTTGGGGCCAGCTGATCAATCTGTTTTACATC CCATCCGGCACAAGCAGAACGGCAGGCTGTCTGCCACCACAGTGGCCACCGAGCGGTACTCTCTGCTG TATATCTCTCTAGCCAGACCACAGACAGCGGCGTACTTCTGTGCCGTGATGGATTCTCTTATAAG CTGATCTTTGGCAGCCGCACCAGGCTGCTGGTCGCGCCCT
	523	MKRILGALLGLLSAQVCCVRGIQVEQSPDLILQEGANSTLRNFSDSVNNLQWFHQNPNWQQLINLFYI PSGTKQNGRLSATTVATERYSLLYISSQTTDSGVYFCVAMDSSYKLI FGSSTRLLVRP
EGFR TCR5 beta chain variable domains	524	ATGCTGCTGCTTCTGCTGCTTCTGGGGCCAGGCTCCGGGCTTGGTGCTGTCGTCTCTCAACATCCGAGC TGGGTATCTGTAAGAGTGGAACCTCTGTGAAGATCGAGTGCCGTTCCCTGGACTTTACAGGCCACAAC TATGTTTTGGTATCGTCAGTTCCCGAAACAGAGTCTCATGCTGATGGCAACTTCCAATGAGGGCTCCAAG GCCACATACGAGCAAGGCGTCGAGAAGGACAAGTTTCTCATCAACCATGCAAGCCTGACCTTGTCCACT CTGACAGTGACCAGTGCCCATCCTGAAGACAGCAGCTTCTACATCTGCAGTGCTCTGCCCGGATTCTCC TACGAGCAGTACTTCGGGCCCGGCACCAGGCTCACGGTCACA
	525	ATGTTATTACTGCTGCTGCTGCTGGGACCAGGCAGCGGACTGGGAGCAGTGGTGAGCCAGCACCCCTTCC TGGGTCATCTGCAAGAGCGGCACATCCGTGAAGATCGAGTGTGGTCTCTGGACTTCCAGGCCACCACA ATGTTCTGGTACAGACAGTTTCTTAAGCAGTCCCTGATGCTGATGGCCACATCTAACGAGGGCAGCAAG GCCACCTATGAGCAGGGCGTGGAGAAGGACAAGTTCTGATCAATCACGCCTCCCTGACCCTGTCTACC CTGACAGTGACCTCCGCCACCCAGAGGATAGCTCCTTTACATCTGCTCTGCCCTGCCAGGCTTCAGC TACGAGCAGTATTTTGGCCCCCGGCACACGGCTGACAGTGACC
	526	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNEGSK ATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICSAALPGFSYEQYFGPGTRTLTVT
EGFR TCR5 alpha chain	527	MKRILGALLGLLSAQVCCVRGIQVEQSPDLILQEGANSTLRNFSDSVNNLQWFHQNPNWQQLINLFYI PSGTKQNGRLSATTVATERYSLLYISSQTTDSGVYFCVAMDSSYKLI FGSSTRLLVRPDIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSK SNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNL SVMGLRILL LKVAGFNLLMTLRLWSS
EGFR TCR5 beta chain	528	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICSAALPGFSYEQYFGPGT RLTVTKDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVS TDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKNS
Peptides	529	QLIMQLMPF
	530	LIMQLMPFGC
	531	MQLMPFGCLL

EMBODIMENTS

[00417] The following embodiments are contemplated within the disclosure:

1. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3, 18, 33, 49, 65, 81, 97, 113, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 401, 417, 534, 547 and 560 and/or wherein the TCR beta chain

construct comprises a complementarity determining region 3 (CDR3) having at least 84% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6, 21, 36, 52, 68, 84, 100, 116, 244, 260, 276, 292, 308, 324, 340, 356, 372, 388, 404, 420, 537, 550, and 563.

2. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from RAS in complex with a human MHC, wherein the epitope from RAS comprises a region having at least 70% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 15, 30, 45, 46, 61, 62, 77, 78, 93, 94, 109, 110, 125, 126, 219-222, 253, 254, 269, 270, 285, 286, 301, 302, 317, 318, 333, 334, 349, 350, 365, 366, 381, 382, 397, 398, 413, 414, 429, 430, 544, 557 and 600.
3. A nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising
 - a. a TCR alpha chain construct and/or
 - b. a TCR beta chain constructwherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A03:01 allele.
4. A nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising
 - a. a TCR alpha chain construct and/or
 - b. a TCR beta chain constructwherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A02:01 allele.
5. A nucleic acid or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes at least one T cell receptor (TCR) comprising
 - a. a TCR alpha chain construct and/or
 - b. a TCR beta chain constructwherein the TCR specifically binds to an epitope from RAS in complex with a human MHC encoded by an HLA-A11:01 allele.
6. The nucleic acid of the embodiment in paragraph 3, wherein the TCR alpha chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 71, 87, 103, 295, 311, 327, 343, 359 and 391.
7. The nucleic acid of embodiment in paragraph 4, wherein the TCR alpha chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 9 and 24.

8. The nucleic acid of embodiment in paragraph 5, wherein the TCR alpha chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs:39, 55, 119, 247, 263, 279, 375, 407, 423, 539, 552, and 565.
9. The nucleic acid of embodiment in paragraph 3, wherein the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 74, 90, 106, 298, 314, 330, 346, 362 and 394.
10. The nucleic acid of embodiment 4, wherein the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 12 and 27.
11. The nucleic acid of embodiment 5, wherein the TCR beta chain construct comprises a variable region having at least 80%, or at least 90%, or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 42, 58, 122, 250, 266, 282, 378, 410, 426, 541, 554, and 567 .
12. The nucleic acid of the embodiments any one of the embodiments in paragraphs 1-3, and 6, wherein the TCR alpha chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 63, 79, 95, 287, 303, 319, 335, 351 and 383.
13. The nucleic acid of the embodiments any one of the embodiments in paragraphs 1-3, and 6, wherein the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 66, 82, 98, 290, 306, 322, 338, 354 and 386.
14. The nucleic acid of any one of the embodiments in paragraphs 1-2, 4 and 7, wherein the TCR alpha chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 1 and 16.
15. The nucleic acid of any one of the embodiments in paragraphs 1-2, 4 and 10, wherein the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 4 and 19.
16. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5 and 8, wherein the TCR alpha chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 31, 47, 111, 239, 255, 271, 367, 399, 415, 532, 545 and 558.
17. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5 and 11, wherein the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs:34, 50, 114, 242, 258, 274, 370, 402, 418, 53, 548 and 561.

18. The nucleic acid of the embodiments any one of the embodiments in paragraphs 1-3, 6, and 12, wherein the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 64, 80, 96, 288, 304, 320, 336, 352 and 384.
19. The nucleic acid of any one of the embodiments in paragraphs 1-3, 6, and 13 wherein the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 67, 83, 99, 291, 307, 323, 339, 355 and 387.
20. The nucleic acid of the embodiments any one of the embodiments in paragraphs 1-2, 4, 7 and 14, wherein the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 2 and 17.
21. The nucleic acid of any one of the embodiments in paragraphs 1-2, 4, 10 and 15, wherein the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 5 and 20.
22. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5, 8, and 16 wherein the TCR alpha chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 32, 48, 112, 240, 256, 272, 368, 400, 416, 533, 546, and 559.
23. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5, 11 and 17 wherein the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 35, 51, 115, 243, 259, 275, 371, 403, 419, 536, 549, and 562.
24. The nucleic acid of the embodiments any one of the in paragraphs 1-3, 6, 12 and 18 wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 65, 81, 97, 289, 305, 321, 337, 353 and 385.
25. The nucleic acid of any one of the embodiments in paragraphs 1-3, 6, 13 and 19 wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 68, 84, 100, 292, 308, 324, 340, 356 and 388.
26. The nucleic acid of the embodiments any one of the embodiments 1-2, 4, 7 14 and 20 wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 3 and 18.

27. The nucleic acid of any one of the embodiments in paragraphs 1-2, 4, 10, 15 and 21 wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 6 and 21.
28. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5, 8, 16 and 22 wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 33, 49, 113, 241, 257, 273, 369, 401, 417, 534, 547, and 560.
29. The nucleic acid of any one of the embodiments in paragraphs 1-2, 5, 11, 17 and 23 wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 36, 52, 116, 244, 260, 276, 372, 404, 420, 537, 550, and 563.
30. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 9; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 12.
31. The nucleic acid of any one of the embodiments in paragraphs 1-5 or 30, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 1,
 - ii. a CDR2 of SEQ ID NO: 2, and
 - iii. a CDR3 of SEQ ID NO: 3; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 4,
 - ii. a CDR2 of SEQ ID NO: 5, and
 - iii. a CDR3 of SEQ ID NO: 6.
32. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 24; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 27.
33. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 32, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 16,
 - ii. a CDR2 of SEQ ID NO: 17, and
 - iii. a CDR3 of SEQ ID NO: 18; and

- b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 19,
 - ii. a CDR2 of SEQ ID NO: 20, and
 - iii. a CDR3 of SEQ ID NO: 21.
- 34. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 39; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 42.
- 35. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 34, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 31,
 - ii. a CDR2 of SEQ ID NO: 32, and
 - iii. a CDR3 of SEQ ID NO: 33; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 34,
 - ii. a CDR2 of SEQ ID NO: 35, and
 - iii. a CDR3 of SEQ ID NO: 36.
- 36. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 55; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 58.
- 37. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 36, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 47,
 - ii. a CDR2 of SEQ ID NO: 48, and
 - iii. a CDR3 of SEQ ID NO: 49; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 50,
 - ii. a CDR2 of SEQ ID NO: 51, and
 - iii. a CDR3 of SEQ ID NO: 52.
- 38. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 71; and

- b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 74.
39. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 38, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 63,
 - ii. a CDR2 of SEQ ID NO: 64, and
 - iii. a CDR3 of SEQ ID NO: 65; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 66,
 - ii. a CDR2 of SEQ ID NO: 67, and
 - iii. a CDR3 of SEQ ID NO: 68.
40. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 87; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 90.
41. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 40, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 79,
 - ii. a CDR2 of SEQ ID NO: 80, and
 - iii. a CDR3 of SEQ ID NO: 81; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 82,
 - ii. a CDR2 of SEQ ID NO: 83, and
 - iii. a CDR3 of SEQ ID NO: 84.
42. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 103; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 106.
43. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 42, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 95,
 - ii. a CDR2 of SEQ ID NO: 96, and
 - iii. a CDR3 of SEQ ID NO: 97; and
 - b. the TCR beta chain construct comprises

- i. a CDR1 of SEQ ID NO: 98,
 - ii. a CDR2 of SEQ ID NO: 99, and
 - iii. a CDR3 of SEQ ID NO: 100.
- 44. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 119; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 122.
- 45. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 44, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 111,
 - ii. a CDR2 of SEQ ID NO: 112, and
 - iii. a CDR3 of SEQ ID NO: 113; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 114,
 - ii. a CDR2 of SEQ ID NO: 115, and
 - iii. a CDR3 of SEQ ID NO: 116.
- 46. The nucleic acid of any one of the embodiments 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 247; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 250.
- 47. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 46, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 239,
 - ii. a CDR2 of SEQ ID NO: 240, and
 - iii. a CDR3 of SEQ ID NO: 241; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 242,
 - ii. a CDR2 of SEQ ID NO: 243, and
 - iii. a CDR3 of SEQ ID NO: 244.
- 48. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 263; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 266.

49. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 48, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 255,
 - ii. a CDR2 of SEQ ID NO: 256, and
 - iii. a CDR3 of SEQ ID NO: 257; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 258,
 - ii. a CDR2 of SEQ ID NO: 259, and
 - iii. a CDR3 of SEQ ID NO: 260.
50. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 279; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 282.
51. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 50, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 271,
 - ii. a CDR2 of SEQ ID NO: 272, and
 - iii. a CDR3 of SEQ ID NO: 273; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 274,
 - ii. a CDR2 of SEQ ID NO: 275, and
 - iii. a CDR3 of SEQ ID NO: 276.
52. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 295; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 298.
53. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 52, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 287,
 - ii. a CDR2 of SEQ ID NO: 288, and
 - iii. a CDR3 of SEQ ID NO: 289; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 290,
 - ii. a CDR2 of SEQ ID NO: 291, and

- iii. a CDR3 of SEQ ID NO: 292.
54. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 311; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 314.
55. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 54, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 303,
 - ii. a CDR2 of SEQ ID NO: 304, and
 - iii. a CDR3 of SEQ ID NO: 305; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 306,
 - ii. a CDR2 of SEQ ID NO: 307, and
 - iii. a CDR3 of SEQ ID NO: 308.
56. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 327; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 330.
57. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 56, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 319,
 - ii. a CDR2 of SEQ ID NO: 320, and
 - iii. a CDR3 of SEQ ID NO: 321; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 322,
 - ii. a CDR2 of SEQ ID NO: 323, and
 - iii. a CDR3 of SEQ ID NO: 324.
58. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 343; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 346.
59. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 58, wherein
- a. the TCR alpha chain construct comprises

- i. a CDR1 of SEQ ID NO: 335,
 - ii. a CDR2 of SEQ ID NO: 336, and
 - iii. a CDR3 of SEQ ID NO: 337; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 338,
 - ii. a CDR2 of SEQ ID NO: 339, and
 - iii. a CDR3 of SEQ ID NO: 340.
- 60. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 359; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 361.
- 61. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 60, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 351,
 - ii. a CDR2 of SEQ ID NO: 352, and
 - iii. a CDR3 of SEQ ID NO: 353; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 354,
 - ii. a CDR2 of SEQ ID NO: 355, and
 - iii. a CDR3 of SEQ ID NO: 356.
- 62. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 375; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 378.
- 63. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 62, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 367,
 - ii. a CDR2 of SEQ ID NO: 368, and
 - iii. a CDR3 of SEQ ID NO: 369; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 370,
 - ii. a CDR2 of SEQ ID NO: 371, and
 - iii. a CDR3 of SEQ ID NO: 372.
- 64. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein

- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 391; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 394.
65. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 64, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 383,
 - ii. a CDR2 of SEQ ID NO: 384, and
 - iii. a CDR3 of SEQ ID NO: 385; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 386,
 - ii. a CDR2 of SEQ ID NO: 387, and
 - iii. a CDR3 of SEQ ID NO: 388.
66. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 407; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 410.
67. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 66, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 399,
 - ii. a CDR2 of SEQ ID NO: 400, and
 - iii. a CDR3 of SEQ ID NO: 401; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 402,
 - ii. a CDR2 of SEQ ID NO: 403, and
 - iii. a CDR3 of SEQ ID NO: 404.
68. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 423; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 426.
69. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 68, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 415,
 - ii. a CDR2 of SEQ ID NO: 416, and

- iii. a CDR3 of SEQ ID NO: 417; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 418,
 - ii. a CDR2 of SEQ ID NO: 419, and
 - iii. a CDR3 of SEQ ID NO: 420.
- 70. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 542; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 543.
- 71. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 70, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 532,
 - ii. a CDR2 of SEQ ID NO: 533, and
 - iii. a CDR3 of SEQ ID NO: 534; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 535,
 - ii. a CDR2 of SEQ ID NO: 536, and
 - iii. a CDR3 of SEQ ID NO: 537.
- 72. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 555; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 556.
- 73. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 72, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 545,
 - ii. a CDR2 of SEQ ID NO: 546, and
 - iii. a CDR3 of SEQ ID NO: 547; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 548,
 - ii. a CDR2 of SEQ ID NO: 549, and
 - iii. a CDR3 of SEQ ID NO: 550.
- 74. The nucleic acid of any one of the embodiments in paragraphs 1-5, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 568; and

- b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 569.
75. The nucleic acid of any one of the embodiments in paragraphs 1-5 and 74, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 558,
 - ii. a CDR2 of SEQ ID NO: 559, and
 - iii. a CDR3 of SEQ ID NO: 560; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 561,
 - ii. a CDR2 of SEQ ID NO: 562, and
 - iii. a CDR3 of SEQ ID NO: 563.
76. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO: 144 and SEQ ID NO: 147.
77. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from TMPRSS2:ERG in complex with a human MHC, wherein the epitope from TMPRSS2:ERG comprises a region having at least 90% sequence identity to amino acid sequence SEQ ID NO: 156.
78. The nucleic acid of the embodiment in paragraph 76 or 77, wherein the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 150.
79. The nucleic acid of the embodiment in paragraph 76 or 77, wherein the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 153.
80. The nucleic acid of any one of the embodiments in paragraphs 76-80, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to SEQ ID NO: 142 or SEQ ID NO: 145 respectively.
81. The nucleic acid of any one of the embodiments in paragraphs 76-80, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to SEQ ID NO: 143 or SEQ ID NO: 146.
82. The nucleic acid of any one of the embodiments in paragraphs 76-81, wherein

- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 150; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 153.
83. The nucleic acid of any one of the embodiments in paragraphs 76-82, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 142,
 - ii. a CDR2 of SEQ ID NO: 143, and
 - iii. a CDR3 of SEQ ID NO: 144; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 145,
 - ii. a CDR2 of SEQ ID NO: 146, and
 - iii. a CDR3 of SEQ ID NO: 147.
84. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in complex with a human MHC, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOS: 129, 132, 191, 194, 206 and 209.
85. A nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant GATA3 peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises
- a. a TCR alpha chain construct and/or
 - b. a TCR beta chain construct.
86. A recombinant nucleic acid, or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR
- a. specifically binds to a mutant GATA3 peptide in complex with an HLA-A02:01, HLA-B07:02 or HLA-B08:01 protein;
 - b. comprises an alpha chain complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to SEQ ID NOS: 129, 132, 191, 194, 206 or 209; and/or
 - c. specifically binds to a mutant GATA3 peptide comprising a region with at least 70% sequence identity to or 100% sequence identity to SEQ ID NO: 141, 203 or 218.
87. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from GATA3 in

complex with a human MHC, wherein the epitope from GATA3 comprises a region having at least 90% sequence identity to or 100% sequence identity to amino acid sequence SEQ ID NO: 141, 203 or 218.

88. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 135, 197 or 212.
89. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 138, 200 or 215.
90. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 127, 130, 189, 192, 204 and 207.
91. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 128, 131, 190, 193, 205 and 208.
92. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 135; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 138.
93. The nucleic acid of embodiment in paragraph 86, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 127,
 - ii. a CDR2 of SEQ ID NO: 128, and
 - iii. a CDR3 of SEQ ID NO: 129; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 130,
 - ii. a CDR2 of SEQ ID NO: 131, and
 - iii. a CDR3 of SEQ ID NO: 132.
94. The nucleic acid of any one of the embodiments in paragraphs 84-87, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 197; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 200.

95. The nucleic acid of the embodiment in paragraph 94, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 189,
 - ii. a CDR2 of SEQ ID NO: 190, and
 - iii. a CDR3 of SEQ ID NO: 191; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 192,
 - ii. a CDR2 of SEQ ID NO: 193, and
 - iii. a CDR3 of SEQ ID NO: 194.
96. The nucleic acid of any one of the embodiments in paragraphs 78-85, wherein
- a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 212; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 215.
97. The nucleic acid of the embodiment in paragraph 90, wherein
- a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 204,
 - ii. a CDR2 of SEQ ID NO: 205, and
 - iii. a CDR3 of SEQ ID NO: 206; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 207,
 - ii. a CDR2 of SEQ ID NO: 208, and
 - iii. a CDR3 of SEQ ID NO: 209.
98. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NO: 161 and SEQ ID NO: 176, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NO: 164 and SEQ ID NO: 179.
99. A nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant BTK peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises
- (a) a TCR alpha chain construct and/or
 - (b) a TCR beta chain construct.

100. A recombinant nucleic acid, or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR
 - a. specifically binds to a mutant BTK peptide in complex with an HLA-A02:01 protein;
 - b. comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to SEQ ID NO: 161, 164, 176, or 179; and/or
 - c. specifically binds to a mutant BTK peptide comprising a region with at least 70% sequence identity to or 100% sequence identity to SEQ ID NO: 173 or 188.
101. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from BTK in complex with a human MHC, wherein the epitope from BTK comprises a region having at least 90% sequence identity to or 100% sequence identity to amino acid sequence SEQ ID NO: 173 or 188.
102. The nucleic acid of any one of the embodiments in paragraphs 98-101, wherein the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 167 or 182.
103. The nucleic acid of any one of the embodiments in paragraphs 98-102, wherein the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 170 or 185.
104. The nucleic acid of any one of the embodiments in paragraphs 98-103, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 159, 162, 174, and 177.
105. The nucleic acid of any one of the embodiments in paragraphs 98-104, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 160, 163, 175 and 178.
106. The nucleic acid of any one of the embodiments in paragraphs 98-105, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 167 or 182; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 170 or 185.
107. The nucleic acid of any one of the embodiments in paragraphs 98-106, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 159 or 174,
 - ii. a CDR2 of SEQ ID NO: 160 or 175, and
 - iii. a CDR3 of SEQ ID NO: 161 or 176; and

- b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 162 or 177,
 - ii. a CDR2 of SEQ ID NO: 163 or 178, and
 - iii. a CDR3 of SEQ ID NO: 164 or 179.
108. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the TCR alpha chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NO: 449, SEQ ID NO: 466, SEQ ID NO: 483, SEQ ID NO: 500, and SEQ ID NO: 517, or wherein the TCR beta chain construct comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NO: 452, SEQ ID NO: 469, SEQ ID NO: 486, SEQ ID NO: 503, and SEQ ID NO: 520.
109. A nucleic acid encoding at least one T cell receptor (TCR) capable of specifically binding to a mutant EGFR peptide in complex with a protein encoded by an HLA allele of a subject with cancer, wherein the TCR comprises
- a. a TCR alpha chain construct and/or
 - b. a TCR beta chain construct.
110. A recombinant nucleic acid, or a cell comprising a recombinant nucleic acid, wherein the nucleic acid encodes a T cell receptor (TCR) comprising a TCR alpha chain construct and/or a TCR beta chain construct, wherein the TCR
- a. specifically binds to a mutant EGFR peptide in complex with an HLA-A02:01 protein;
 - b. comprises a complementarity determining region 3 (CDR3) having at least 90% sequence identity to or 100% sequence identity to SEQ ID NO: 449, 466, 483, 500, 517, 452, 469, 486, 503, or 520; and/or
 - c. specifically binds to a mutant EGFR peptide comprising a region with at least 70% sequence identity to or 100% sequence identity to SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.
111. A nucleic acid encoding at least one T cell receptor (TCR) comprising a TCR alpha chain construct and/or TCR beta chain construct capable of specifically binding to an epitope from EGFR in complex with a human MHC, wherein the epitope from EGFR comprises a region having at least 90% sequence identity to or 100% sequence identity to amino acid sequence SEQ ID NO: 461, 462, 463, 478, 479, 480, 495, 496, 497, 512, 513, 514, 529, 530 or 531.
112. The nucleic acid of any one of the embodiments in paragraphs 108-111, wherein the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 455, 472, 489, 506 or 526.

113. The nucleic acid of any one of the embodiments in paragraphs 108-112, wherein the TCR beta chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 458, 475, 492, 509, or 526.
114. The nucleic acid of any one of the embodiments in paragraphs 108-113, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 1 (CDR1) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 447, 464, 481, 498, 515, 450, 467, 484, 501, and 518.
115. The nucleic acid of any one of the embodiments in paragraphs 108-114, wherein the TCR alpha chain construct and/or the TCR beta chain construct comprises a complementarity determining region 2 (CDR2) having at least 90% sequence identity to or 100% sequence identity to an amino acid sequence selected from SEQ ID NOs: 448, 465, 482, 499, 516, 451, 468, 485, 502, and 519.
116. The nucleic acid of any one of the embodiments in paragraphs 108-115, wherein
 - a. the TCR alpha chain construct comprises a variable region having at least 80% sequence identity to or 100% sequence identity to SEQ ID NO: 455, 472, 489, 506, or 523; and
 - b. the TCR beta chain construct comprises a variable region having at least 80% sequence identity to SEQ ID NO: 458, 475, 492, 509 or 526.
117. The nucleic acid of any one of the embodiments in paragraphs 108-116, wherein
 - a. the TCR alpha chain construct comprises
 - i. a CDR1 of SEQ ID NO: 447, 464, 481, 498 or 515,
 - ii. a CDR2 of SEQ ID NO: 448, 465, 482, 499 or 516, and
 - iii. a CDR3 of SEQ ID NO: 449, 466, 483, 500 or 517; and
 - b. the TCR beta chain construct comprises
 - i. a CDR1 of SEQ ID NO: 450, 467, 484, 501 or 518,
 - ii. a CDR2 of SEQ ID NO: 451, 468, 485, 502, or 519, and
 - iii. a CDR3 of SEQ ID NO: 452, 469, 486, 503, or 520.
118. The nucleic acid of any one of the embodiments in paragraphs 1-117, wherein the epitope comprises a mutation selected from the group consisting of a point mutation, a splice-site mutation, a frameshift mutation, a read-through mutation, a resistance mutation, a gene fusion mutation and any combination thereof
119. The nucleic acid of any one of the embodiments 1-69, wherein the human MHC is encoded by either HLA-A02:01 allele, or HLA-A03:01 allele or HLA-A11:01 allele.
120. The nucleic acid of any one of the embodiments in paragraphs 1-69, wherein the epitope comprises a point mutation.
121. The nucleic acid of the embodiment in paragraph 120, wherein the point mutation is a G12V mutation.

122. The nucleic acid of the embodiment in paragraph 120, wherein the point mutation is a G12C mutation.
123. The nucleic acid of the embodiment in paragraph 120, wherein the point mutation is a G12D mutation.
124. The nucleic acid of any one of the embodiments in paragraphs 76-83, wherein the human MHC is encoded by HLA-A02:01 allele.
125. The nucleic acid of any one of the embodiments in paragraphs 76-83 and 124, wherein the epitope comprises a gene fusion mutation.
126. The nucleic acid of any one of the embodiments in paragraphs 84-97, wherein the human MHC is encoded by HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.
127. The nucleic acid of any one of the embodiments in paragraphs 84-97 and 126, wherein the epitope comprises a frameshift mutation.
128. The nucleic acid of any one of the embodiments in paragraphs 98-107, wherein the human MHC is encoded by HLA-A02:01 allele.
129. The nucleic acid of any one of the embodiments in paragraphs 98-107 and 128, wherein the epitope comprises a point mutation.
130. The nucleic acid of the embodiment in paragraph 129, wherein the point mutation is C481S mutation.
131. The nucleic acid of any one of the embodiments in paragraphs 108-117, wherein the human MHC is encoded by HLA-A02:01 allele.
132. The nucleic acid of any one of the embodiments in paragraphs 108-117, wherein the epitope comprises a point mutation.
133. The nucleic acid of embodiment in paragraph 132, wherein the point mutation is T790M.
134. The nucleic acid of any one of the embodiments in paragraphs 1-130, wherein the epitope has a length of at least 8 amino acids.
135. The nucleic acid of any one of the embodiments in paragraphs 1-134, wherein the epitope has a length of at least 16 amino acids.
136. The nucleic acid of any one of the embodiments 1-135, wherein the epitope has a length of from 8-25 amino acids.
137. The nucleic acid of any one of the embodiments 1-136, wherein the epitope has a length of from 8-12 amino acids.
138. The nucleic acid of any one of the embodiments in paragraphs 1-136, wherein the epitope has a length of from 16-25 amino acids.
139. The nucleic acid of any one of the embodiments in paragraphs 1-136, wherein the epitope has a length of 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids.
140. The nucleic acid of any one of the embodiments in paragraphs 1-139, wherein the epitope binds to the human MHC with a greater affinity than a corresponding wild-type epitope.

141. The nucleic acid of any one of the embodiments in paragraphs 1-140, wherein the epitope binds to the human MHC with a KD or an IC50 less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM.
142. The nucleic acid of any one of the embodiments 108-141, wherein the mutation is not present in non-cancer cells of a subject.
143. The nucleic acid of any one of the embodiments in paragraphs 1-142, wherein the epitope is encoded by a gene or an expressed gene of a subject's cancer cells.
144. The nucleic acid of any one of the embodiments in paragraphs 1-143, wherein the TCR binds to a MHC-peptide complex with a KD or an IC50 of less than 500 nM, 250 nM, 150 nM, 100 nM, 50 nM, 25 nM or 10 nM.
145. The nucleic acid of any one of the embodiments in paragraphs 1-144, wherein the nucleic acid is operably linked to a promoter.
146. A vector comprising the nucleic acid of any one of the embodiments in paragraphs 1-145.
147. The vector of the embodiment in paragraph 146, wherein the vector is a self-amplifying RNA replicon, plasmid, phage, transposon, cosmid, virus, or virion.
148. The vector of the embodiment in paragraphs 146 or 147, wherein the vector is a viral vector.
149. The vector of the embodiment in paragraph 148, wherein the vector is derived from a retrovirus, lentivirus, adenovirus, adeno-associated virus, herpes virus, pox virus, alpha virus, vaccinia virus, hepatitis B virus, human papillomavirus or a pseudotype thereof.
150. The vector of the embodiment in paragraphs 146 or 147, wherein the vector is a non-viral vector.
151. The vector of the embodiment in paragraph 150, wherein the non-viral vector is a nanoparticle, a cationic lipid, a cationic polymer, a metallic nanopolymer, a nanorod, a liposome, a micelle, a microbubble, a cell-penetrating peptide, or a liposphere.
152. A protein encoded by the nucleic acid of any one of the embodiments in paragraphs 1-145.
153. A cell comprising the nucleic acid of any one embodiment in paragraphs 1-149, the vector of any one of the embodiments 144-149, or the protein of embodiment 146.
154. The cell of the embodiment 153, wherein the cell is a CD4+ T cell.
155. The cell of the embodiment 153, wherein the cell is a CD8+ T cell.
156. The cell of the embodiment 153, wherein the cell is an autologous cell.
157. The cell of the embodiment 153, wherein the cell is an allogeneic cell.
158. The cell of the embodiment 153, wherein the cell is a natural killer cell, a B cell, or an immortalized cell line.
159. The cell of any one of the embodiments in paragraphs 153-156, wherein the cell is a human cell.
160. A pharmaceutical composition comprising the nucleic acid of any one of the embodiments in paragraphs 1-143, the vector of any one of the embodiments in paragraphs 146-151, the protein of

- embodiment in paragraph 152, or the cell of any one of the embodiments in paragraphs 153-159; and a pharmaceutically acceptable excipient or diluent.
161. The pharmaceutical composition of the embodiment in paragraphs 160, further comprising an immunomodulatory agent or an adjuvant.
162. The pharmaceutical composition of the embodiment in paragraph 161, wherein the immunomodulatory agent is a cytokine.
163. The pharmaceutical composition of any one of the embodiments in paragraphs 160-162 wherein the adjuvant is poly I:C.
164. The pharmaceutical composition of any one of the embodiments in paragraphs 160-163, for use in treating an immune disease or cancer.
165. Use of the pharmaceutical composition of any one of the embodiments in paragraphs 160-164, for treating an immune disease or cancer.
166. Use of the nucleic acid of any one of the embodiments in paragraphs 1-145, the vector of any one of the embodiments in paragraphs 146-151, the protein of embodiment in paragraph 152, or the cell of any one of the embodiments 153-159, for manufacture of a medicament for treating an immune disease or cancer.
167. The use of the embodiment in paragraph 166, wherein the medicament is an adoptive T cell therapy or a TCR gene therapy.
168. A method of treating a subject with a disease or condition, comprising administering to the subject the pharmaceutical composition of any one of the embodiments in paragraphs 160-164.
169. A method of treating a subject with cancer comprising administering to the subject the pharmaceutical composition of any one of the embodiments in paragraphs 160-164.
170. A method of treating a subject with cancer comprising administering to the subject the pharmaceutical composition of any one of the embodiments in paragraphs 160-164; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01 allele, an HLA-B07:02, an HLA-B08:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele of the subject's genome.
171. A method of treating a subject with cancer comprising administering a TCR or T cell expressing the TCR to the subject, wherein the TCR specifically binds to a mutant RAS peptide in complex with a protein encoded by an HLA-A02:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the subject expresses the HLA allele.

172. A method of treating a subject with cancer comprising administering to the subject the pharmaceutical composition of any one of the embodiments in paragraphs 154-158; wherein the TCR binds to a mutant RAS peptide comprising a mutation at G12 in complex with an HLA-A02:01, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01; wherein the subject is identified as expressing a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele.
173. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises at least one mutant amino acid and is fragment of at least 8 contiguous amino acids of a mutant GATA3 protein arising from a mutation in a GATA3 gene of a cancer cell; wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.
174. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises one or more mutant GATA3 amino acids encoded by a GATA3 neoORF sequence, wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.
175. A method of treating a subject with cancer comprising administering a TCR or T cell expressing the TCR to the subject; wherein the TCR specifically binds to a mutant GATA3 peptide in complex with a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele; wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.
176. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant TMPRSS2:ERG peptide in complex with an HLA protein; wherein the mutant TMPRSS2:ERG peptide comprises at least one mutant amino acid and is a fragment of a TMPRSS2:ERG gene fusion mutation; wherein the mutant TMPRSS2:ERG peptide binds to a protein encoded by an HLA-A02:01 allele.
177. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises at least one mutant amino acid; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.
178. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA

protein; wherein the mutant BTK peptide comprises a resistance mutation or a point mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.

179. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a C481S mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.
180. A method of treating a subject with cancer comprising administering to the subject a composition comprising a T cell receptor (TCR) or a T cell expressing the TCR to the subject, wherein the TCR specifically binds to a mutant EGFR peptide in complex with a protein encoded by an HLA-A02:01; wherein the mutant EGFR peptide comprises a resistance mutation or a point mutation, wherein the subject is identified as expressing or expresses a protein encoded by an HLA-A02:01 allele.
181. The method of embodiment in paragraph 178, wherein the mutant EGFR peptide comprises a T790M mutation.
182. A method of preventing resistance to a cancer therapy, the method comprising administering to a subject in need thereof the pharmaceutical composition of any one of the embodiments in paragraph 160-164.
183. A method of inducing an immune response, the method comprising administering to a subject in need thereof the pharmaceutical composition of any one of the embodiments in paragraphs 160-164.
184. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as a subject that expresses a protein encoded by an HLA-A02:01 allele, an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the therapeutic is the pharmaceutical composition of any one of the embodiments in paragraphs 160-164.
185. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant GATA3 peptide in complex with an HLA protein; wherein the mutant GATA3 peptide comprises at least one mutant amino acid and is fragment of at least 8 contiguous amino acids of a mutant GATA3 protein arising from a mutation in a GATA3 gene of a cancer cell; wherein the mutant GATA3 peptide binds to a protein encoded by an HLA-A02:01, HLA-B07:02 or HLA-B08:01 allele.
186. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant RAS peptide comprising a

mutation at G12 in complex with an HLA protein; wherein the mutant RAS peptide binds to a protein encoded by an HLA-A03:01 allele, an HLA-A11:01 allele, an HLA-A03:02 allele, an HLA-A30:01 allele, an HLA-A31:01 allele, an HLA-A33:01 allele, an HLA-A33:03 allele, an HLA-A68:01 allele, or an HLA-A74:01 allele.

187. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant TMPRSS2:ERG peptide in complex with an HLA protein; wherein the mutant TMPRSS2:ERG peptide comprises at least one mutant amino acid and is a fragment of a TMPRSS2:ERG gene fusion mutation; wherein the mutant TMPRSS2:ERG peptide binds to a protein encoded by an HLA-A02:01 allele.
188. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises at least one mutant amino acid; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.
189. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a resistance mutation or a point mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.
190. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic a T cell receptor (TCR) specific for a mutant BTK peptide in complex with an HLA protein; wherein the mutant BTK peptide comprises a C481S mutation; wherein the mutant BTK peptide binds to a protein encoded by an HLA-A02:01 allele.
191. A method of identifying a subject with cancer as a candidate for a therapeutic, the method comprising identifying the subject as one that expresses a protein encoded by an HLA-A02:01 allele, wherein the therapeutic comprises a T cell receptor (TCR) specific for a mutant EGFR peptide in complex with an HLA protein; wherein the mutant EGFR peptide comprises at least one mutant amino acid T790M; wherein the mutant EGFR peptide binds to a protein encoded by an HLA-A02:01 allele.
192. The method of any one of the embodiments in paragraphs 162-185, wherein the cancer is selected from the group consisting of breast cancer, lung cancer, non-small cell lung cancer, pancreatic cancer, colorectal cancer, uterine cancer, melanoma, ovarian cancer, prostate cancer, endometrial cancer, chronic lymphocytic leukemia (CLL) and liver cancer.
193. The method of any one of the embodiments in paragraphs 162-185, wherein the subject has a breast cancer that is resistant to anti-estrogen therapy, is an MSI breast cancer, is a metastatic breast cancer,

is a Her2 negative breast cancer, is a Her2 positive breast cancer, is an ER negative breast cancer, is an ER positive breast cancer is a recurrent breast cancer, is a metastatic breast cancer, or any combination thereof.

194. The method of the embodiment 193, wherein the breast cancer expresses an estrogen receptor with a mutation.
195. The method of any one of the embodiments in paragraphs 169-191, wherein the subject has a breast cancer that is resistant to anti-estrogen therapy.
196. The method of the embodiment in paragraph 195, wherein the breast cancer expresses an estrogen receptor with a mutation.
197. The method of any one of the embodiments in paragraphs 169-196, wherein the subject has a CLL that is resistant to ibrutinib therapy.
198. The method of the embodiment in paragraph 197, wherein the CLL expresses a Bruton tyrosine kinase (BTK) with a mutation, such as a C481S mutation.
199. The method of any one of the embodiments in paragraph 169-197, wherein the subject has a lung cancer that is resistant to a tyrosine kinase inhibitor.
200. The method of the embodiment in paragraphs 199, wherein the lung cancer expresses an epidermal growth factor receptor (EGFR) with a mutation, such as a T790M, L792F, or C797S mutation.
201. The method of any one of the embodiments in paragraphs 169-200, further comprising administering at least one additional therapeutic agent or modality.
202. The method of any one of the embodiments in paragraphs in paragraphs 168-200, wherein an immune response is elicited in the subject.
203. The method of the embodiment in paragraph 200, wherein the immune response is a humoral response.
204. The method of the embodiment in paragraph 200, wherein the immune response is a cytotoxic T cell response.
205. The method of any one of the embodiments in paragraphs 168-204, further comprising administering at least one additional therapeutic agent or modality.
206. The method of the embodiment in paragraphs 205, wherein the at least one additional therapeutic agent or modality is surgery, a checkpoint inhibitor, an antibody or fragment thereof, a chemotherapeutic agent, radiation, a vaccine, a small molecule, a T cell, a vector, and APC, a polynucleotide, an oncolytic virus or any combination thereof.
207. The method of the embodiment in paragraph 206, wherein the at least one additional therapeutic agent is an anti-PD-1 agent and anti-PD-L1 agent, an anti-CTLA-4 agent, or an anti-CD40 agent.
208. The method of the embodiment in paragraph 206 or 207, wherein the additional therapeutic agent is administered before, simultaneously, or after administering the pharmaceutical composition of any one of the embodiments 160-164.

209. The method of any one of the embodiments in paragraphs 169-183, or any one of the embodiments in paragraphs 201-208 wherein administering comprises administering subcutaneously or intravenously.
210. The method of any one of the embodiments in paragraphs 169-209, wherein the subject is a subject that has had disease progression following endocrine therapy in combination with a CDK 4/6 inhibitor.
211. A method comprising:
- identifying neoantigen-specific T cells from a sample comprising a population of T cells;
 - identifying one or more peptides of a peptide-MHC complex that are presented by an antigen presenting cell (APC);
 - identifying a variable sequence of a T cell receptor (TCR) from the neoantigen-specific T cells;
 - expressing a recombinant TCR comprising the variable sequence of the TCR identified in a TCR cell; and
 - performing a functional assay, wherein the functional assay comprises contacting the TCR cell to a peptide-MHC complex comprising a peptide of the one or more peptides identified.
212. The method of the embodiment in paragraph 211, wherein the method comprises obtaining the sample comprising the population of cells comprising the neoantigen-specific T cells.
213. The method of the embodiment in paragraph 212, wherein obtaining the sample comprises obtaining a T cell sample from a healthy subject or from a subject with cancer.
214. The method of the embodiment in paragraph 213, wherein the T cell sample is from a healthy donor.
215. The method of the embodiment in paragraph 213 or 214, wherein the T cell sample is a peripheral blood mononuclear cell (PBMC) sample.
216. The method of any one of the embodiments in paragraphs 211-215, wherein identifying neoantigen-specific T cells comprises contacting the population of T cells to at least one peptide-MHC multimer complex comprising a neoantigen peptide.
217. The method of any one of the embodiments in paragraphs 205-209, wherein identifying neoantigen-specific T cells comprises contacting the population of T cells to a peptide-MHC complex comprising a neoantigen peptide.
218. The method of the embodiment in paragraph 211, wherein identifying neoantigen-specific T cells comprises contacting the population of T cells to an APC comprising the peptide-MHC complex.
219. The method of any one of the embodiments in paragraphs 216-218, wherein identifying neoantigen-specific T cells further comprises isolating T cells of the T cell population specific to the peptide-MHC complex.
220. The method of any one of the embodiments 216-218, wherein identifying neoantigen-specific T cells further comprises identifying or predicting T cells of the of the T cell population specific to the peptide-MHC complex based on TCR clonality.

221. The method of the embodiment in paragraphs 220, wherein identifying a variable sequence of a TCR from the neoantigen-specific T cells is performed before identifying neoantigen-specific T cells.
222. The method of any one of the embodiments in paragraphs 211-221, wherein identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing DNA, RNA, or amplified products thereof from one or more neoantigen-specific T cells that encode the variable sequence.
223. The method of any one of the embodiments in paragraphs 211-222, wherein identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing DNA, RNA, or amplified products thereof from a single neoantigen-specific T cell that encodes the variable sequence.
224. The method of any one of the embodiments in paragraphs 215-223, wherein identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises sequencing barcoded DNA or barcoded RNA, or amplified products thereof, from one or more neoantigen-specific T cells that encode the variable sequence.
225. The method of any one of the embodiments in paragraphs 221-224, wherein identifying a variable sequence of a TCR from the neoantigen-specific T cells comprises pairing a TCR-alpha chain with a TCR-beta chain.
226. The method of any one of the embodiments in paragraphs 211-225, wherein expressing a recombinant TCR comprises expressing the variable sequence identified from a polynucleotide comprising a sequence encoding the variable sequence identified.
227. The method of the embodiment in paragraph 226, wherein the polynucleotide is a vector.
228. The method of the embodiment in paragraph 227, wherein the vector is a viral vector.
229. The method of the embodiment in paragraph 228, wherein the viral vector is a lentiviral vector.
230. The method of any one of the embodiments in paragraphs 226-229, wherein expressing a recombinant TCR comprises transducing or transfecting the polynucleotide into cells.
231. The method of embodiment in paragraph 230, wherein the cells are a T cell line or healthy donor PMBCs.
232. The method of any one of the embodiments in paragraphs 211-231, wherein identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises expressing the one or more peptides in cells.
233. The method of any one of the embodiments in paragraphs 211-231, wherein identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises loading the one or more peptides onto MHCs of cells.
234. The method of any one of the embodiments in paragraphs 211-233, wherein identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises eluting or isolating a peptide of the one or more peptides from a peptide MHC complex.

235. The method of any one of the embodiments in paragraphs 211-234, wherein identifying one or more peptides of a peptide-MHC complex that are presented by an APC comprises performing mass spectrometry on a peptide of the one or more peptides that was isolated or eluted from a peptide-MHC complex.
236. The method of any one of the embodiments in paragraphs 211-235, wherein performing a functional assay comprises determining expression of one or more cell markers.
237. The method of embodiment in paragraph 236, the one or more cell markers comprise TNF- α , IFN- γ , LAMP-1, 4-1BB, IL-2, IL-17A, Granzyme B, PD-1, CD25, CD69, TIM3, LAG3, CTLA-4, CD62L, CD45RA, CD45RO, FoxP3, or any combination thereof.

CLAIMS

What is claimed is:

1. A recombinant nucleic acid encoding a T cell receptor (TCR) comprising a TCR beta chain construct comprising a beta chain complementarity determining region 1 (CDR1), a beta chain complementarity determining region 2 (CDR2), and a beta chain complementarity determining region 3 (CDR3); and a TCR alpha chain construct comprising an alpha chain CDR1, an alpha chain CDR2, and an alpha chain CDR3, wherein

(a) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 50, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 51, the beta chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 52, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 47, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 48, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 49, wherein the TCR specifically binds to a mutated RAS epitope from human RAS in complex with a human MHC encoded by an HLA-A11:01 allele; or

(b) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 66, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 67, the beta chain CDR3 has an amino acid sequence set forth in SEQ ID NO: 68, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 63, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 64, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 65, wherein the TCR specifically binds to the mutated epitope from the human RAS in complex with a human MHC encoded by an HLA-A03:01 allele; or

(c) the beta chain CDR1 has an amino acid sequence set forth in SEQ ID NO: 82, the beta chain CDR2 has an amino acid sequence set forth in SEQ ID NO: 83, the beta chain CDR3 has an amino acid sequence set forth in SEQ ID NO: 84, the alpha chain CDR1 has an amino acid sequence as set forth in SEQ ID NO: 79, the alpha chain CDR2 has an amino acid sequence as set forth in SEQ ID NO: 80, and the alpha chain CDR3 has an amino acid sequence as set forth in SEQ ID NO: 81, wherein the TCR specifically binds to the mutated epitope from the human RAS in complex with the human MHC encoded by the HLA-A03:01 allele;

wherein the mutated epitope from human RAS is characterized by a G12V mutation, wherein the mutated epitope comprises a sequence of VVGAVGVGK or VVVGAVGVGK.

2. The recombinant nucleic acid of claim 1, wherein (b) comprises the TCR beta chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 74.

3. The recombinant nucleic acid of claim 1 or 2, wherein (b) comprises the TCR alpha chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 71.
4. The recombinant nucleic acid of claim 1, wherein (c) comprises the TCR beta chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 90.
5. The recombinant nucleic acid of claim 1 or 4, wherein (c) comprises the TCR alpha chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 87.
6. The recombinant nucleic acid of claim 1, wherein (a) comprises the TCR beta chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 58.
7. The recombinant nucleic acid of claim 1 or 6, wherein (a) comprises the TCR alpha chain construct comprising a variable region having an amino acid sequence with at least 80% sequence identity to an amino acid sequence set forth in SEQ ID NO: 55.
8. The recombinant nucleic acid of any one of the preceding claims, wherein the recombinant nucleic acid is a vector.
9. The recombinant nucleic acid of any one of the preceding claims, wherein the epitope has a length of from 8-25 amino acids.
10. The recombinant nucleic acid of any one of the preceding claims, wherein the epitope binds to the human MHC with a greater affinity than a corresponding wild-type epitope.
11. The recombinant nucleic acid of any one of the preceding claims, wherein the mutation is not present in non-cancer cells of a subject.
12. The recombinant nucleic acid of any one of the preceding claims, wherein the nucleic acid is operably linked to a promoter.
13. A T cell comprising the recombinant nucleic acid of any one of the preceding claims, capable of expressing the TCR that specifically binds to the mutated epitope of human RAS in complex with a human MHC.
14. The T cell of claim 13, wherein the T cell is a CD4⁺ T cell or a CD8⁺ T cell.
15. The T cell of claim 13, wherein the T cell is isolated from a subject having a RAS mutation.
16. A pharmaceutical composition comprising:
 - a. the recombinant nucleic acid of any one of claims 1-12; or the cell of any one of claims 13-15; and,

- b. a pharmaceutically acceptable excipient or diluent.
17. A method of treating a subject having a cancer associated with a mutated RAS, comprising administering to the subject the cell of any one of claims 13-15 or the pharmaceutical composition of claim 16, wherein the mutated RAS is characterized by a G12V mutation comprising a sequence of VVGAVGVGK or VVVGAVGVGK.
18. The method of claim 17, wherein the cancer is a cancer selected from the group consisting of adenocarcinoma of the biliary tract, transitional cell carcinoma of the bladder, breast carcinoma, cervical adenocarcinoma, colon adenocarcinoma, colon adenoma, neuroblastoma (autonomic ganglia), acute myeloid leukemia, chronic myeloid leukemia, chronic myelomonocytic leukemia, juvenile myelomonocytic leukemia, acute lymphoblastic leukemia, Burkitt's lymphoma, Hodgkin's lymphoma, plasma cell myeloma, hepatocellular carcinoma, large cell carcinoma, non-small cell carcinoma, ductal carcinoma, endocrine tumor, prostate adenocarcinoma, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, angiosarcoma, leiomyosarcoma, liposarcoma, rhabdomyosarcoma, myxoma, malignant fibrous histiocytoma, pleomorphic sarcoma, germinoma, seminoma, anaplastic carcinoma, follicular carcinoma, papillary carcinoma and Hurthle cell carcinoma.
19. Use of the recombinant nucleic acid of any one of claims 1-12, or the cell of any one of claims 13-15, in the manufacture of a medicament for treating cancer associated with a RAS G12V mutation, wherein the RAS G12V mutation comprises a sequence of VVGAVGVGK or VVVGAVGVGK.

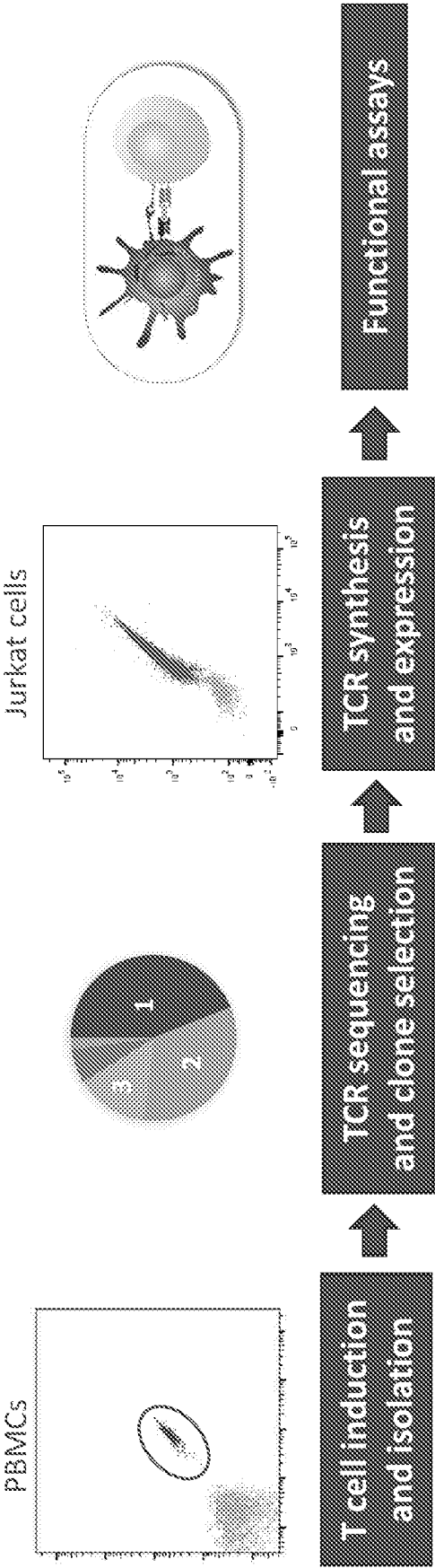


FIG. 1

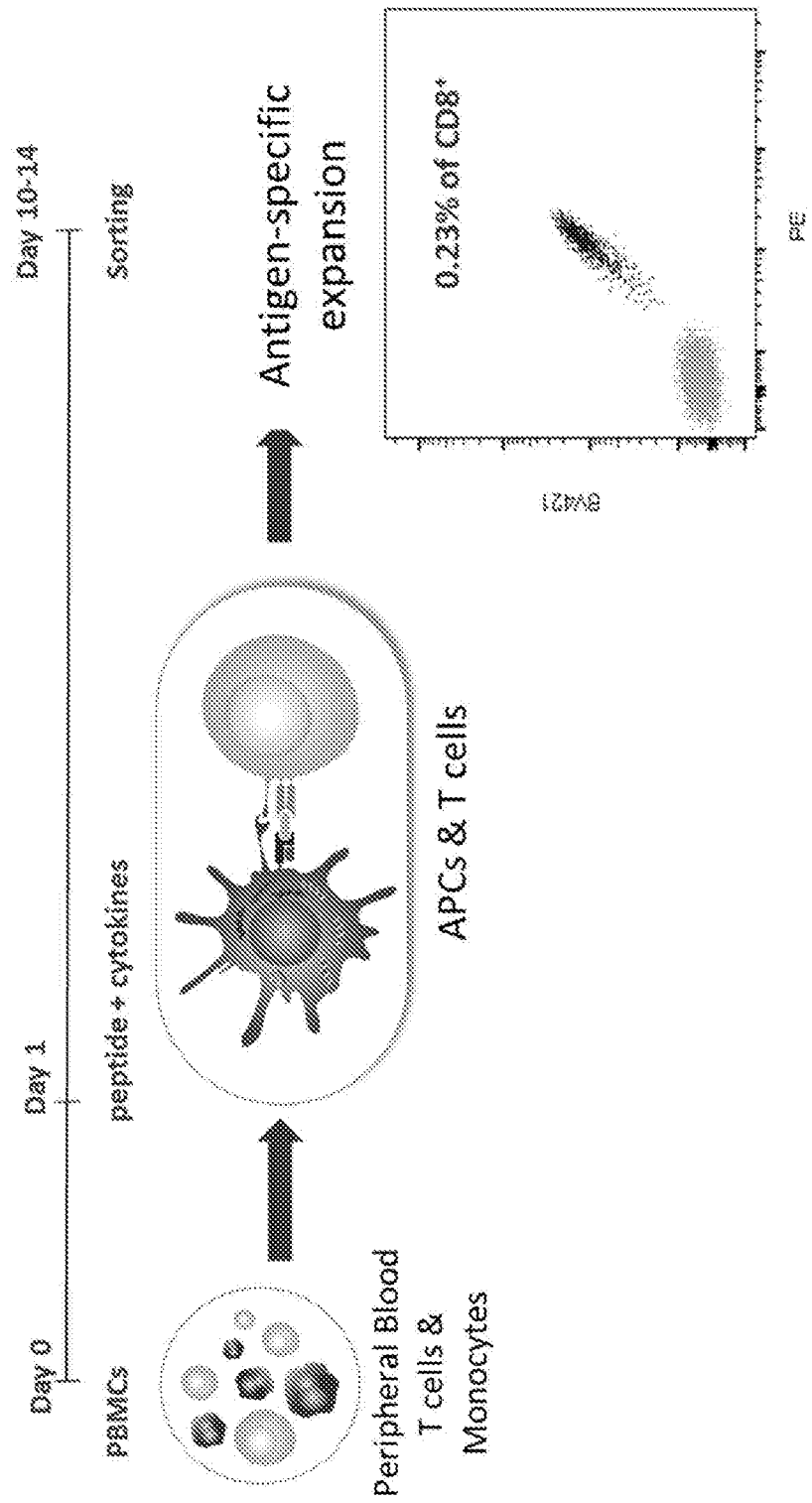


FIG. 2

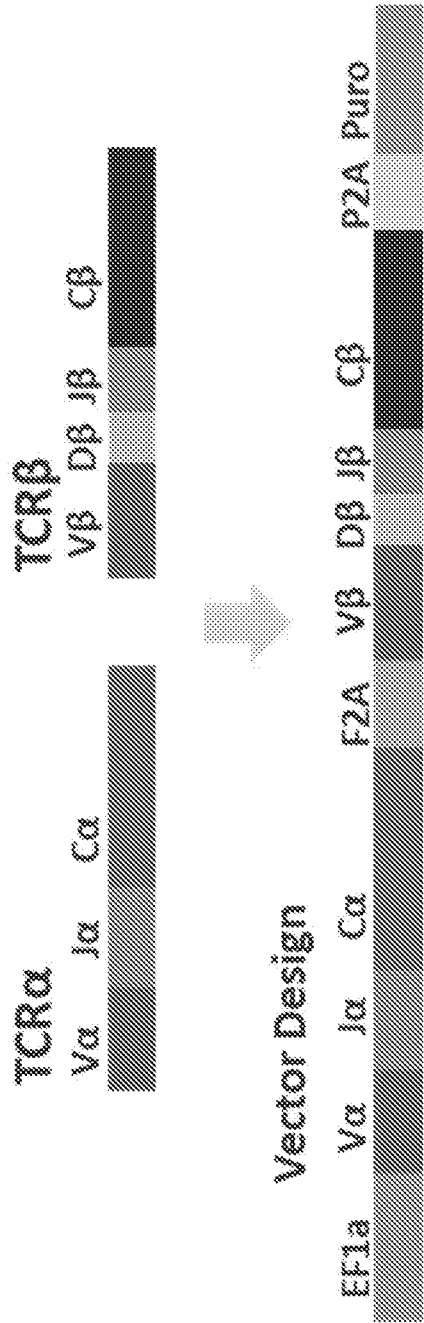
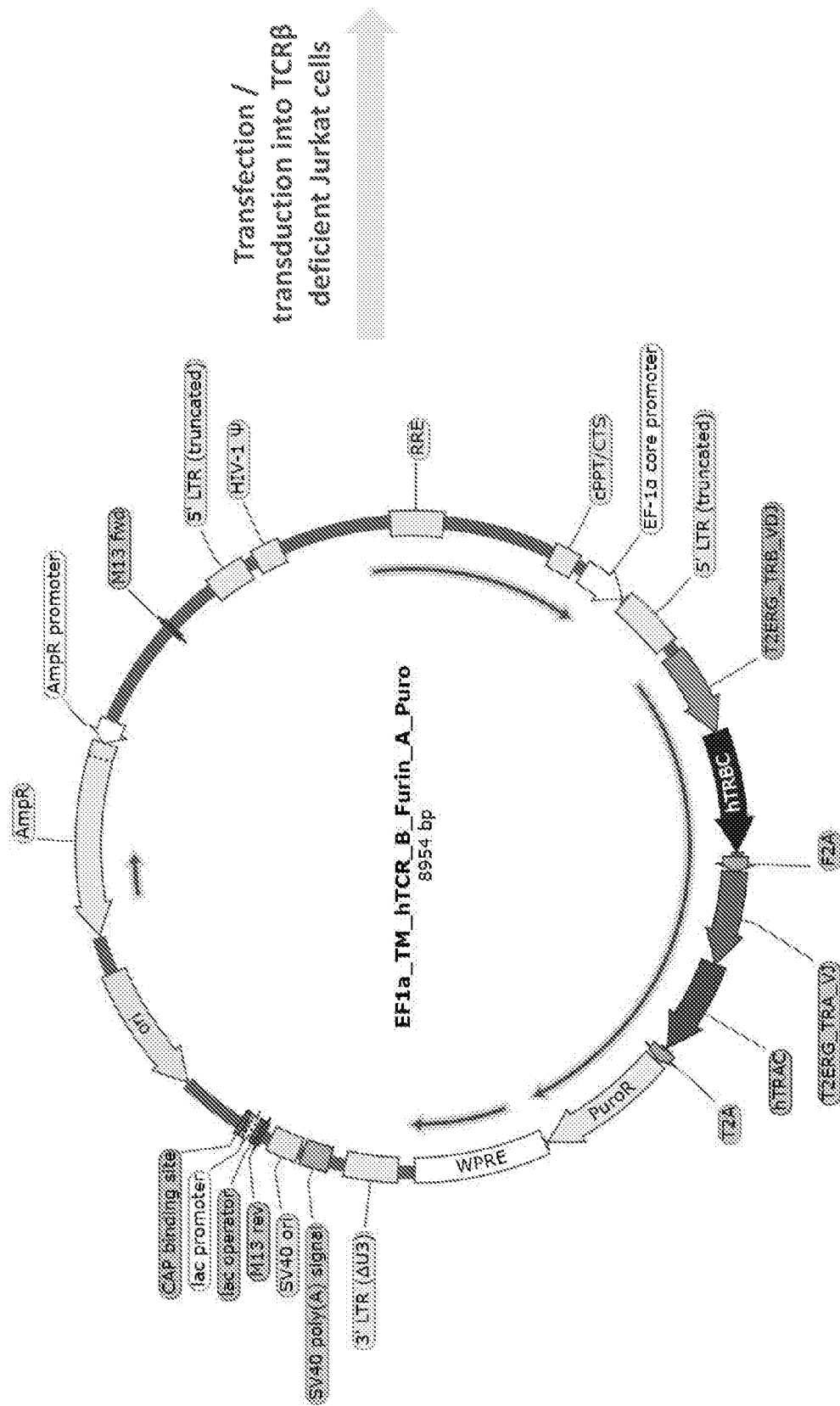


FIG. 3A



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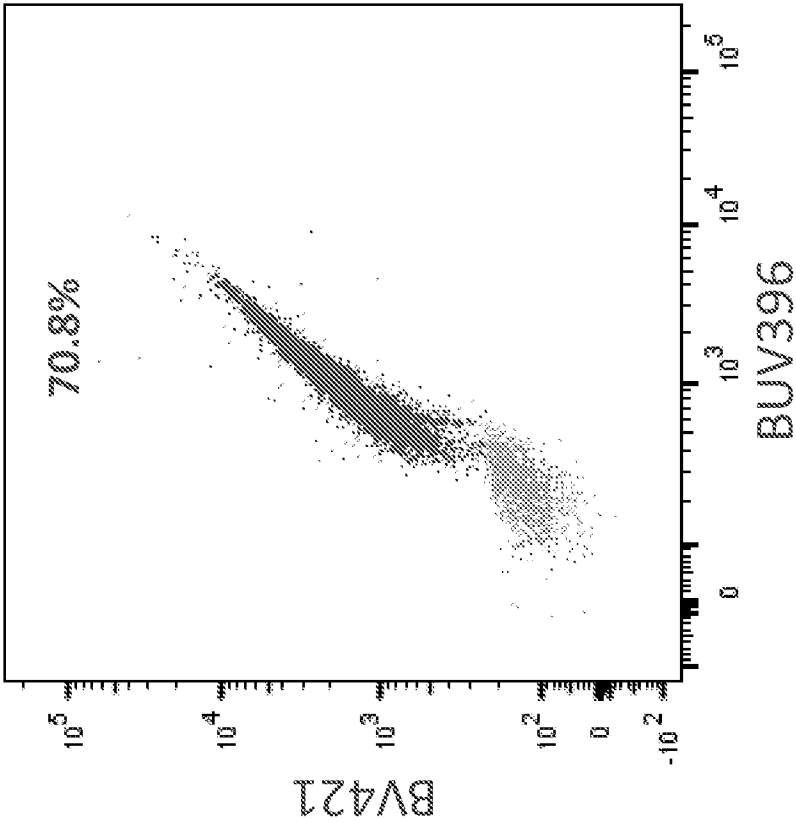


FIG. 4B

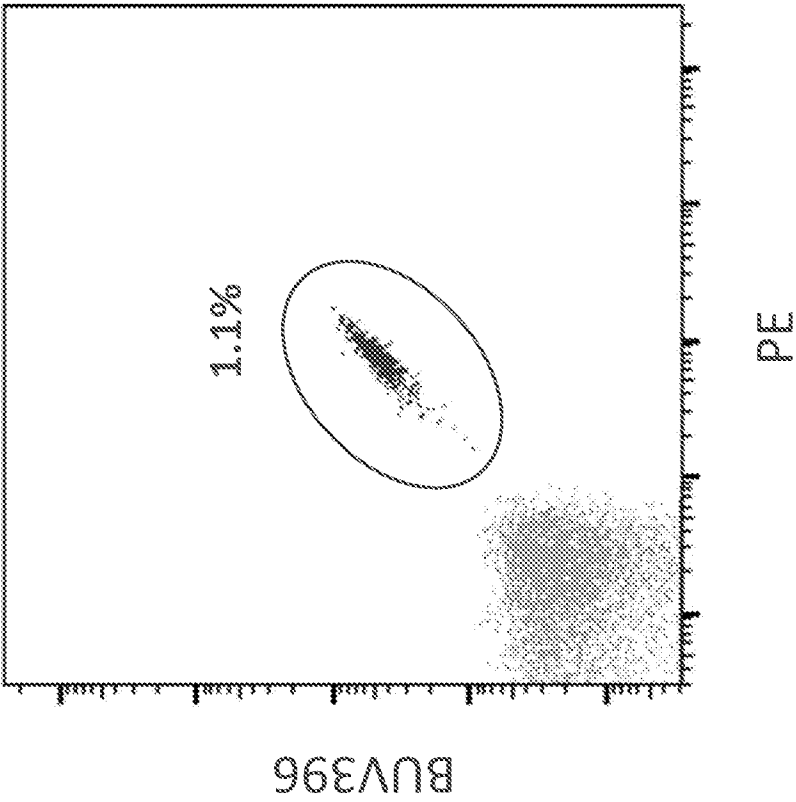
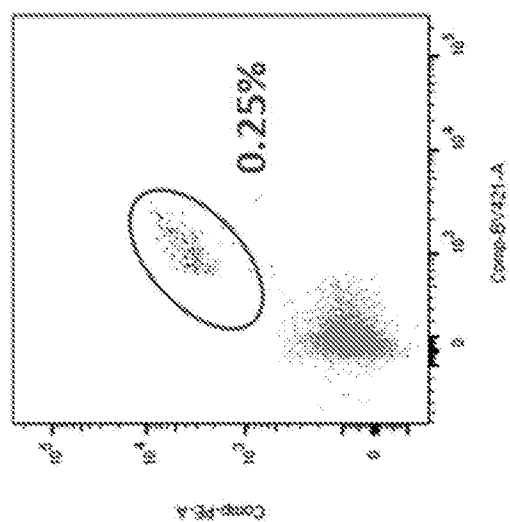
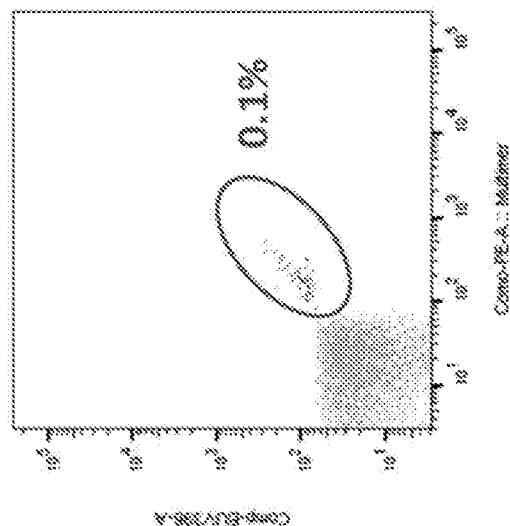
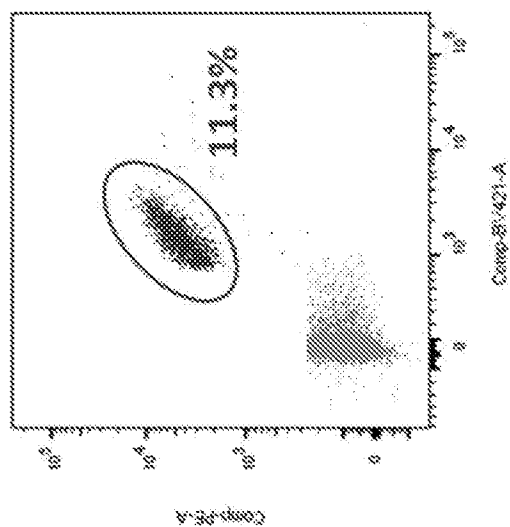


FIG. 4A

RAS G12V

RAS G12C

RASGL2D



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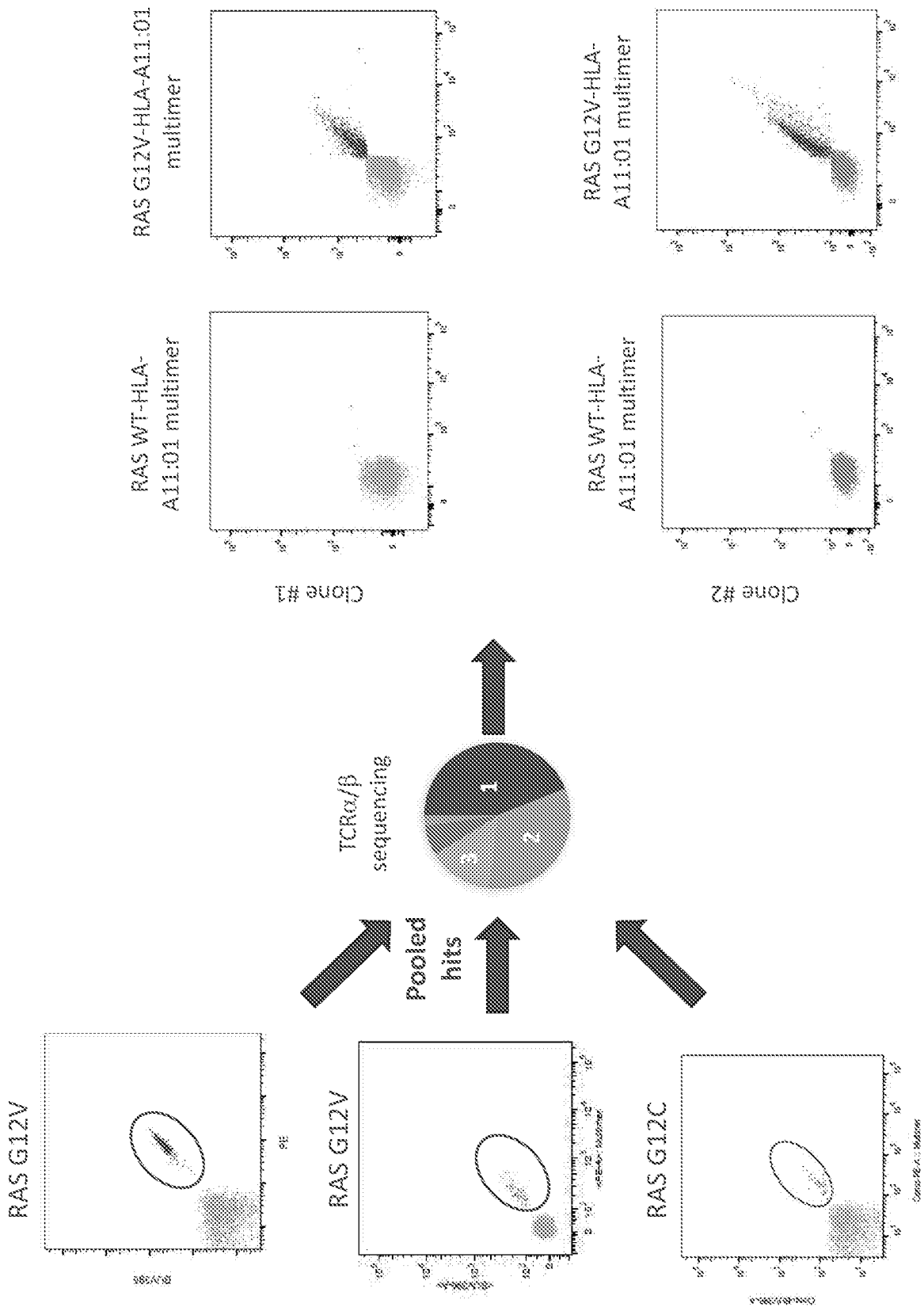


FIG. 6A

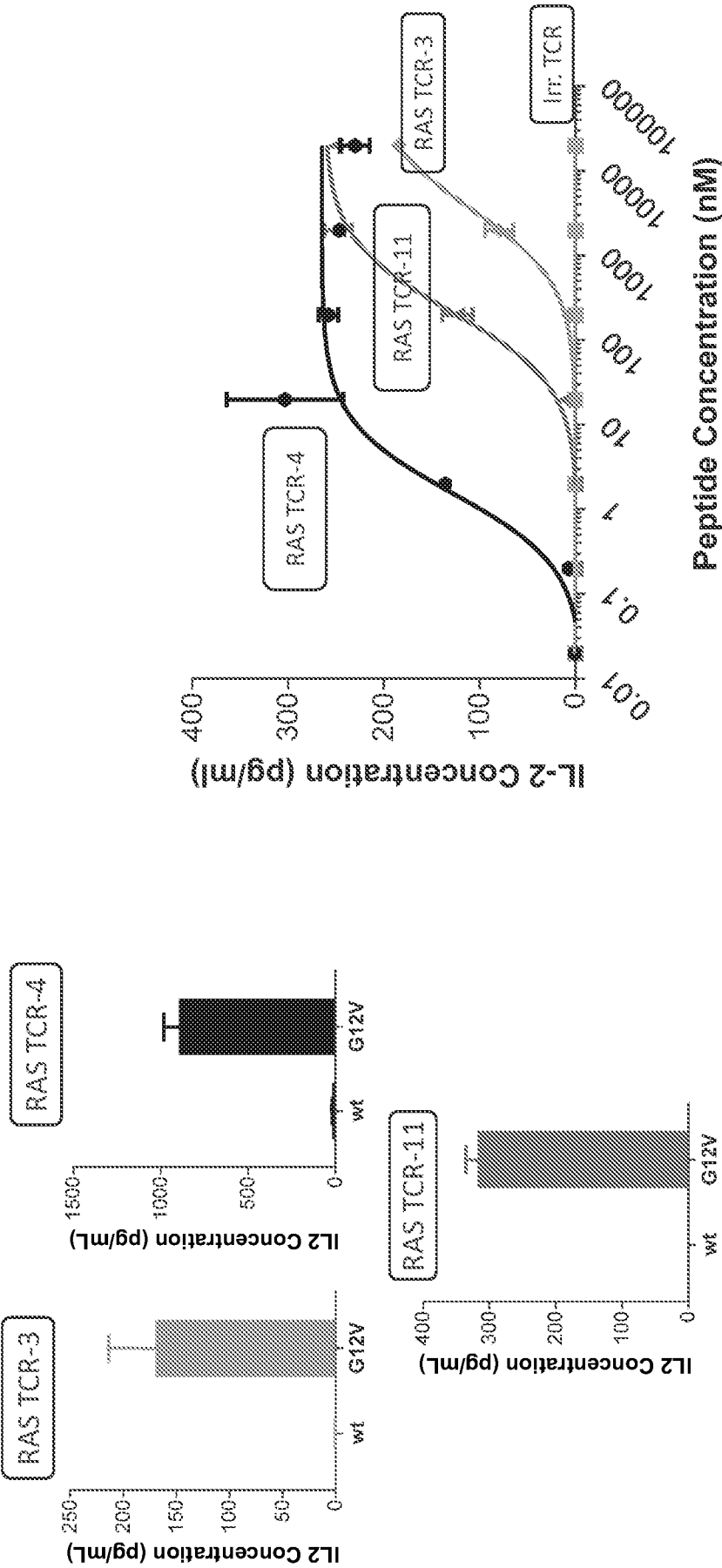


FIG. 6B

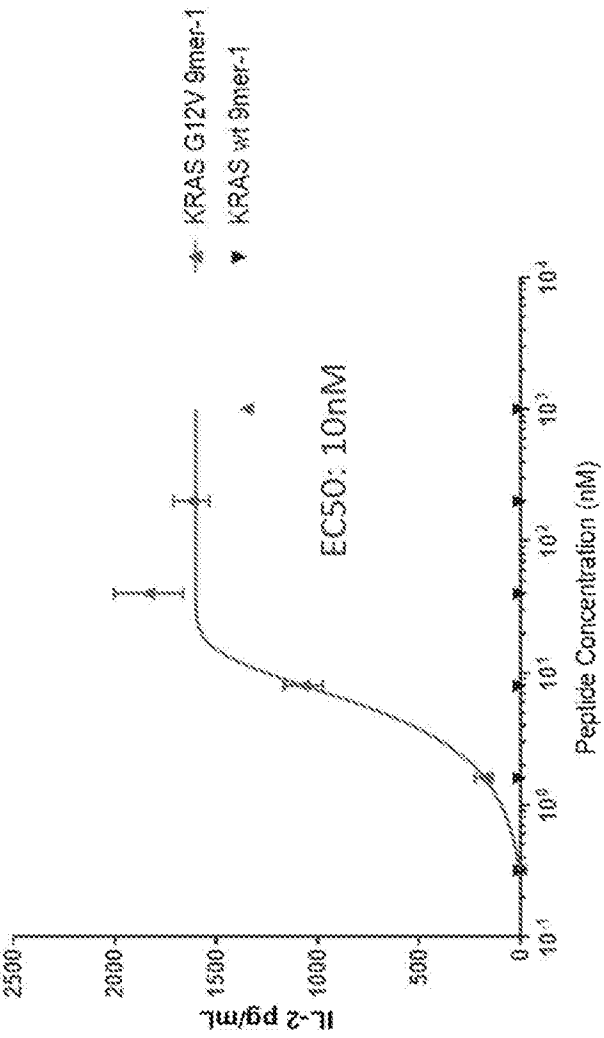


FIG. 7A

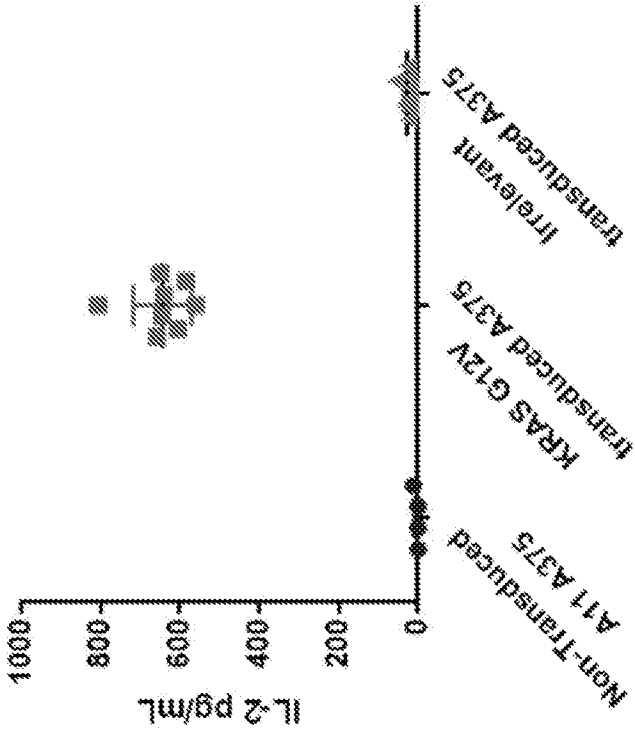


FIG. 7B

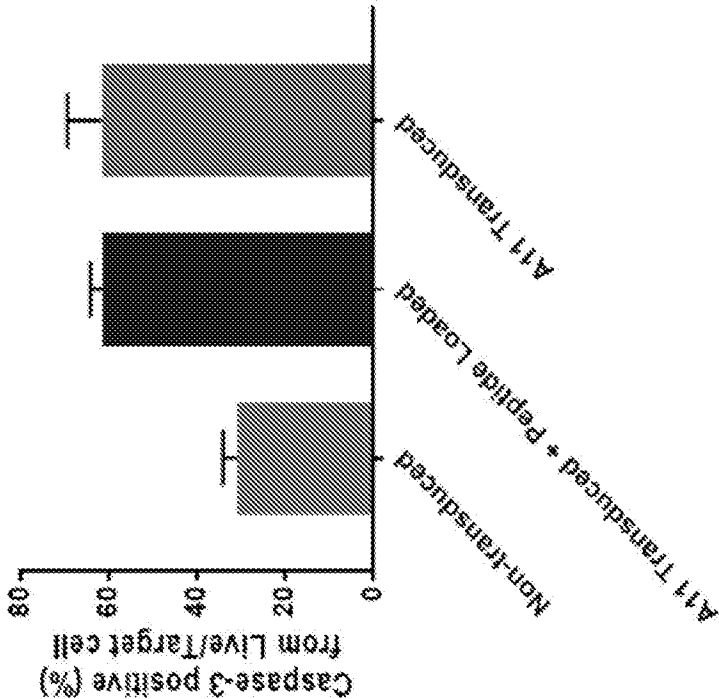


FIG. 8B

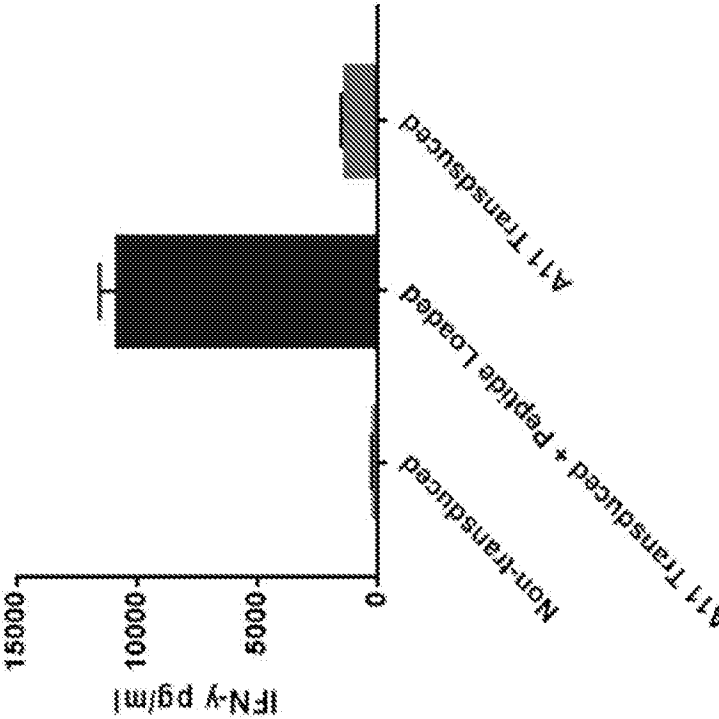


FIG. 8A

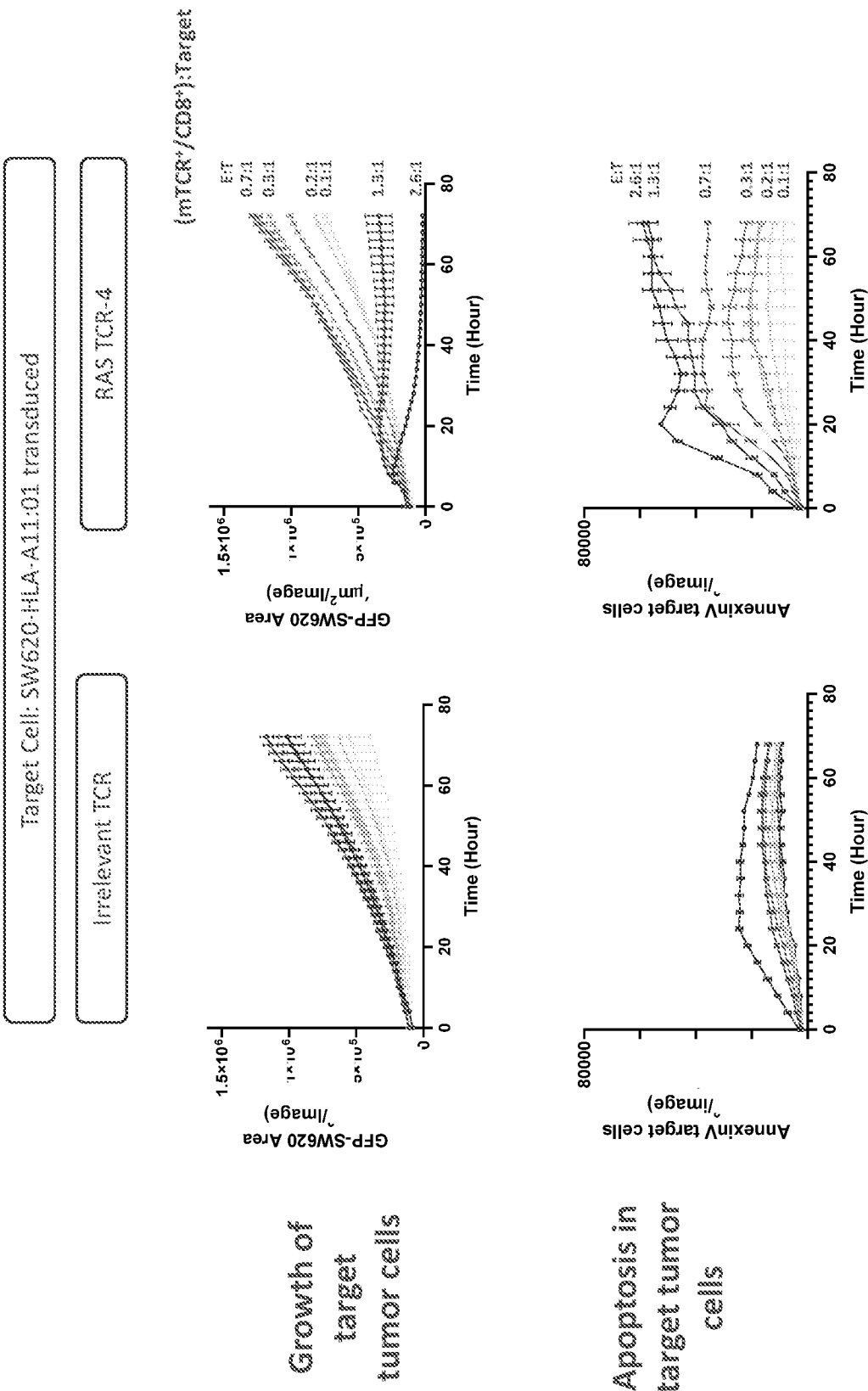


FIG. 8C

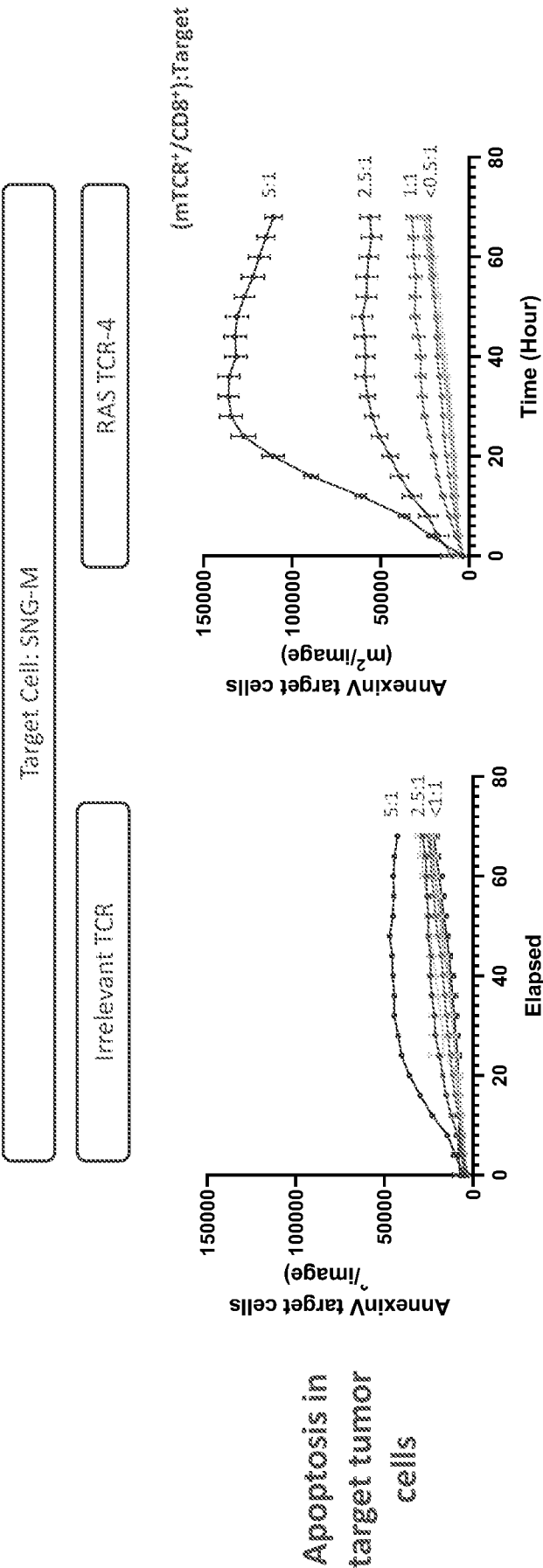
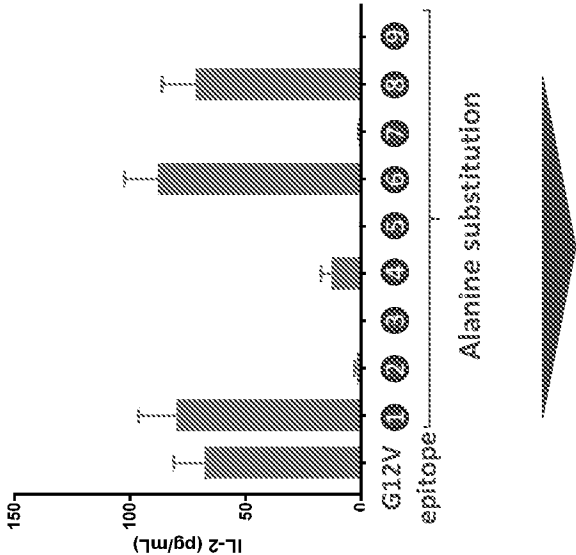


FIG. 8D

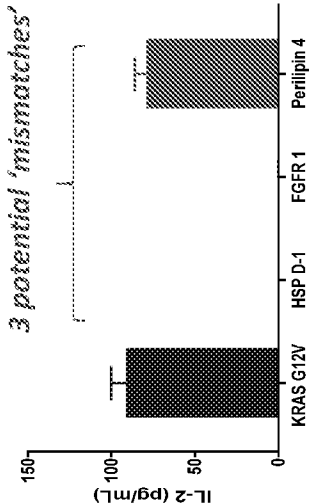
Alanine scan shows positions
1,4,6,8 are substitutable

Only 1 mismatch peptide
recognized by RAS TCR-4

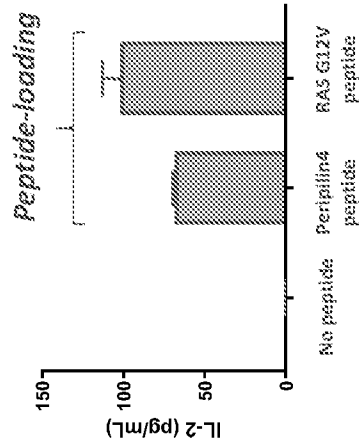
Recognized peptide is not
endogenously processed



Identified 3 potential mismatch
peptides in human proteome scan

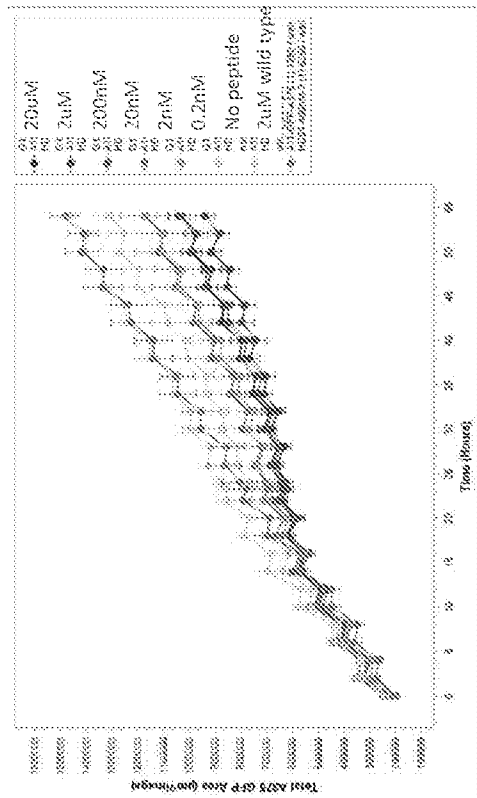
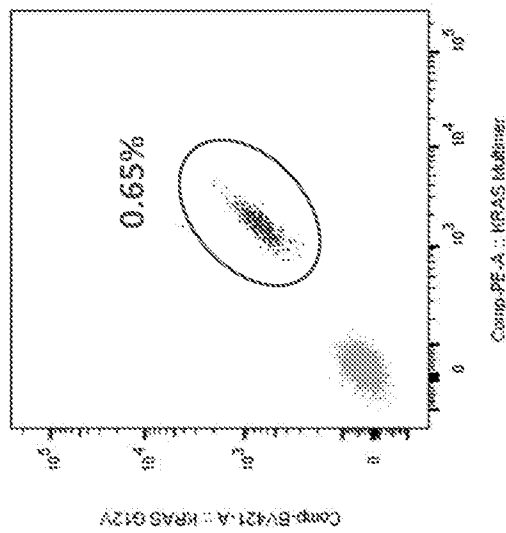


Peptide-loaded A375-HLA-A11:01 cells
+ RAS TCR-transduced Jurkat
(5:1 E:T ratio, 2µM peptide)



A375-HLA-A11:01 cells transduced with Perilipin4
+ RAS TCR-transduced Jurkat
(5:1 E:T ratio, 2µM peptide)

FIG. 8E



Cytotoxicity assay at 48Hr

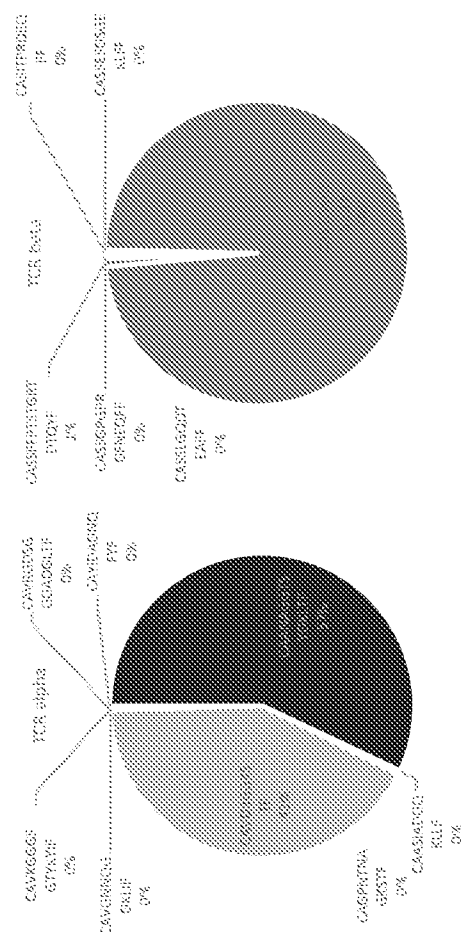
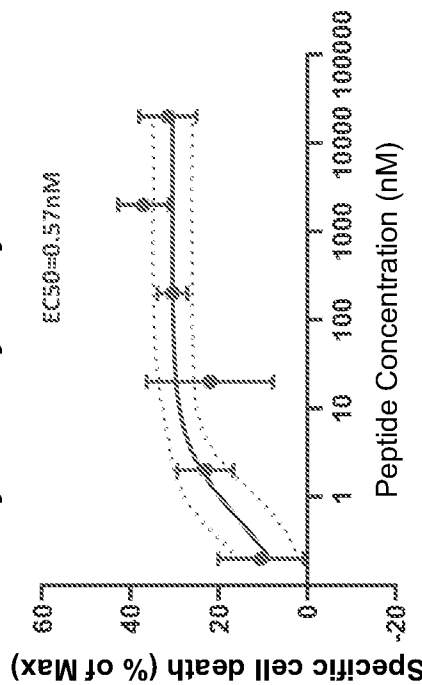
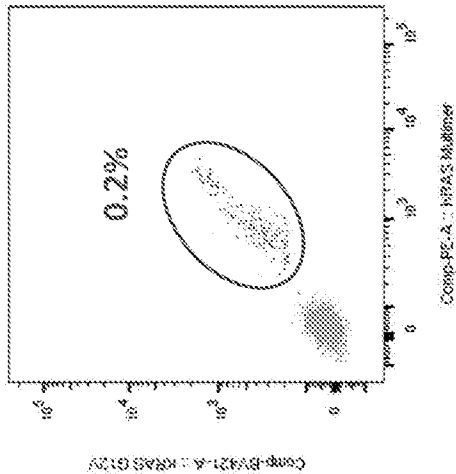
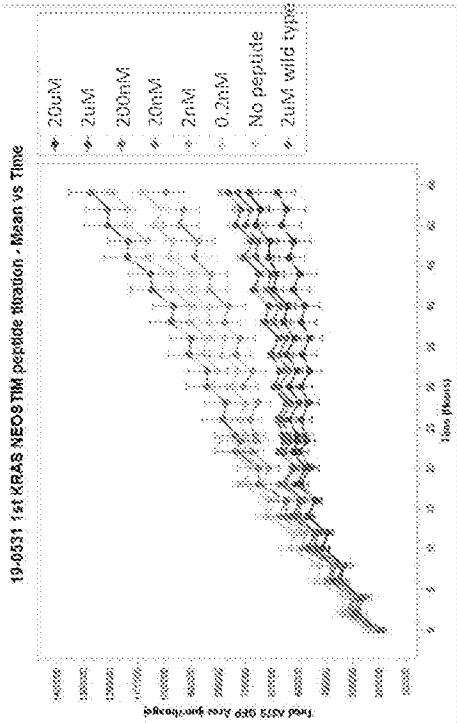


FIG. 8F



Cytotoxicity assay at 48Hr

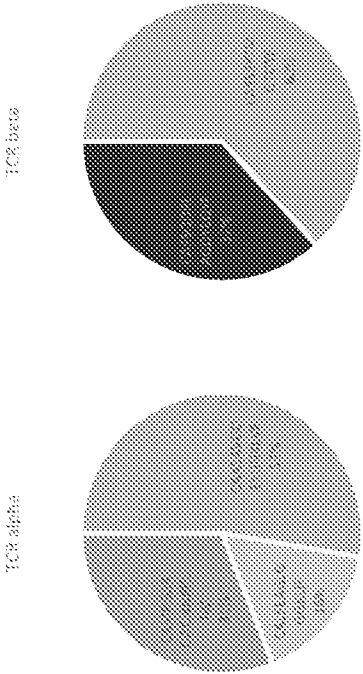
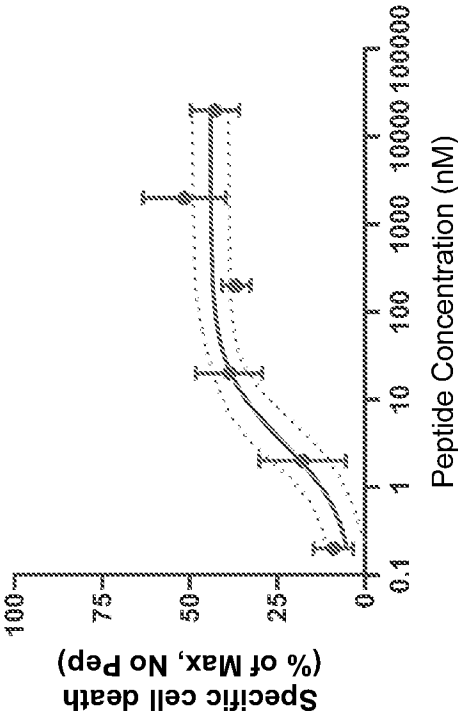


FIG. 8G

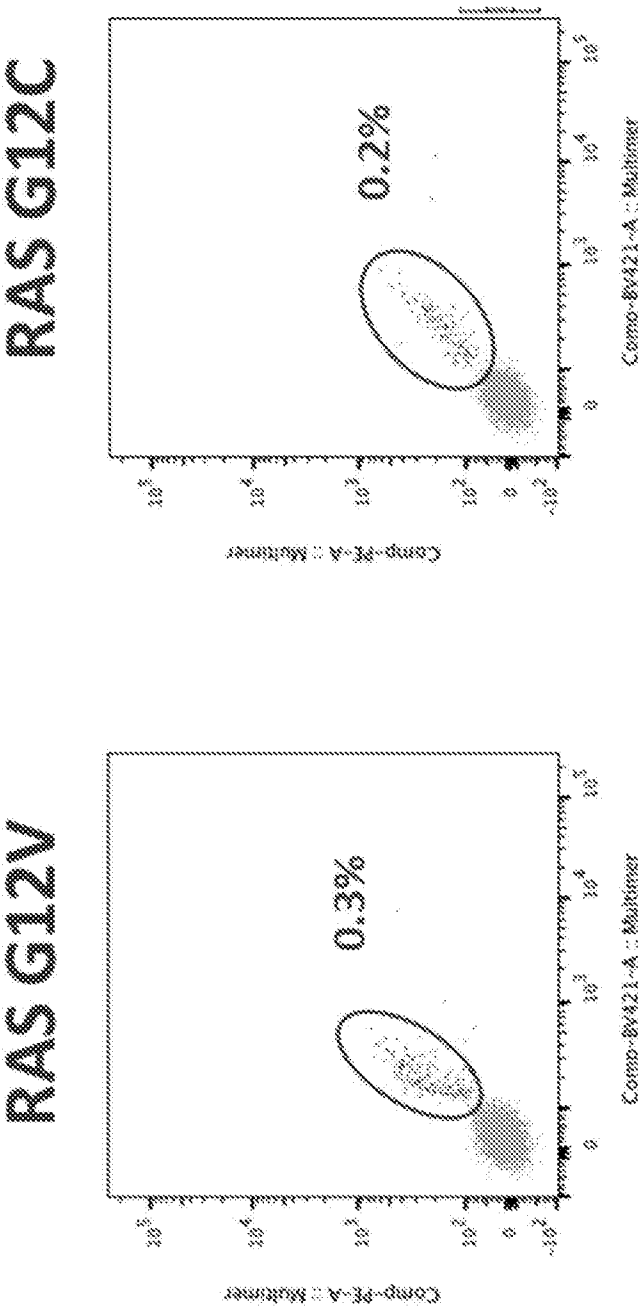


FIG. 9

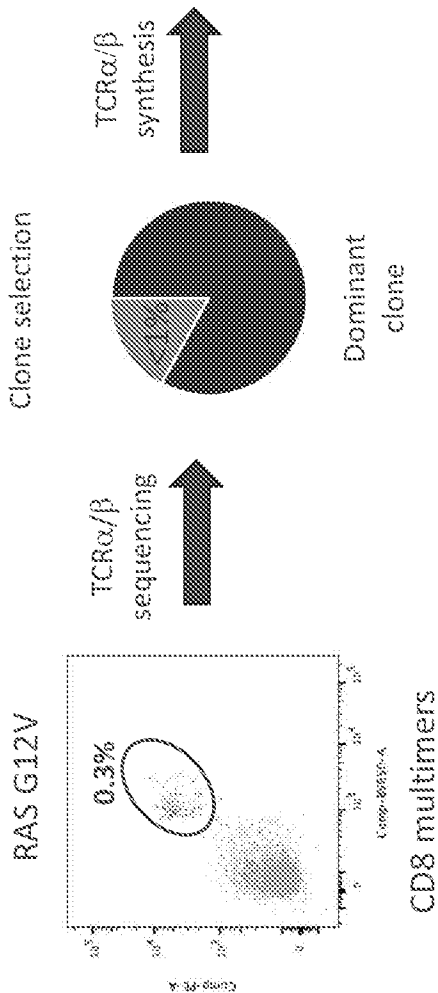
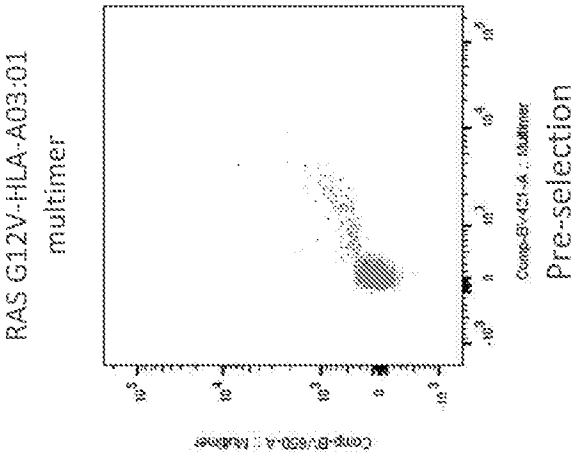


FIG. 10A

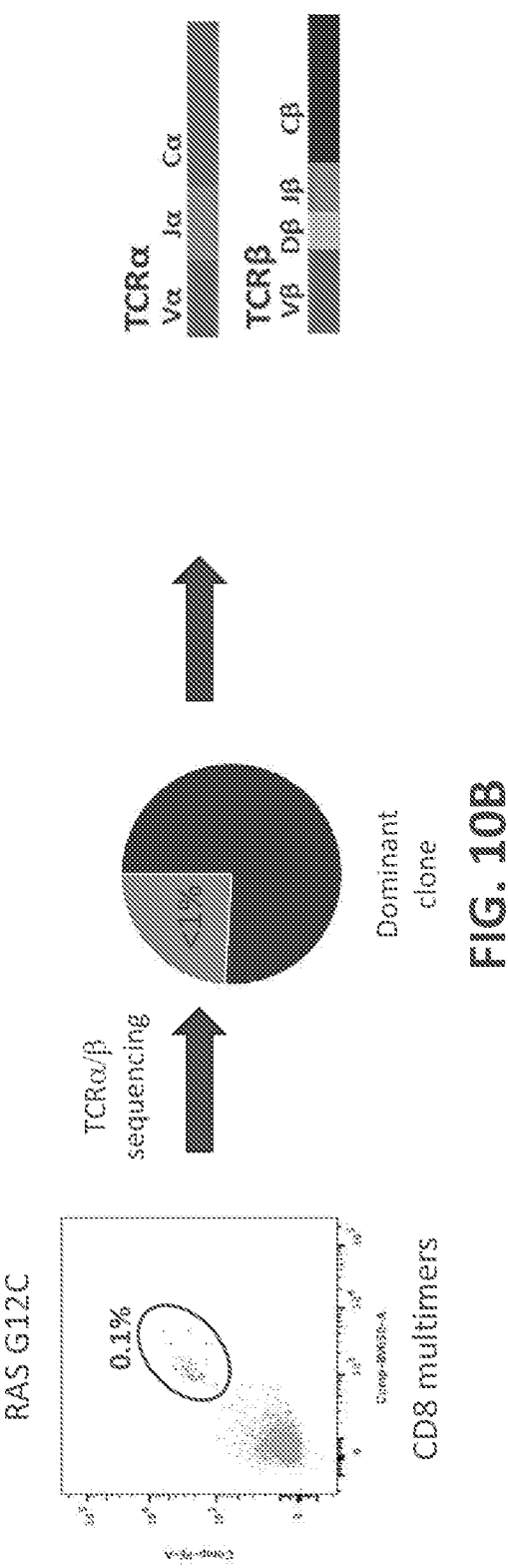


FIG. 10B

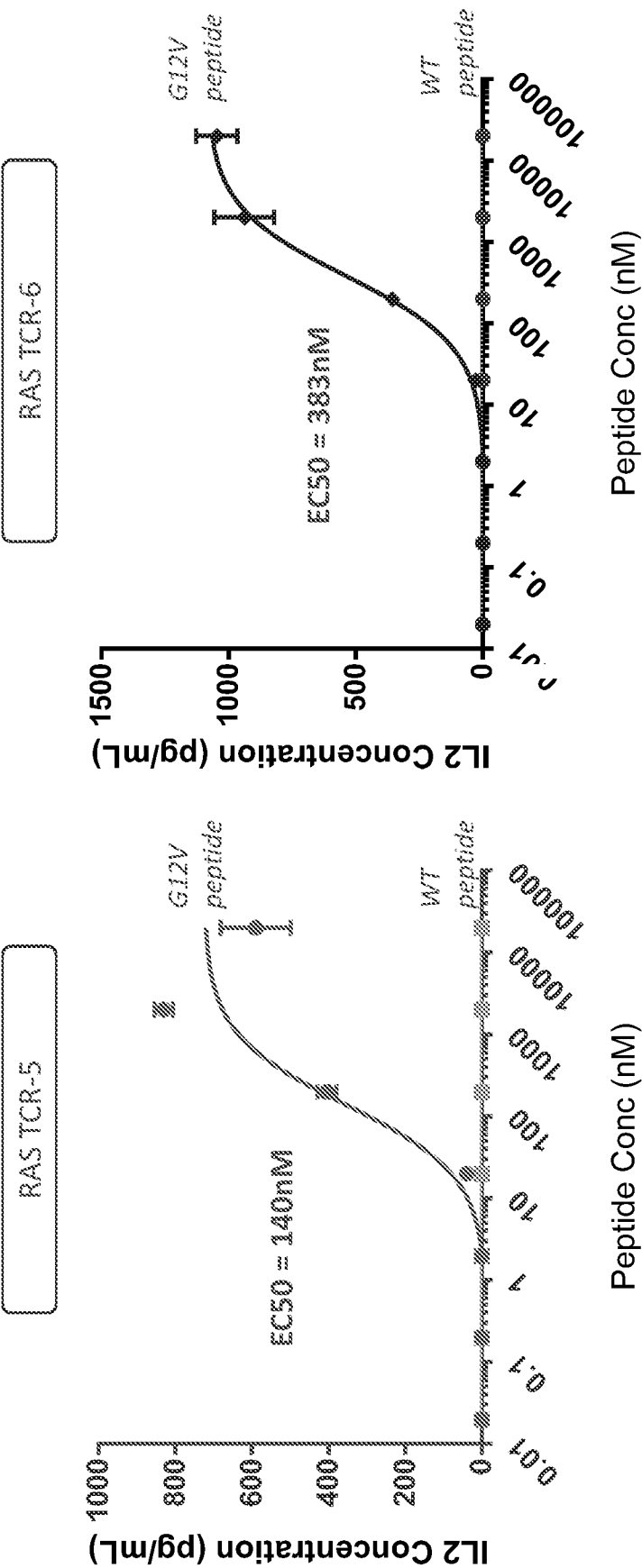
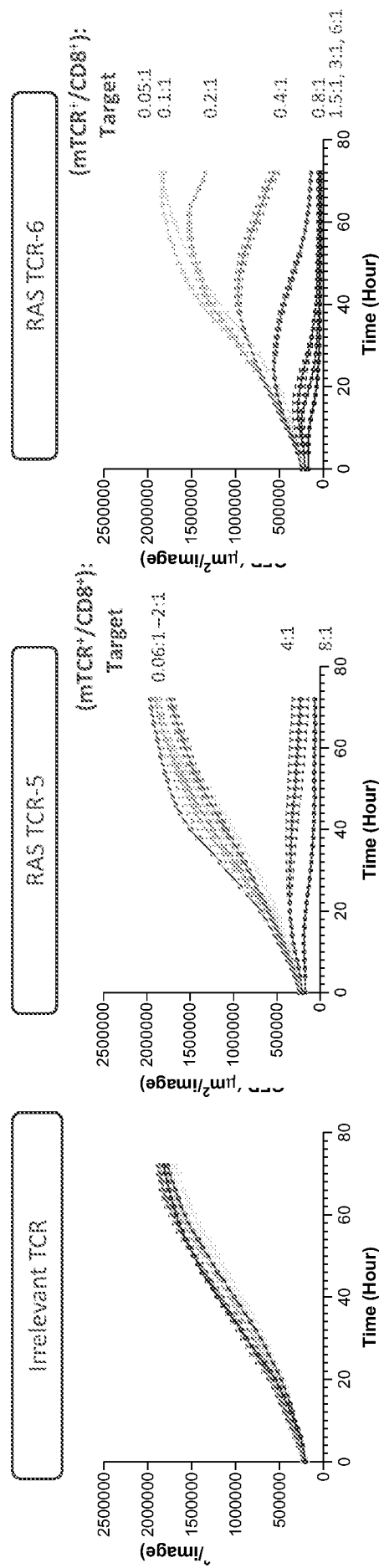
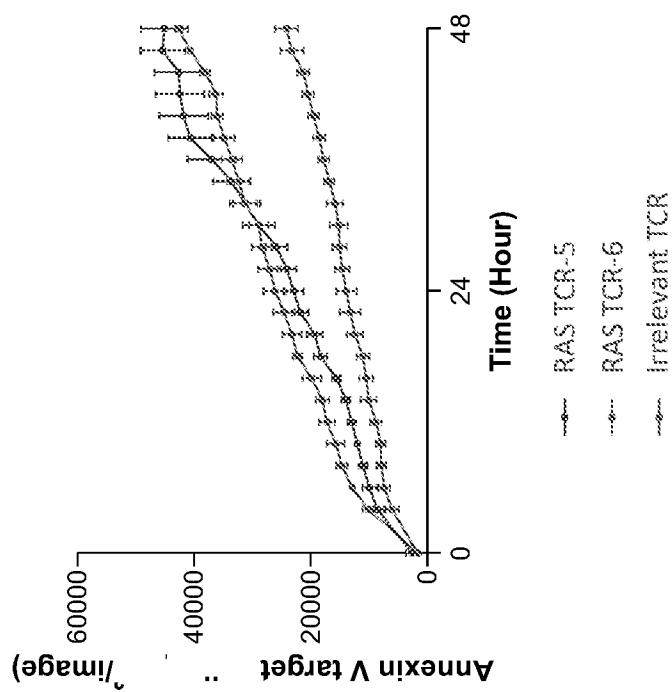


FIG. 10C



Co-culture of TCR-transduced PBMCs with A375-HLA-A03:01 transduction across range of E:T ratios

FIG. 10D



Co-culture of TCR-transduced PBMCs with NCI-H441 at
20:1 total E:T (~4:1 specific E:T)

FIG. 10E

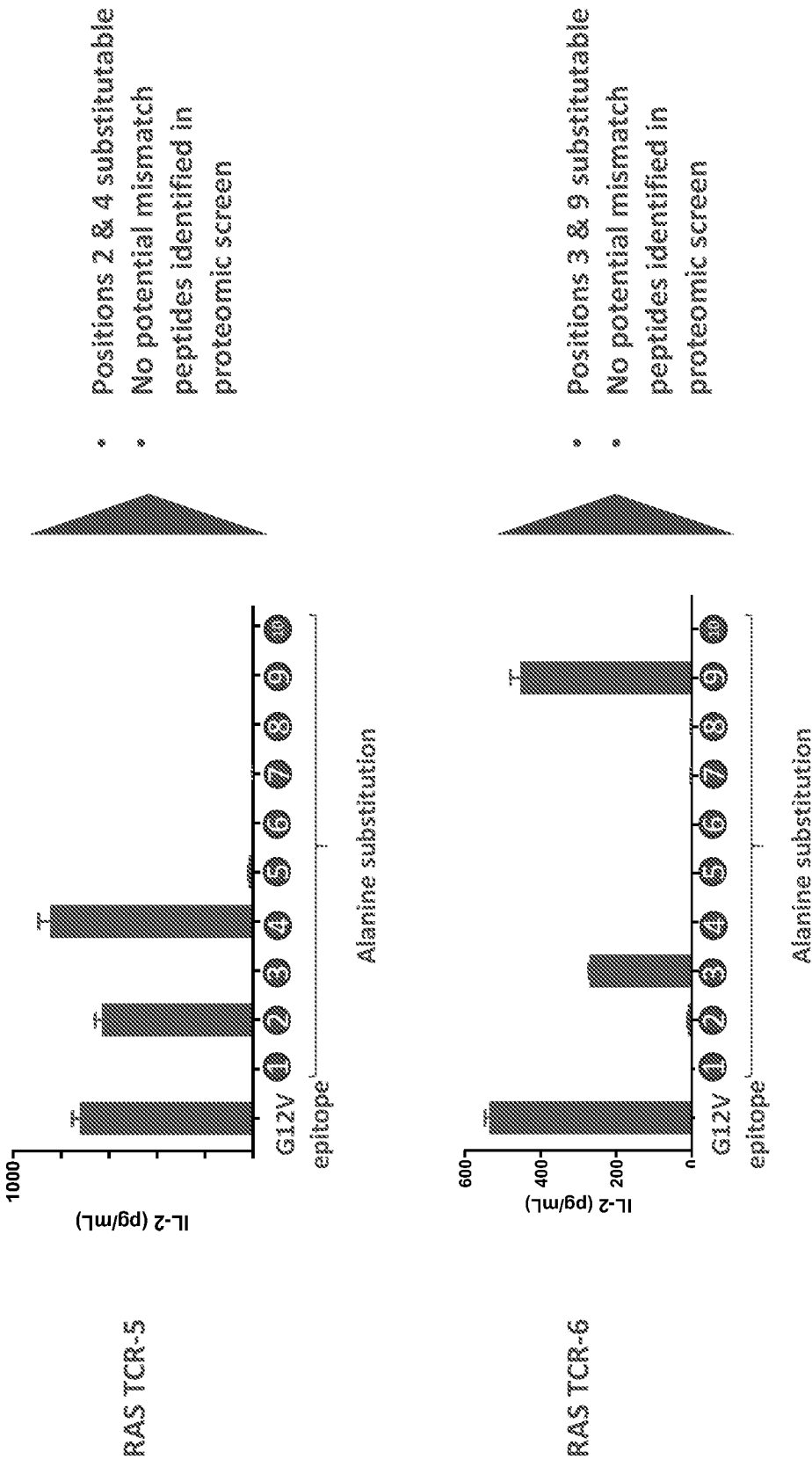


FIG. 10F

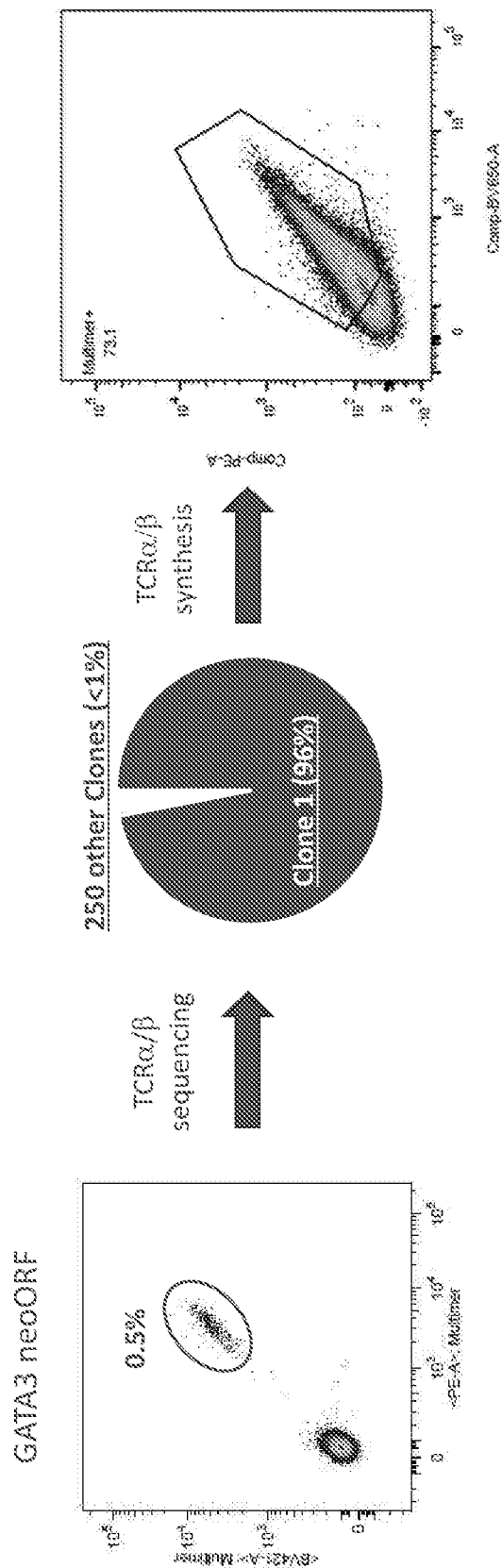


FIG. 11

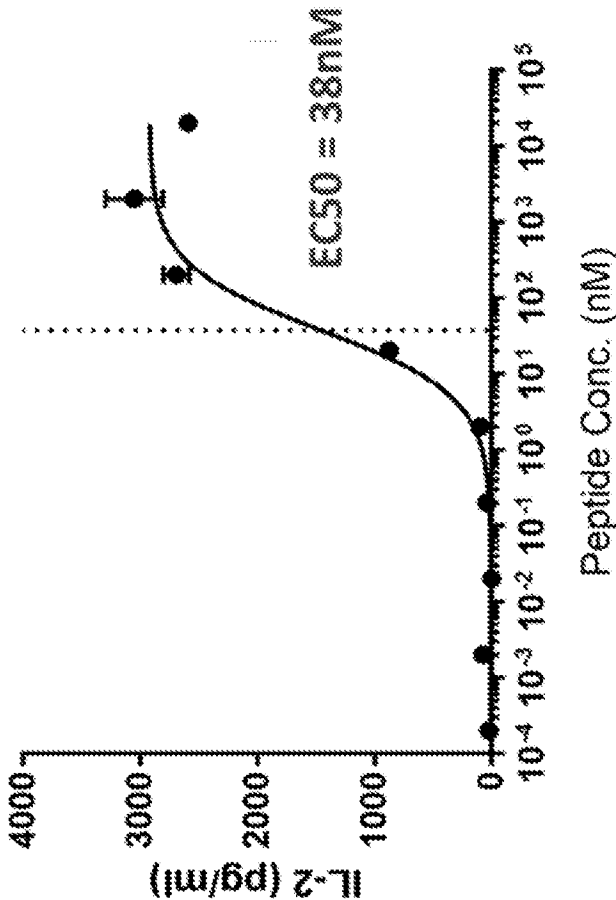


FIG. 12A

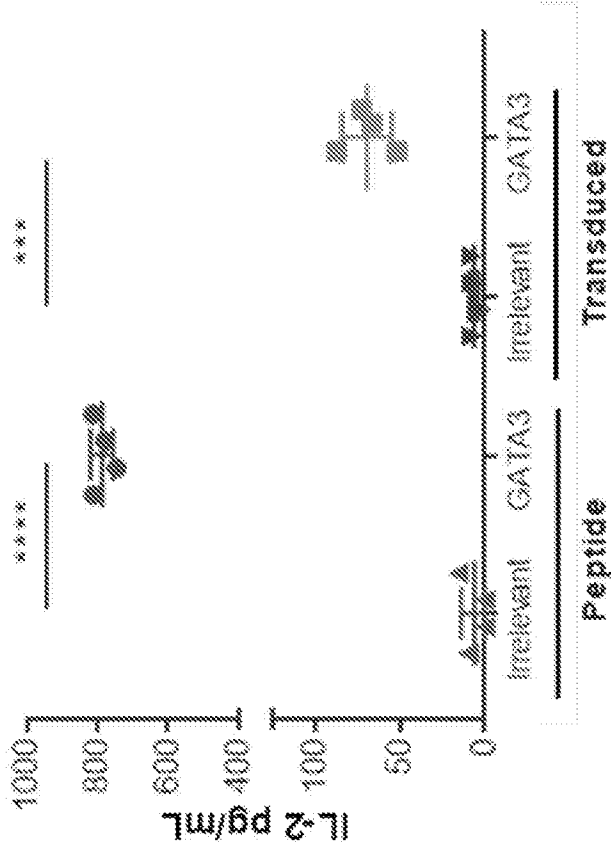


FIG. 12B

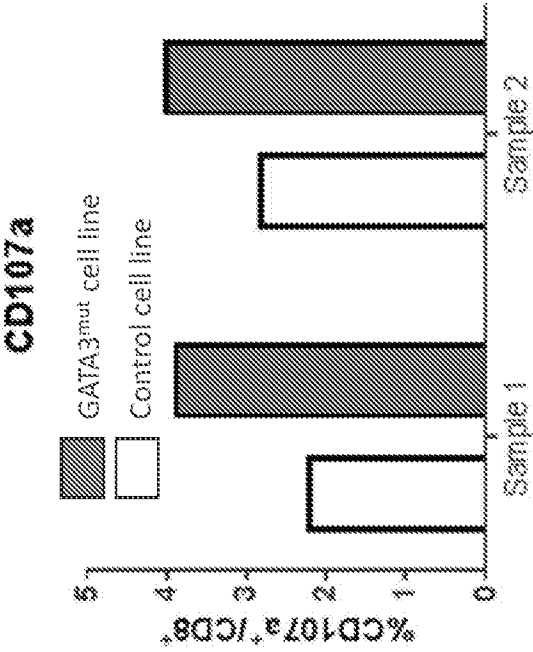


FIG. 12D

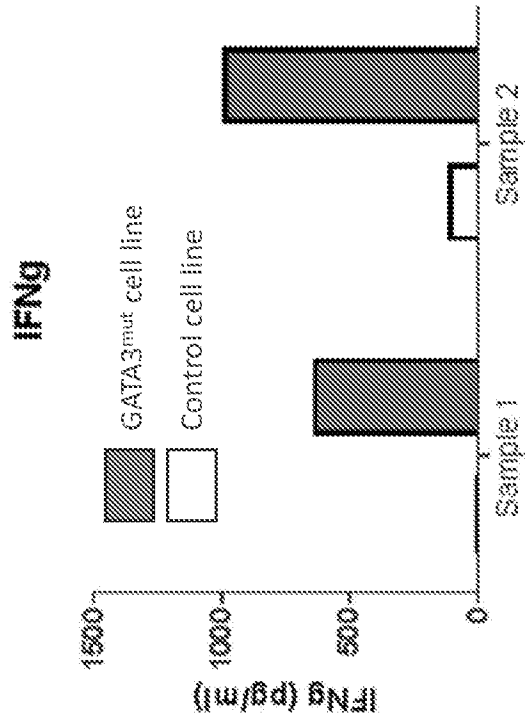


FIG. 12C

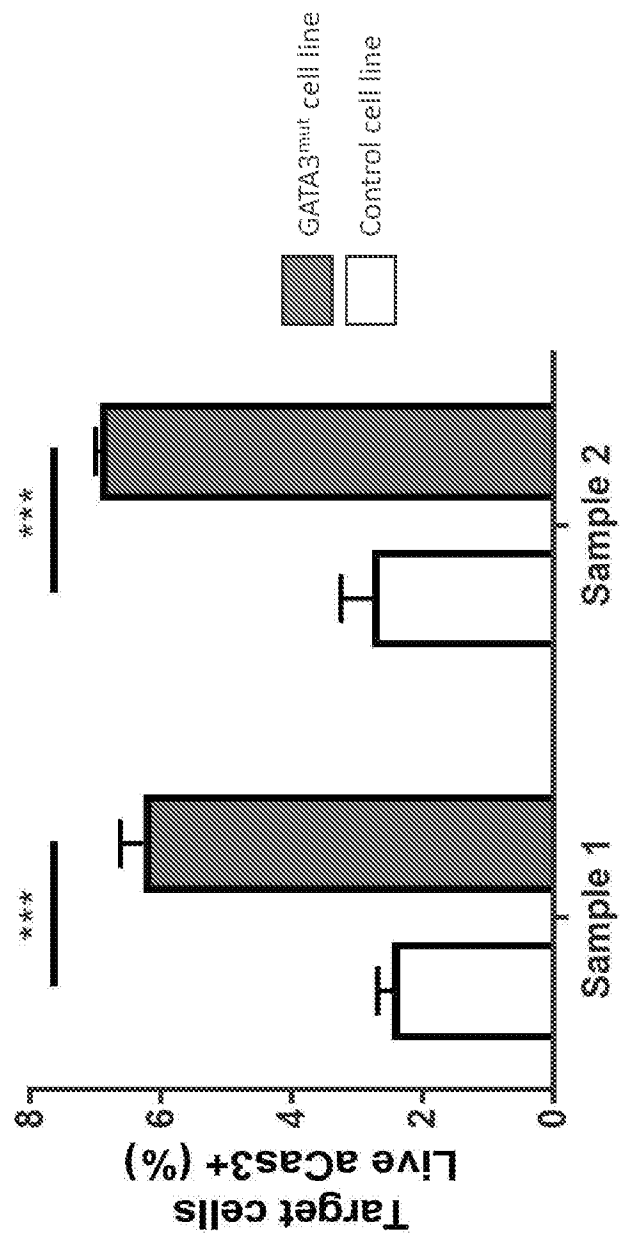


FIG. 12E

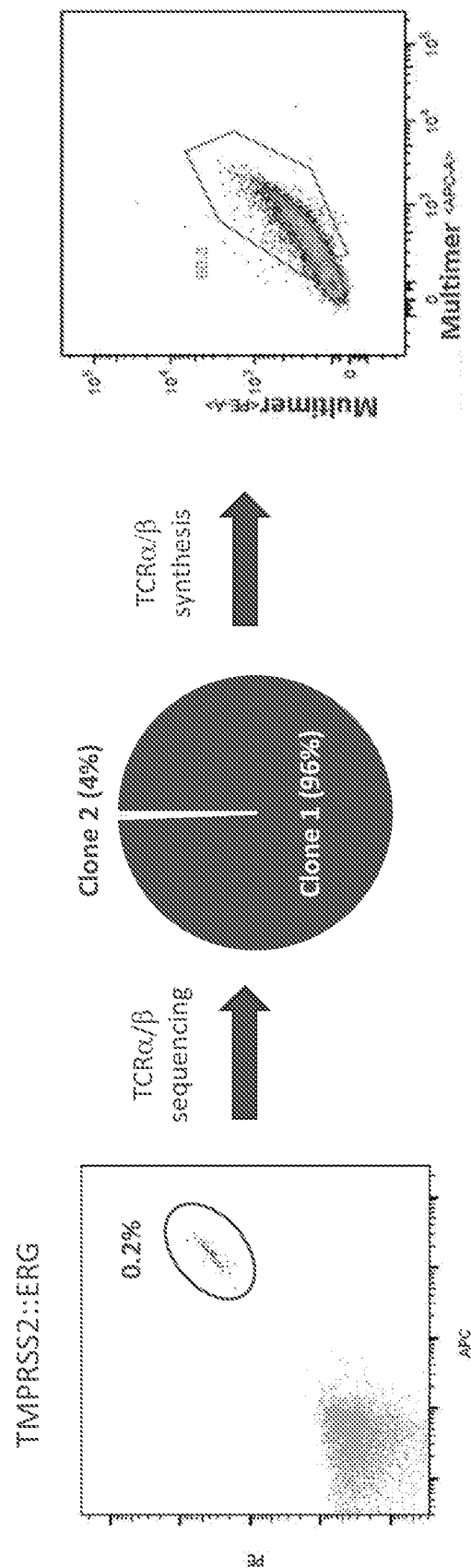


FIG. 13

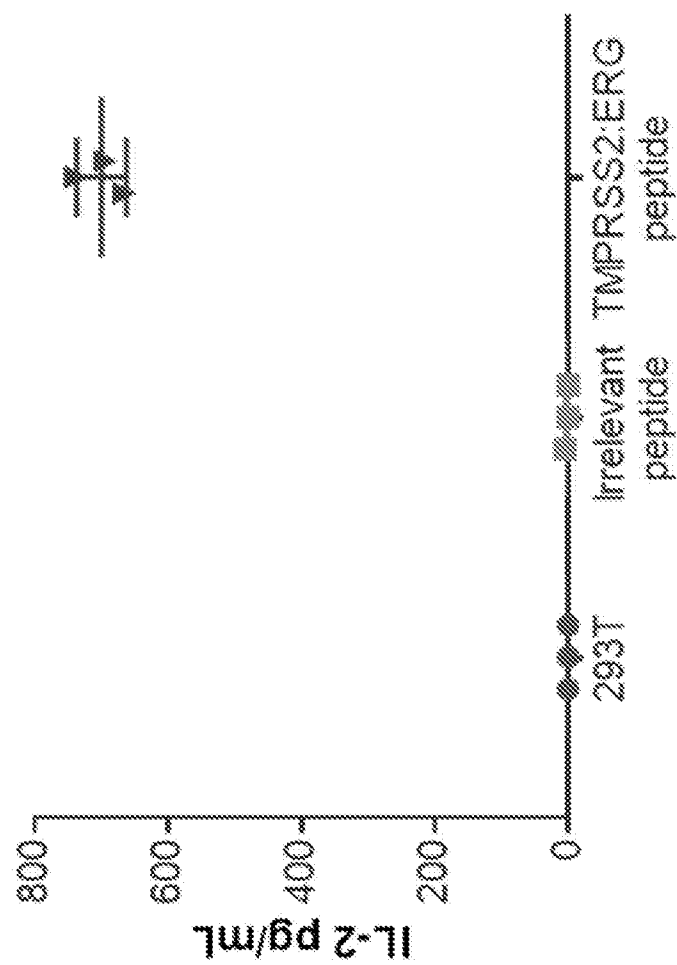


FIG. 14

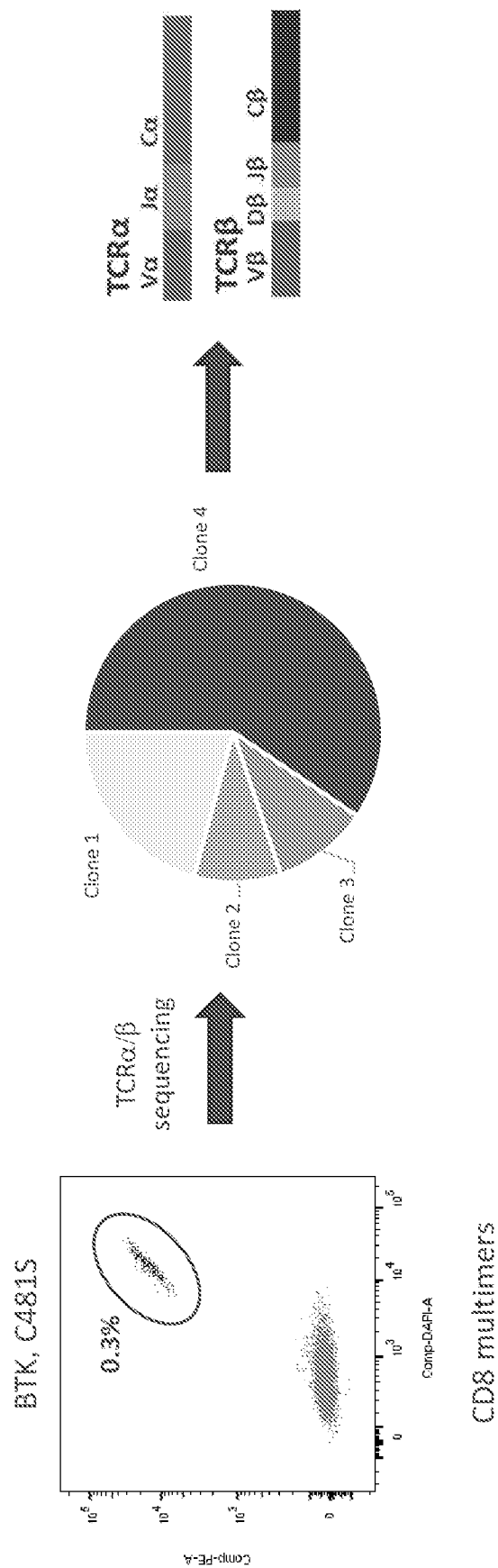


FIG. 15

EGFR T790M TCRs

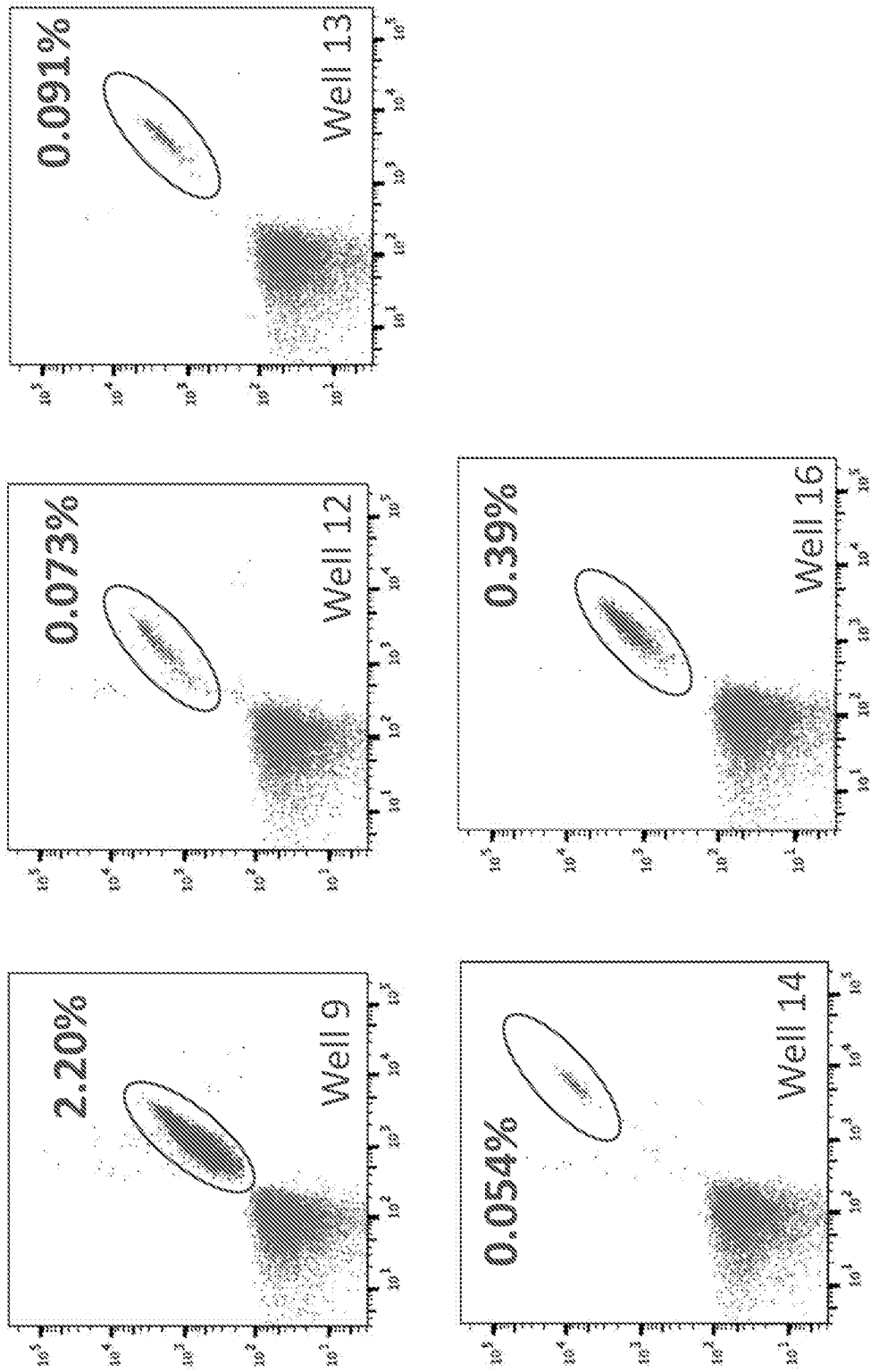


FIG. 16A

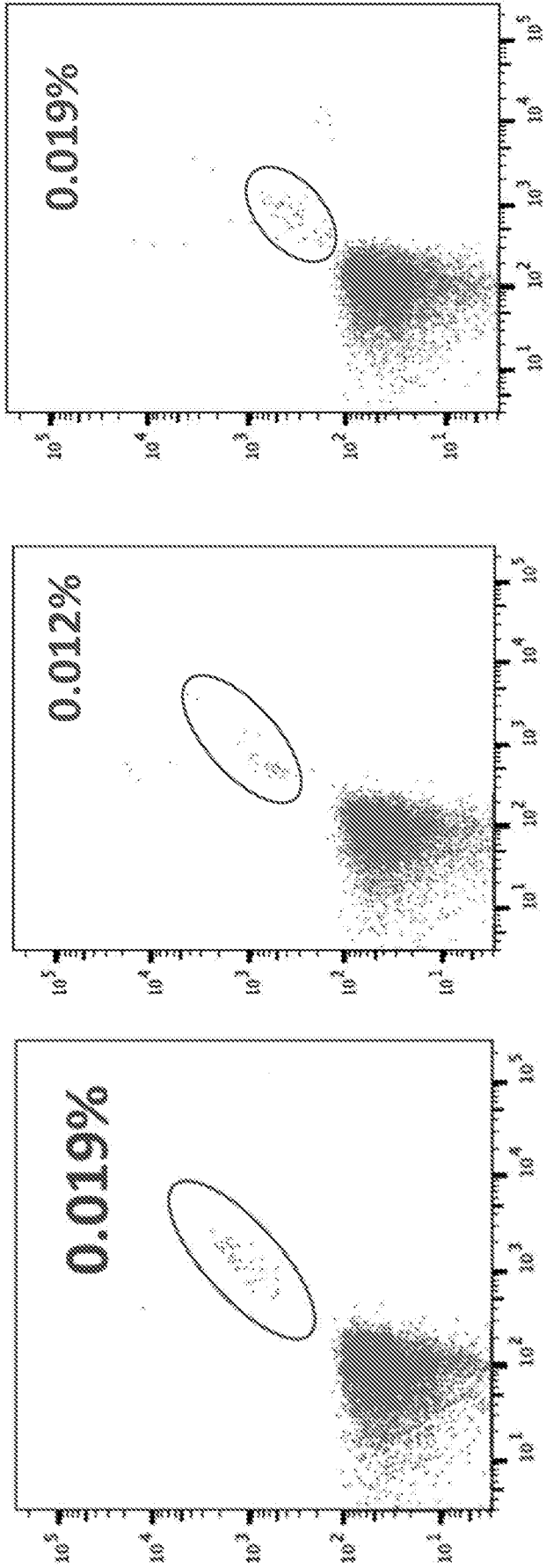


FIG. 16B

SEQUENCE LISTING

<110> NEON THERAPEUTICS, INC.

<120> T CELL RECEPTOR CONSTRUCTS AND USES THEREOF

<130> 50401-726.601

<140> PCT/US2019/046876

<141> 2019-08-16

<150> 62/810,112

<151> 2019-02-25

<150> 62/764,817

<151> 2018-08-16

<160> 621

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 1

Ser Ile Phe Asn Thr

1 5

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<210> 3

<211> 13

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 3

Cys Ala Gly Arg Asn Phe Gly Asn Glu Lys Leu Thr Phe
1 5 10

<210> 4

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

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Asp Phe Gln Ala Thr Thr
1 5

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 5

Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 6
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 6
Ser Ala Arg Asp Arg Gly Leu Val Ser Leu Pro Ser Val Glu Ala Phe
1 5 10 15

Phe

<210> 7
<211> 387
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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120
tgcacttctt caagcatatt taacacctgg ctatggtaca agcaggaccc tggggaaggt
180
cctgtcctct tgatagcctt atataaggct ggtgaattga cctcaaattgg aagactgact
240
gctcagtttg gtataaccag aaaggacagc ttcctgaata tctcagcatc catacctagt
300
gatgtaggca tctacttctg tgctgggaga aactttggaa atgagaaatt aacctttggg
360

a c t g g a a c a a
387

g a c t c a c c a t

c a t a c c c

<210> 8

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

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cagctgaatc agagtcctca atctatgttt atccaggaag gagaagatgt ctccatgaac
120

tgcactttctt caagcatatt taacacctgg ctatggtaca agcaggaccc tggggaaggt
180

cctgtcctct tgatagcctt atataaggct ggtgaattga cctcaaattgg aagactgact
240

gctcagtttg gtataaccag aaaggacagc ttcctgaata tctcagcatc catacctagt
300

gatgtaggca tctactttctg tgctgggaga aactttggaa atgagaaatt aacctttggg
360

a c t g g a a c a a
387

g a c t c a c c a t

c a t a c c c

<210> 9

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

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polypeptide

<400> 9

Met Leu Leu Glu His Leu Leu Ile Ile Leu Trp Met Gln Leu Thr Trp
1 5 10 15

Val Ser Gly Gln Gln Leu Asn Gln Ser Pro Gln Ser Met Phe Ile Gln
20 25 30

Glu Gly Glu Asp Val Ser Met Asn Cys Thr Ser Ser Ser Ile Phe Asn
35 40 45

Thr Trp Leu Trp Tyr Lys Gln Asp Pro Gly Glu Gly Pro Val Leu Leu
50 55 60

Ile Ala Leu Tyr Lys Ala Gly Glu Leu Thr Ser Asn Gly Arg Leu Thr
65 70 75 80

Ala Gln Phe Gly Ile Thr Arg Lys Asp Ser Phe Leu Asn Ile Ser Ala
85 90 95

Ser Ile Pro Ser Asp Val Gly Ile Tyr Phe Cys Ala Gly Arg Asn Phe
100 105 110

Gly Asn Glu Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu Thr Ile Ile
115 120 125

Pro

<210> 10

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

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60

catccgagca gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccttg
120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg
180

atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag
240

tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct
300

gaagacagca gcttctacat ctgcagtgct cgcgacaggg ggcttgtatc gttgccgtcg
360

gtagaagctt tctttggaca aggcaccaga ctcacagttg tactg
405

<210> 11

<211> 405

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg
180

atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag
240

tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct
300

gaagacagca gcttctacat ctgcagtgtc cgcgacaggg ggcttgtatc gttgccgtcg
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gtagaagctt tcttttgaca aggcaccaga ctcacagttg tactg
405

<210> 12

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 12

Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Pro	Gly	Ser	Gly	Leu	Gly	Ala
1				5				10					15		

Val	Val	Ser	Gln	His	Pro	Ser	Arg	Val	Ile	Cys	Lys	Ser	Gly	Thr	Ser
			20					25					30		

Val	Lys	Ile	Glu	Cys	Arg	Ser	Leu	Asp	Phe	Gln	Ala	Thr	Thr	Met	Phe
	35						40					45			

Trp	Tyr	Arg	Gln	Phe	Pro	Lys	Gln	Ser	Leu	Met	Leu	Met	Ala	Thr	Ser
50						55					60				

Asn	Glu	Gly	Ser	Lys	Ala	Thr	Tyr	Glu	Gln	Gly	Val	Glu	Lys	Asp	Lys
65					70					75					80

Phe	Leu	Ile	Asn	His	Ala	Ser	Leu	Thr	Leu	Ser	Thr	Leu	Thr	Val	Thr
				85					90					95	

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp
100 105 110

Arg Gly Leu Val Ser Leu Pro Ser Val Glu Ala Phe Phe Gly Gln Gly
115 120 125

Thr Arg Leu Thr Val Val
130

<210> 13

<211> 270

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 13

Met Leu Leu Glu His Leu Leu Ile Ile Leu Trp Met Gln Leu Thr Trp
1 5 10 15

Val Ser Gly Gln Gln Leu Asn Gln Ser Pro Gln Ser Met Phe Ile Gln
20 25 30

Glu Gly Glu Asp Val Ser Met Asn Cys Thr Ser Ser Ser Ile Phe Asn
35 40 45

Thr Trp Leu Trp Tyr Lys Gln Asp Pro Gly Glu Gly Pro Val Leu Leu
50 55 60

Ile Ala Leu Tyr Lys Ala Gly Glu Leu Thr Ser Asn Gly Arg Leu Thr
65 70 75 80

Ala Gln Phe Gly Ile Thr Arg Lys Asp Ser Phe Leu Asn Ile Ser Ala
85 90 95

Ser Ile Pro Ser Asp Val Gly Ile Tyr Phe Cys Ala Gly Arg Asn Phe
100 105 110

Gly Asn Glu Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu Thr Ile Ile
115 120 125

Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
130 135 140

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
145 150 155 160

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
165 170 175

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
180 185 190

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
195 200 205

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
210 215 220

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
225 230 235 240

Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
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Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265 270

<210> 14
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 14
Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Arg Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp
100 105 110

Arg Gly Leu Val Ser Leu Pro Ser Val Glu Ala Phe Phe Gly Gln Gly
115 120 125

Thr Arg Leu Thr Val Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
130 135 140

Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
260 265 270

Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 15
Lys Leu Val Val Val Gly Ala Cys Gly Val
1 5 10

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 16
Val Ser Gly Asn Pro Tyr
1 5

<210> 17
<211> 8
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 17
Tyr Ile Thr Gly Asp Asn Leu Val
1 5

<210> 18
<211> 14
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 18

Cys Ala Val Arg Asp Gln Ser Gly Ala Asn Asn Leu Phe Phe
1 5 10

<210> 19

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

Ser Glu His Asn Arg
1 5

<210> 20

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Phe Gln Asn Glu Ala Gln
1 5

<210> 21

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 21

Ala Ser Tyr Leu Ser Gly Ser Ile Tyr Asn Glu Gln Phe Phe
1 5 10

<210> 22

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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60

cagtcagtgg ctcagccgga agatcaggtc aacgttgctg aagggaatcc tctgactgtg
120

aaatgcacct attcagtctc tggaaaccct tatctttttt ggtatgttca ataccccaac
180

cgaggcctcc agttccttct gaaatacatc acaggggata acctgggttaa aggcagctat
240

ggctttgaag ctgaatttaa caagagccaa acctccttcc acctgaagaa accatctgcc
300

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360

ctctttctttg ggactggaac gagactcacc gttattccc
399

<210> 23

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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caaagcgtgg cccaacctga ggatcaggtg aatgtagcgg agggcaatcc gttgacagtt
120

aagtgtacat actccgtatc aggcaatccg tacttgtttt ggtatgtgca gtaccccaat
180

cgggggccttc aattcttgct gaagtacatt acaggcgata atctggtaaa aggtagttat
240

ggttttgagg ccgaattcaa caaatcacia acatcatttc atcttaaaaa gccaaagcga
300

cttgtcagtg actcagcgct ttatttctgt gcagtcagag accaatcagg ggcaaataat
360

ctgtttctttg ggacagggac tagattgact gttataccc
399

<210> 24

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 24

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1 5 10 15

Gly Leu Arg Ala Gln Ser Val Ala Gln Pro Glu Asp Gln Val Asn Val
20 25 30

Ala Glu Gly Asn Pro Leu Thr Val Lys Cys Thr Tyr Ser Val Ser Gly
35 40 45

Asn Pro Tyr Leu Phe Trp Tyr Val Gln Tyr Pro Asn Arg Gly Leu Gln
50 55 60

Phe Leu Leu Lys Tyr Ile Thr Gly Asp Asn Leu Val Lys Gly Ser Tyr
65 70 75 80

Gly Phe Glu Ala Glu Phe Asn Lys Ser Gln Thr Ser Phe His Leu Lys
85 90 95

Lys Pro Ser Ala Leu Val Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val
100 105 110

Arg Asp Gln Ser Gly Ala Asn Asn Leu Phe Phe Gly Thr Gly Thr Arg
115 120 125

Leu Thr Val Ile Pro
130

<210> 25

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

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120

aggtgtgatc caatttctga acacaaccgc ctttattggt accgacagac cctggggcag
180

ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc
240

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300

acagagcagg gggactcggc catgtatctc tgtgccagct acctgagcgg ttccatttac
360

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402

<210> 26

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

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acagggctct cccaagatcc cagacataaa atcacaaaac ggggccagaa cgttaccttt
120

cgctgcgata cgatatcaga gcataatcga ctgtattggt ataggcaaac tctcggggcaa
180

gggcctgagt tcctcactta tttccaaaat gaggcgcaac tggaaaagag ccggttggtg
240

agtgataggt tttccgcaga gcgacccaag gggagcttct caacactgga gatacaaagg
300

accgaacaag gtgattccgc aatgtatctc tgtgctagtt atttgagcgg ctccatatat
360

aacgaacagt ttttcggacc gggcactcgc ctgaccgtac ta
402

<210> 27
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 27
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Tyr Leu Ser Gly Ser Ile Tyr Asn Glu Gln Phe Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Leu
130

<210> 28
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 28
Met Ala Ser Ala Pro Ile Ser Met Leu Ala Met Leu Phe Thr Leu Ser
1 5 10 15

Gly Leu Arg Ala Gln Ser Val Ala Gln Pro Glu Asp Gln Val Asn Val
20 25 30

Ala Glu Gly Asn Pro Leu Thr Val Lys Cys Thr Tyr Ser Val Ser Gly
35 40 45

Asn Pro Tyr Leu Phe Trp Tyr Val Gln Tyr Pro Asn Arg Gly Leu Gln
50 55 60

Phe Leu Leu Lys Tyr Ile Thr Gly Asp Asn Leu Val Lys Gly Ser Tyr
65 70 75 80

Gly Phe Glu Ala Glu Phe Asn Lys Ser Gln Thr Ser Phe His Leu Lys
85 90 95

Lys Pro Ser Ala Leu Val Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val
100 105 110

Arg Asp Gln Ser Gly Ala Asn Asn Leu Phe Phe Gly Thr Gly Thr Arg
115 120 125

Leu Thr Val Ile Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln

130

135

140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser

<210> 29

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 29

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Tyr Leu Ser Gly Ser Ile Tyr Asn Glu Gln Phe Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu
130 135 140

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu

165

170

175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
 245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr
 260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
 275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
 290 295 300

Met Val Lys Arg Lys Asp Phe
 305 310

<210> 30

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 30

Leu Val Val Val Gly Ala Cys Gly Val
1 5

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 31

Asn Ser Met Phe Asp Tyr
1 5

<210> 32

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 32

Ile Ser Ser Ile Lys Asp Lys
1 5

<210> 33

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 33

Ala Ala Ser Gly Gly Gly Gly Ala Asp Gly Leu Thr
1 5 10

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 34

Met Asn His Asn Tyr
1 5

<210> 35

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 35

Ser Val Gly Ala Gly Ile
1 5

<210> 36

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 36

Ala Ser Ser Tyr Ser Thr Glu Arg Gly Thr Ile Tyr
1 5 10

<210> 37
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 37
atggccatgc tcctgggggc atcagtgctg attctgtggc ttcagccaga ctgggtaaac
60
agtcaacaga agaatgatga ccagcaagtt aagcaaaatt caccatccct gagcgtccag
120
gaaggaagaa tttctattct gaactgtgac tatactaaca gcatgtttga ttatttccta
180
tggtacaaaa aataccctgc tgaaggctct acattcctga tatctataag ttccattaag
240
gataaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct
300
ctgcacattg tgccctccca gcctggagac tctgcagtgt acttctgtgc agcaagcggg
360
ggaggagggtg ctgacggact cacctttggc aaagggactc atctaatacat ccagccc
417

<210> 38
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 38
atggccatgc tgctgggcgc cagcgtgctg attttatggc tgcagcccga ctgggtgaac
60

agccagcaga agaacgacga ccagcaagtg aagcagaact ccccttcttt aagcgtgcaa
120

gaaggtcgta tcagcatttt aaactgcgac tacaccaaca gcatgttcga ctacttttta
180

tggtacaaga agtaccgccg cgagggcccc acctttttaa tcagcatcag cagcatcaag
240

gacaagaacg aggacggtcg tttcaccgtg tttttaaaca agagcgccaa gcatttatct
300

ttacacatcg tgccctccca gcccggtgat agcgccgtgt acttctgcgc cgccagcgga
360

ggaggaggcg ccgatggact gaccttcggc aagggcaccc atttaatcat ccagccc
417

<210> 39

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39

Met	Ala	Met	Leu	Leu	Gly	Ala	Ser	Val	Leu	Ile	Leu	Trp	Leu	Gln	Pro
1			5						10					15	

Asp	Trp	Val	Asn	Ser	Gln	Gln	Lys	Asn	Asp	Asp	Gln	Gln	Val	Lys	Gln
			20					25					30		

Asn	Ser	Pro	Ser	Leu	Ser	Val	Gln	Glu	Gly	Arg	Ile	Ser	Ile	Leu	Asn
		35					40					45			

Cys	Asp	Tyr	Thr	Asn	Ser	Met	Phe	Asp	Tyr	Phe	Leu	Trp	Tyr	Lys	Lys
	50					55					60				

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Gly Gly Gly Gly Ala Asp Gly Leu Thr
115 120 125

Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro
130 135

<210> 40

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 40

atgagggtctc agaatgactt ccttgagagt cctgttcccc tttcatcaat gcacagatac
60

agaagacccc tccgtcctgg agcacctgcc atgagcatca gcctcctgtg ctgtgcagcc
120

tttcctctcc tgtgggcagg tccagtgaat gctgggtgtca ctcagacccc aaaattccgc
180

atcctgaaga taggacagag catgacactg cagtgtaccc aggatatgaa ccataactac
240

atgtactggg atcgacaaga cccaggcatg gggctgaagc tgatttatta ttcagttggt
300

gctggtatca ctgataaagg agaagtcccg aatggctaca acgtctccag atcaaccaca
360

gaggatttcc cgctcaggct ggagttggct gctccctccc agacatctgt gtacttctgt
420

gccagcagtt actcgacgga acgcgggacc atatattttg gagagggaag ttggctcact
480

g t t g t a
486

<210> 41

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

**<223> Description of Artificial Sequence: Synthetic
polynucleotide**

<400> 41

atgaggagcc agaacgactt tttagagagc cccgtgcctc tgagcagcat gcataggtat
60

aggaggcctc tgagaccggt tgccccgct atgagcatct ctttactgtg ctgtgctgcc
120

tttcctttac tgtgggctgg ccccgttaac gctggcgtga cccagacccc caagtttagg
180

attttaaaga tcggccagtc catgacttta cagtgcaccc aagatatgaa ccacaactac
240

atgtactggg atcgtcaaga tcccggcatg ggtttaaagc tgatttacta cagcgtggga
300

gccggcatca ccgacaaggg cgaggtgccc aacggctaca atgtgtctcg tagcaccacc
360

gaggacttcc ctctgagact ggagctggcc gccctagcc agacaagcgt gtacttctgc
420

gcctcctcct acagcaccga gaggggcacc atctacttcg gcgagggcag ctggctgacc
480

g t g g t g
486

<210> 42

<211> 162

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Met Arg Ser Gln Asn Asp Phe Leu Glu Ser Pro Val Pro Leu Ser Ser
1 5 10 15

Met His Arg Tyr Arg Arg Pro Leu Arg Pro Gly Ala Pro Ala Met Ser
20 25 30

Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala Gly Pro
35 40 45

Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Arg Ile Leu Lys Ile
50 55 60

Gly Gln Ser Met Thr Leu Gln Cys Thr Gln Asp Met Asn His Asn Tyr
65 70 75 80

Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys Leu Ile Tyr
85 90 95

Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val Pro Asn Gly
100 105 110

Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Glu
115 120 125

Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr
130 135 140

Ser Thr Glu Arg Gly Thr Ile Tyr Phe Gly Glu Gly Ser Trp Leu Thr
145 150 155 160

Val Val

<210> 43

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro
1 5 10 15

Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln
20 25 30

Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn
35 40 45

Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys
50 55 60

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Gly Gly Gly Gly Ala Asp Gly Leu Thr
115 120 125

Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro Asp Ile Gln Asn Pro
130 135 140

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
145 150 155 160

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
165 170 175

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg
180 185 190

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
195 200 205

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
210 215 220

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu
225 230 235 240

Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val
245 250 255

Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
260 265 270

Met Thr Leu Arg Leu Trp Ser Ser
275 280

<210> 44

<211> 339

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Met Arg Ser Gln Asn Asp Phe Leu Glu Ser Pro Val Pro Leu Ser Ser
1 5 10 15

Met His Arg Tyr Arg Arg Pro Leu Arg Pro Gly Ala Pro Ala Met Ser
20 25 30

Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala Gly Pro
35 40 45

Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Arg Ile Leu Lys Ile
50 55 60

Gly Gln Ser Met Thr Leu Gln Cys Thr Gln Asp Met Asn His Asn Tyr
65 70 75 80

Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys Leu Ile Tyr
85 90 95

Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val Pro Asn Gly
100 105 110

Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Glu
115 120 125

Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr
130 135 140

Ser Thr Glu Arg Gly Thr Ile Tyr Phe Gly Glu Gly Ser Trp Leu Thr
145 150 155 160

Val Val Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe
165 170 175

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
180 185 190

Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
195 200 205

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro
210 215 220

Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
225 230 235 240

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
245 250 255

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
260 265 270

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
275 280 285

Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val
290 295 300

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
305 310 315 320

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg
325 330 335

Lys Asp Phe

<210> 45

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 45

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 47

<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 47

Thr Ser Ile Asn Asn
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 48

Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 49

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 49

Ala Thr Asp Arg Gln Ser Ser Gly Asp Lys Leu Thr
1 5 10

<210> 50

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 50

Ser Gly His Ala Thr
1 5

<210> 51

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 51

Phe Gln Asn Asn Gly Val
1 5

<210> 52

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 52

Ala Ser Ser Leu Ala Asp Ile Tyr Glu Gln Tyr
1 5 10

<210> 53

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 53

atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggaggggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaata ttttaatacgt tcaaatagaaa gagagaaaca cagtgggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acggaccgtc aaagcagcgg agacaagctg
360

a c t t t t g g g a c c g g g a c t c g t t t a g c a g t t a g g c c c
396

<210> 54

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 54

atggagactt tactgggagcgt gtcttttagtg attttatggc tgcagctggc tcgtgtgaat
60

agccagcaag gtgaagagga cccccaagct ttaagcatcc aagaaggcga gaacgccacc
120

atgaactgct cctacaagac cagcatcaac aatttacagt ggtatcgtca gaacagcgg
180

cgtgggttag tgcatttaata ttttaattcgt agcaacgaga gggagaagca cagcggtcgt
240

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Arg Gln Ser Ser Gly Asp Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Ala Val Arg Pro
130

<210> 56

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 56

atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa
60

gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt
120

tggtgcaatc ctatatctgg ccatgctacc ctttactggg accagcagat cctgggacag
180

ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct
240

aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct
300

gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttagccga catctacgag
360

c a g t a c t t c g g g c c g g g c a c c a g g c t c a c g g t c a c a
396

<210> 57

<213> Artificial Sequence

<220>

polynucleotide

<400> 57

60

120

180

240

300

360

396

<210> 58

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

polypeptide

<400> 58

15

Glu	Leu	Thr	Glu	Ala	Gly	Val	Ala	Gln	Ser	Pro	Arg	Tyr	Lys	Ile	Ile
			20					25					30		
Glu	Lys	Arg	Gln	Ser	Val	Ala	Phe	Trp	Cys	Asn	Pro	Ile	Ser	Gly	His
		35					40					45			
Ala	Thr	Leu	Tyr	Trp	Tyr	Gln	Gln	Ile	Leu	Gly	Gln	Gly	Pro	Lys	Leu
	50					55					60				
Leu	Ile	Gln	Phe	Gln	Asn	Asn	Gly	Val	Val	Asp	Asp	Ser	Gln	Leu	Pro
65					70					75				80	
Lys	Asp	Arg	Phe	Ser	Ala	Glu	Arg	Leu	Lys	Gly	Val	Asp	Ser	Thr	Leu
				85					90					95	
Lys	Ile	Gln	Pro	Ala	Lys	Leu	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala
			100					105					110		
Ser	Ser	Leu	Ala	Asp	Ile	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Thr												
	130														
<210> 59															
<211> 273															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Description of Artificial Sequence: Synthetic polypeptide															
<400> 59															
Met	Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Arg Gln Ser Ser Gly Asp Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Ala Val Arg Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
180 185 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
195 200 205

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
210 215 220

Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 60

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Leu Ala Asp Ile Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Phe
305

<210> 61

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 61

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 62

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

peptide

<400> 62

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 63

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 63

Thr Ser Gly Phe Asn Gly
1 5

<210> 64

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 64

Asn Val Leu Asp Gly Leu
1 5

<210> 65

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 65

Cys Ala Pro Gly Asp Asn Phe Asn Lys Phe Tyr Phe
1 5 10

<210> 66

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 66

Ser Gly His Arg Ser

1 5

<210> 67

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 67

Tyr Phe Ser Glu Thr Gln

1 5

<210> 68

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 68

Cys Ala Ser Ser Ala Arg Asn Asp Glu Ala Phe Phe

1 5 10

<210> 69
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 69
atgtggggag ttttccttct ttatgtttcc atgaagatgg gaggcactac aggacaaaac
60

attgaccagc ccactgagat gacagctacg gaaggtgcca ttgtccagat caactgcacg
120

taccagacat ctgggttcaa cgggctgttc tgggtaccagc aacatgctgg cgaagcacc
180

acatttctgt cttacaatgt tctggatggg ttggaggaga aaggtcgttt ttcttcattc
240

cttagtcggt ctaaagggtg cagttacctc cttttgaagg agctccagat gaaagactct
300

gcctcttacc tctgtgctcc cggggacaac ttcaacaaat tttactttgg atctgggacc
360

a a a c t c a a t g t a a a a c c a
378

<210> 70
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 70
atgtggggcg tgtttctgct gtacgtgtcc atgaagatgg gcggcaccac aggccagaac
60

atcgaccagc caaccgagat gaccgccaca gagggcgcca tcgtgcagat caactgcacc
120

taccagacat ctggcttcaa tggcctgttt tggatatcagc agcacgcagg agaggcaccc
180

acattcctga gctataatgt gctggatggc ctggaggaga agggcagggtt ctcctctttt
240

ctgtctcgca gcaagggcta ctcctatctg ctgctgaagg agctgcagat gaaggactcc
300

gcctcttacc tgtgcgcccc tggcgataac ttttaataagt tctatttcgg ctctggcacc
360

a a g c t g a a t g t g a a g c c a
378

<210> 71

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Pro Gly Asp Asn Phe Asn
100 105 110

Lys Phe Tyr Phe Gly Ser Gly Thr Lys Leu Asn Val Lys Pro
115 120 125

<210> 72

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 72

atgggctcca ggctgctctg ttgggtgctg ctttgtctcc tgggagcagg cccagtaaag
60

gctggagtca ctcaaactcc aagatatctg atcaaaacga gaggacagca agtgacactg
120

agctgctccc ctatctcttg gcataggagt gtatcctggt accaacagac cccaggacag
180

ggccttcagt tcctctttga atacttcagt gagacacaga gaaacaaagg aaacttcct
240

ggtcgattct cagggcgcca gttctctaac tctcgctctg agatgaatgt gagcaccttg
300

gagctggggg actcggccct ttatctttgc gccagcagcg cgagaaatga tgaagctttc
360

t t t g g a c a a g
390

g c a c c a g a c t

c a c a g t t g t a

<210> 73

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 73

atgggcagcc ggctgctgtg ctgggtgctg ctgtgcctgc tgggagcagg accagtgaag
60

gcaggcgtga cccagacacc tcggtacctg atcaagacca gaggccagca ggtgacctg
120

agctgctccc caatctccgg ccacagatct gtgagctggg accagcagac cccaggacag
180

ggactgcagt tcctgtttga gtatttctcc gagacacaga ggaacaaggg caatttcct
240

ggccgggtttt ctggcagaca gttttccaac tctcgcagcg agatgaatgt gagcacctg
300

gagctgggcg actccgccct gtacctgtgc gccagctccg ccaggaacga tgaggccttc
360

t t t g g c c a g g
390

g c a c c c g g c t

g a c a g t g g t g

<210> 74

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 74

Met Gly Ser Arg Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Lys Ala Gly Val Thr Gln Thr Pro Arg Tyr Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Ser Cys Ser Pro Ile Ser Gly His
35 40 45

Arg Ser Val Ser Trp Tyr Gln Gln Thr Pro Gly Gln Gly Leu Gln Phe
50 55 60

Leu Phe Glu Tyr Phe Ser Glu Thr Gln Arg Asn Lys Gly Asn Phe Pro
65 70 75 80

Gly Arg Phe Ser Gly Arg Gln Phe Ser Asn Ser Arg Ser Glu Met Asn
85 90 95

Val Ser Thr Leu Glu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Ala Arg Asn Asp Glu Ala Phe Phe Gly Gln Gly Thr Arg Leu Thr
115 120 125

Val Val
130

<210> 75

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Pro Gly Asp Asn Phe Asn
100 105 110

Lys Phe Tyr Phe Gly Ser Gly Thr Lys Leu Asn Val Lys Pro Asp Ile
115 120 125

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
130 135 140

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
145 150 155 160

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
165 170 175

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
180 185 190

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
195 200 205

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
210 215 220

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
225 230 235 240

Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
245 250 255

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 76

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 76

Met Gly Ser Arg Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Lys Ala Gly Val Thr Gln Thr Pro Arg Tyr Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Ser Cys Ser Pro Ile Ser Gly His
35 40 45

Arg Ser Val Ser Trp Tyr Gln Gln Thr Pro Gly Gln Gly Leu Gln Phe
50 55 60

Leu Phe Glu Tyr Phe Ser Glu Thr Gln Arg Asn Lys Gly Asn Phe Pro
65 70 75 80

Gly Arg Phe Ser Gly Arg Gln Phe Ser Asn Ser Arg Ser Glu Met Asn
85 90 95

Val Ser Thr Leu Glu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Ala Arg Asn Asp Glu Ala Phe Phe Gly Gln Gly Thr Arg Leu Thr
115 120 125

Val Val Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe
130 135 140

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
145 150 155 160

Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro
180 185 190

Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
210 215 220

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
225 230 235 240

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
245 250 255

Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val
260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
275 280 285

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg
290 295 300

Lys Asp Phe
305

<210> 77

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 77

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 78

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 78

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 79

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 79

Asp Arg Gly Ser Gln Ser
1 5

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 80

Ile Tyr Ser Asn Gly Asp
1 5

<210> 81

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 81

Cys Ala Val Lys Ser Arg Ala Gly Ser Tyr Gln Leu Thr Phe
1 5 10

<210> 82

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 82

Ser Gly His Asn Ser
1 5

<210> 83

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 83

Phe Asn Asn Asn Val Pro
1 5

<210> 84

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 84

Cys Ala Ser Ser Leu Gly Asp Ser Glu Gln Tyr Phe
1 5 10

<210> 85
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 85
atgaaatcct tgagagtttt actagtgatc ctgtggcttc agttgagctg ggtttggagc
60

caacagaagg aggtggagca gaattctgga cccctcagtg ttccagaggg agccattgcc
120

tctctcaact gcacttacag tgaccgaggt tcccagtcct tcttctggta cagacaatat
180

tctgggaaaa gccctgagtt gataatgttc atatactcca atgggtgacaa agaagatgga
240

aggtttacag cacagctcaa taaagccagc cagtatgttt ctctgctcat cagagactcc
300

cagcccagtg attcagccac ctacctctgt gccgtgaagt caagggctgg gagttaccaa
360

ctcactttcg ggaaggggac caaactctcg gtcatacca
399

<210> 86
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 86
atgaagagcc tgcgggtgct gctggtcatc ctgtggctgc agctgtcctg ggtgtggtct
60

cagcagaagg aggtggagca gaatagcgga ccactgtccg tgccagaggg agccatcgcc
120

tccctgaact gcacatactc tgacaggggc tcccagtctt tcttttggtta ccgccagtat
180

agcggcaagt cccccgagct gatcatgttc atctactcta atggcgacaa ggaggatggc
240

aggtttaccg cccagctgaa caaggcctct cagtatgtga gcctgctgat ccgcgacagc
300

cagcctagcg attccgccac atacctgtgc gcagtgaagt cccgggcagg ctcttatcag
360

ctgacctttg gcaagggcac aaagctgagc gtgatccca
399

<210> 87

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 87

Met	Lys	Ser	Leu	Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ser
1				5					10					15	

Trp	Val	Trp	Ser	Gln	Gln	Lys	Glu	Val	Glu	Gln	Asn	Ser	Gly	Pro	Leu
			20					25					30		

Ser	Val	Pro	Glu	Gly	Ala	Ile	Ala	Ser	Leu	Asn	Cys	Thr	Tyr	Ser	Asp
		35					40					45			

Arg	Gly	Ser	Gln	Ser	Phe	Phe	Trp	Tyr	Arg	Gln	Tyr	Ser	Gly	Lys	Ser
	50					55					60				

Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly
65 70 75 80

Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu
85 90 95

Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val
100 105 110

Lys Ser Arg Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr Lys
115 120 125

Leu Ser Val Ile Pro
130

<210> 88

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 88

atggactcct ggaccttctg ctgtgtgtcc ctttgcattc tggtagcgaa gcatacagat
60

gctggagtta tccagtcacc ccgccatgag gtgacagaga tgggacaaga agtgactctg
120

agatgtaaac caatttcagg ccacaactcc cttttctggt acagacagac catgatgcgg
180

ggactggagt tgctcattta ctttaacaac aacgttccga tagatgattc agggatgccc
240

gaggatcgat tctcagctaa gatgcctaata gcatcattct ccactctgaa gatccagccc
300

tcagaaccca gggactcagc tgtgtacttc tgtgccagca gtctcgggga cagcgagcag
360

t a c t t c g g g c c g g g c a c c a g g c t c a c g g t c a c a
393

<210> 89

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 89

atggacagct ggaccttctg ctgcgtgagc ctgtgcatcc tgggtggccaa gcacacagat
60

gcaggcgtga tccagtcccc aaggcacgag gtgaccgaga tgggacagga ggtgacactg
120

aggtgtaagc ctatctctgg ccacaatagc ctgttctggt acaggcagac catgatgcgc
180

ggcctggagc tgctgatcta cttcaacaat aacgtgccta tcgacgattc cggcatgcca
240

gaggacagat tctctgccaa gatgcccaac gcctcctttt ctacactgaa gatccagcca
300

agcgagccta gggactccgc cgtgtacttc tgcgccagct ccctgggcga tagcgagcag
360

t a t t t t g g c c c t g g c a c c c g g c t g a c c g t g a c a
393

<210> 90

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 90

Met Asp Ser Trp Thr Phe Cys Cys Val Ser Leu Cys Ile Leu Val Ala
1 5 10 15

Lys His Thr Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr
20 25 30

Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His
35 40 45

Asn Ser Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu
50 55 60

Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro
65 70 75 80

Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
100 105 110

Ser Ser Leu Gly Asp Ser Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Thr
130

<210> 91

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91

Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu Ser
1 5 10 15

Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu
20 25 30

Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp
35 40 45

Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser
50 55 60

Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly
65 70 75 80

Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu
85 90 95

Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val
100 105 110

Lys Ser Arg Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr Lys
115 120 125

Leu Ser Val Ile Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
130 135 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser

<210> 92

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92

Met Asp Ser Trp Thr Phe Cys Cys Val Ser Leu Cys Ile Leu Val Ala
1 5 10 15

Lys His Thr Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr
20 25 30

Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His
35 40 45

Asn Ser Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu
50 55 60

Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro
65 70 75 80

Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
100 105 110

Ser Ser Leu Gly Asp Ser Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val
130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Phe
305

<210> 93

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 93

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 94
Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 95
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 95
Ser Ser Tyr Ser Pro Ser
1 5

<210> 96
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 96
Tyr Thr Ser Ala Ala Thr Leu Val
1 5

<210> 97

<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 97

Cys	Val	Val	Ser	Gly	Gly	Gly	Ser	Ser	Asn	Thr	Gly	Lys	Leu	Ile	Phe
1				5					10					15	

<210> 98

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 98

Ser	Gly	His	Ala	Thr
1				5

<210> 99

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 99

Phe	Gln	Asn	Asn	Gly	Val
1				5	

<210> 100

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 100

Cys	Ala	Ser	Ser	Gln	Arg	Ser	Asn	Thr	Gly	Glu	Leu	Phe	Phe
1				5					10				

<210> 101

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 101

atgctcctgc tgctcgtccc agtgctcgag gtgattttta ctctgggagg aaccagagcc
60

cagtcggtga cccagcttga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg
120

agggtgcaact actcatcttc ttattcacca tctctcttct ggtatgtgca acaccccaac
180

aaaggactcc agcttctcct gaagtacaca tcagcggcca ccctgggttaa aggcataaac
240

ggttttgagg ctgaatttaa gaagagtga acctccttcc acctgacgaa accctcagcc
300

catatgagcg acgcggctga gtacttctgt gttgtgagtg ggggaggctc tagcaacaca
360

ggcaaactaa tctttgggca agggacaact ttacaagtaa aacca
405

<210> 102

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 102

atgctgctgc tgctggtgcc cgtgctggaa gtgatcttca ccctgggagg aacaagggca
60

cagagcgtga cccagctgga ctcccacgtg tccgtgtctg agggcacacc cgtgctgctg
120

agatgcaact actcctctag ctatagcccc tccctgttct ggtacgtgca gcaccctaat
180

aagggcctgc agctgctgct gaagtatacc tccgccgcca cactggtgaa gggcatcaac
240

ggcttcgagg ccgagtttaa gaagagcgag acctccttcc acctgacaaa gccttctgcc
300

cacatgagcg atgccgccga gtacttttgc gtggtgagcg gcggcggctc ctctaatacc
360

ggcaagctga tcttcggcca gggcaccaca ctgcagggtga agcca
405

<210> 103

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 103

Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
1 5 10 15

Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val
20 25 30

Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr
35 40 45

Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln
50 55 60

Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn
65 70 75 80

Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr
85 90 95

Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val
100 105 110

Ser Gly Gly Gly Ser Ser Asn Thr Gly Lys Leu Ile Phe Gly Gln Gly
115 120 125

Thr Thr Leu Gln Val Lys Pro
130 135

<210> 104

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 104

atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa
60

gctggagttg ccagtcctcc cagatataag attatagaga aaaggcagag tgtggcctttt
120

tggtgcaatc ctatatctgg ccatgctacc ctttactggg accagcagat cctgggacag
180

ggcccaaagc ttctgattca gtttcagaat aacgggtgtg tggatgattc acagttgcct
240

aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccaacct
300

gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gccagaggtc gaacaccggg
360

g a g c t g t t t t t t g g a g a a g g c t c t a g g c t g a c c g t a c t g
399

<210> 105

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 105

atgggcaccc ggctgctgtg ctgggccgcc ctgtgcctgc tgggagcaga gctgacagag
60

gcaggagtgg cccagtcccc acggtacaag atcatcgaga agagacagtc cgtggccttt
120

tggtgcaacc ccatctctgg ccacgccacc ctgtactggg atcagcagat cctgggccag
180

ggccctaagc tgctgatcca gttccagaac aatggcgtgg tggacgattc tcagctgcca
240

aaggacaggt ttagcgccga gcgcctgaag ggcgtggata gcaccctgaa gatccagcct
300

gccaagctgg aggacagcgc cgtgtatctg tgcgccagct cccagcggtc caatacaggc
360

g a g c t g t t c t t t g g c g a g g g c t c t a g g c t g a c c g t g c t g
399

<210> 106

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Gln Arg Ser Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu
130

<210> 107

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 107

Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
1 5 10 15

Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val
20 25 30

Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr
35 40 45

Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln
50 55 60

Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn
65 70 75 80

Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr
85 90 95

Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val
100 105 110

Ser Gly Gly Gly Ser Ser Asn Thr Gly Lys Leu Ile Phe Gly Gln Gly
115 120 125

Thr Thr Leu Gln Val Lys Pro Asp Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
180 185 190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
275

<210> 108

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 108

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Gln Arg Ser Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val
130 135 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
225 230 235 240

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
245 250 255

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln
260 265 270

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
275 280 285

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
290 295 300

Val Lys Arg Lys Asp Phe
305 310

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 109

Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 110

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 110

Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10

<210> 111

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 111

Thr Ser Ile Asn Asn
1 5

<210> 112

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 112

Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 113

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 113

Cys Ala Thr Asp Ala Gly Gly Gly Ala Asp Gly Leu Thr Phe
1 5 10

<210> 114

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 114

Ser Gly Asp Leu Ser
1 5

<210> 115

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 115

Tyr Tyr Asn Gly Glu Glu
1 5

<210> 116

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 116

Cys Ala Ser Gly Gly Arg Asp Ser Thr Asp Thr Gln Tyr Phe
1 5 10

<210> 117

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 117

atggaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggaggggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaat tttaatacgt tcaaataaaa gagagaaaca cagtggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acggacgccg gaggaggtgc tgacggactc
360

acctttggca aagggaactca tctaatactc cagccc
396

<210> 118

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 118

atggagacac tgctgggcgt gtccctggtc atcctgtggc tgcagctggc caggggtgaac
60

agccagcagg gagaggagga cccccaggcc ctgtctatcc aggagggcga gaacgccacc
120

atgaattgct cttacaagac aagcatcaac aatctgcagt ggtatagaca gaactccggc
180

aggggcctgg tgcacctgat cctgatccgc tccaatgagc gggagaagca ctctggccgg
240

ctgagagtga ccctggatac atctaagaag tcctctagcc tgctgatcac cgccagccgg
300

gcagcagaca cagcctccta cttttgtgcc accgatgccg ggggcggagc agacggactg
360

acattcggga aggggaactca cctgattatc cagcca
396

<210> 119

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 119

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Ala Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu
115 120 125

Ile Ile Gln Pro
130

<210> 120

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 120

atggggcttca ggctcctctg ctgtgtggcc ttttgtctcc tgggagcagg cccagtggat
60

tctggagtca cacaaacccc aaagcacctg atcacagcaa ctggacagcg agtgacgctg
120

agatgctccc ctaggtcttg agacctctct gtgtactggg accaacagag cctggaccag
180

ggcctccagt tcctcattca gtattataat ggagaagaga gagcaaaagg aaacattctt
240

gaacgattct ccgcacaaca gttccctgac ttgcactctg aactaaacct gagctctctg
300

gagctggggg actcagcttt gtatttctgt gccagcgggg gacgggattc cacagatacg
360

c a g t a t t t t g g c c c a g g c a c c c g g c t g a c a g t g c t c
396

<210> 121

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 121

atggggctttc ggctgctgtg ctgcgtggct ttttgcctgc tgggggctgg gcctgtggat
60

agcgggggtca ctcagacacc taaacatctg atcacccgcaa caggacagag ggtgaccctg
120

agggtgctctc ctcggagcgg cgacctgagc gtgtactggg atcagcagag cctggatcag
180

ggcctgcagt tcctgatcca gtactataac ggcgaggagc gcgccaaggg caatatcctg
240

gagcggttct ctgccagca gtttcagac ctgcacagcg agctgaacct gagctccctg
300

gagctgggcg atagcgccct gtacttctgc gcctccggcg gcagagactc taccgataca
360

cagtat t t t t g g c c c c g g c a c c a g a c t g a c a g t g c t g
396

<210> 122

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 122

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

Ala Thr Gly Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Gly Gly Arg Asp Ser Thr Asp Thr Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Thr Val Leu
130

<210> 123

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 123

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Ala Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu
115 120 125

Ile Ile Gln Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
180 185 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
195 200 205

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
210 215 220

Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 124

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 124

Met	Gly	Phe	Arg	Leu	Leu	Cys	Cys	Val	Ala	Phe	Cys	Leu	Leu	Gly	Ala
1				5				10						15	

Gly	Pro	Val	Asp	Ser	Gly	Val	Thr	Gln	Thr	Pro	Lys	His	Leu	Ile	Thr
			20					25					30		

Ala	Thr	Gly	Gln	Arg	Val	Thr	Leu	Arg	Cys	Ser	Pro	Arg	Ser	Gly	Asp
		35					40					45			

Leu	Ser	Val	Tyr	Trp	Tyr	Gln	Gln	Ser	Leu	Asp	Gln	Gly	Leu	Gln	Phe
	50					55					60				

Leu	Ile	Gln	Tyr	Tyr	Asn	Gly	Glu	Glu	Arg	Ala	Lys	Gly	Asn	Ile	Leu
65					70					75					80

Glu	Arg	Phe	Ser	Ala	Gln	Gln	Phe	Pro	Asp	Leu	His	Ser	Glu	Leu	Asn
				85					90					95	

Leu	Ser	Ser	Leu	Glu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Ser
			100					105					110		

Gly	Gly	Arg	Asp	Ser	Thr	Asp	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg
		115					120					125			

Leu Thr Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Phe
305

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 125
Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 126
Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 127
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 127
Asn Tyr Ser Pro Ala Tyr
1 5

<210> 128
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 128
Ile Arg Glu Asn Glu Lys Glu
1 5

<210> 129
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 129
Ala Leu Asp Ile Tyr Gly Asn Asn Arg Leu Ala
1 5 10

<210> 130
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 130
Met Asp His Glu Asn
1 5

<210> 131
<211> 6

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 131
Ser Tyr Asp Val Lys Met
1 5

<210> 132
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 132
Ala Ser Ser Leu Asp Phe Val Leu Ala Gly Ser Tyr Ser Tyr Asn Glu
1 5 10 15

Gln Phe

<210> 133
<211> 453
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 133
atggccttttt ggctgagaag gctgggtcta catttcaggc cacatttggg gagacgaatg
60
gagtcattcc tgggaggtgt tttgctgatt ttgtggcttc aagtggactg ggtgaagagc
120

caaaagatag aacagaattc cgaggccctg aacattcagg agggtaaaac ggccaccctg
180

acctgcaact atacaaacta ttctccagca tacttacagt ggtaccgaca agatccagga
240

agaggccctg ttttcttgct actcatacgt gaaaatgaga aagaaaaaag gaaagaaaga
300

ctgaagggtca cctttgatac cacccttaaa cagagtttgt ttcatatcac agcctcccag
360

cctgcagact cagctaccta cctctgtgct ctagacattt atgggaacaa cagactcgct
420

t t t g g g a a g g g g a a c c a a g t g g t g g t c a t a c c a
453

<210> 134

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 134

atggccttct ggctgaggag actgggttta cacttcagac cccatttagg cagaagaatg
60

gagagctttt taggcggcgt gctgctgatt ttatggctgc aagttgactg ggtgaagagc
120

cagaagatcg agcagaacag cgaggcttta aacattcaag aaggcaagac agccacttta
180

acttgtaact ataccaacta ctcccccgct tatttacagt ggtacagaca agatcccggc
240

agaggccccg tgtttttact gctgattcgt gagaacgaga aggagaagag gaaggagaga
300

360

420

453

<210> 135

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 135

1

5

10

15

G

20

25

30

L

35

40

45

A

50

55

60

65

70

75

80

A

85

90

95

A

100

105

110

Leu Phe His Ile Thr Ala Ser Gln Pro Ala Asp Ser Ala Thr Tyr Leu
115 120 125

Cys Ala Leu Asp Ile Tyr Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly
130 135 140

Asn Gln Val Val Val Ile Pro
145 150

<210> 136

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 136

atgggaatca ggctcctctg tcgtgtggcc ttttgtttcc tggctgtagg cctcgtagat
60

gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg
120

gaatgtgtcc aggatatgga ccatgaaaat atgttcttgt atcgacaaga cccaggtctg
180

gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct
240

gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtccgcc
300

agcaccaacc agacatctat gtacctctgt gccagcagtt tagattttgt gctagcgggg
360

tcctactcct acaatgagca gttcttcggg ccaggggacac ggctcaccgt gcta
414

<210> 137
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 137
atgggcattc gtctgctgtg tcgtgtggcc ttctgctttt tagccgtggg tttagtggac
60
gtgaagggtga cccagtcctc tcgttattta gtgaagagga ccggcgagaa ggtgttttta
120
gaatgctgtc aagatatgga ccacgagaac atgttctggt acagacaaga tcccggactg
180
ggtttaaggc tgatctactt cagctacgac gtgaagatga aggagaaggg cgacatcccc
240
gagggctact ccgtgtctcg tgagaagaag gagaggttct ctttaatttt agagtccgcc
300
agcaccaacc agaccagcat gtatttatgc gccagctctt tagactttgt gctggccggc
360
agctacagct acaacgagca gttcttcggc cccggcacca gactgaccgt gctg
414

<210> 138
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 138
Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val

1	5	10	15												
Gly	Leu	Val	Asp	Val	Lys	Val	Thr	Gln	Ser	Ser	Arg	Tyr	Leu	Val	Lys
			20					25					30		
Arg	Thr	Gly	Glu	Lys	Val	Phe	Leu	Glu	Cys	Val	Gln	Asp	Met	Asp	His
		35					40					45			
Glu	Asn	Met	Phe	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Leu
	50					55					60				
Ile	Tyr	Phe	Ser	Tyr	Asp	Val	Lys	Met	Lys	Glu	Lys	Gly	Asp	Ile	Pro
65					70					75					80
Glu	Gly	Tyr	Ser	Val	Ser	Arg	Glu	Lys	Lys	Glu	Arg	Phe	Ser	Leu	Ile
				85					90					95	
Leu	Glu	Ser	Ala	Ser	Thr	Asn	Gln	Thr	Ser	Met	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Leu	Asp	Phe	Val	Leu	Ala	Gly	Ser	Tyr	Ser	Tyr	Asn	Glu	Gln	Phe
		115					120					125			
Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu						
	130					135									

<210> 139

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139

Met Ala Phe Trp Leu Arg Arg Leu Gly Leu His Phe Arg Pro His Leu
 1 5 10 15

Gly Arg Arg Met Glu Ser Phe Leu Gly Gly Val Leu Leu Ile Leu Trp
 20 25 30

Leu Gln Val Asp Trp Val Lys Ser Gln Lys Ile Glu Gln Asn Ser Glu
 35 40 45

Ala Leu Asn Ile Gln Glu Gly Lys Thr Ala Thr Leu Thr Cys Asn Tyr
 50 55 60

Thr Asn Tyr Ser Pro Ala Tyr Leu Gln Trp Tyr Arg Gln Asp Pro Gly
 65 70 75 80

Arg Gly Pro Val Phe Leu Leu Leu Ile Arg Glu Asn Glu Lys Glu Lys
 85 90 95

Arg Lys Glu Arg Leu Lys Val Thr Phe Asp Thr Thr Leu Lys Gln Ser
 100 105 110

Leu Phe His Ile Thr Ala Ser Gln Pro Ala Asp Ser Ala Thr Tyr Leu
 115 120 125

Cys Ala Leu Asp Ile Tyr Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly
 130 135 140

Asn Gln Val Val Val Ile Pro Asp Ile Gln Asn Pro Asp Pro Ala Val
 145 150 155 160

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
 165 170 175

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp

180

185

190

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
 195 200 205

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
 210 215 220

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
 225 230 235 240

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
 245 250 255

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
 260 265 270

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
 275 280 285

Leu Trp Ser Ser
 290

<210> 140

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 140

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
 1 5 10 15

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
20 25 30

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Leu Asp Phe Val Leu Ala Gly Ser Tyr Ser Tyr Asn Glu Gln Phe
115 120 125

Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Asn Lys Val
130 135 140

Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser
145 150 155 160

His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro
165 170 175

Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser
180 185 190

Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn

195

200

205

Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe
210 215 220

Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly
225 230 235 240

Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr
245 250 255

Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr
260 265 270

Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu
275 280 285

Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu
290 295 300

Val Leu Met Ala Met Val Lys Arg Lys Asp Phe
305 310 315

<210> 141

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 141

Met Leu Thr Gly Pro Pro Ala Arg Val
1 5

<210> 142
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 142
Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 143
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 143
Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 144
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 144
Ala Leu Ser Glu Ala Arg Val Phe Asn Gly Ala Asn Ser Lys Leu Thr
1 5 10 15

<210> 145
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 145

Ser Gly His Asp Asn

1 5

<210> 146

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 146

Phe Val Lys Glu Ser Lys

1 5

<210> 147

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 147

Ala Ser Ser Gln Ala Asp Ser Pro Leu His

1 5 10

<210> 148

<211> 417

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 148

atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg
60

gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc
120

ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca
180

ccaagtggag aattggtttt ccttattcgt cggaactctt ttgatgagca aaatgaaata
240

agtggtcggt attcttgga cttccagaaa tccaccagtt ccttcaactt caccatcaca
300

gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgagtgaggc ccgcgttttc
360

aatggagcca atagtaagct gacatttgga aaaggaataa ctctgagtgt tagacca
417

<210> 149

<211> 417

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 149

atgctgaccg ccagcctgct gagggctgtg atcgccagca tctgcgtcgt gtccagcatg
60

gctcaaaagg tcacacaggc ccagacagag atctccgtcg tcgagaaaga ggacgtgacc
120

ctcgactgcg tgtatgagac cagggacacc acatactacc tgttttggta caagcagccc
180

cccagcggag agctcgtggt tctgatcaga aggaacagct ttgatgaaca gaatgagatc
240

tccggcaggt actcctggaa cticcagaag agcacctcca gcttcaactt cacaattaca
300

gcttcccagg tgggtggatag cgccgtgtat ttctgcgctc tcagcgaggc caggggtgttc
360

aacggcgcca attccaaact gaccttcggc aaaggcatca cactgtccgt gagaccc
417

<210> 150

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 150

Met	Leu	Thr	Ala	Ser	Leu	Leu	Arg	Ala	Val	Ile	Ala	Ser	Ile	Cys	Val
1				5					10					15	

Val	Ser	Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser
			20					25					30		

Val	Val	Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg
		35					40					45			

Asp	Thr	Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu
	50					55					60				

Leu	Val	Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile
65					70					75				80	

Ser	Gly	Arg	Tyr	Ser	Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	Asn
				85					90					95	

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Ser Glu Ala Arg Val Phe Asn Gly Ala Asn Ser Lys Leu Thr
115 120 125

Phe Gly Lys Gly Ile Thr Leu Ser Val Arg Pro
130 135

<210> 151

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 151

atggtttcca ggcttctcag tttagtgtcc ctttgtctcc tgggagcaaa gcacatagaa
60

gctggagtta ctcagttccc cagccacagc gtaatagaga agggccagac tgtgactctg
120

agatgtgacc caatttctgg acatgataat ctttattggg atcgacgtgt tatgggaaaa
180

gaaataaaat ttctgttaca ttttgtgaaa gagtctaaac aggatgaatc cggtatgccc
240

aacaatcgat tcttagctga aaggactgga gggacgtatt ctactctgaa ggtgcagcct
300

gcagaactgg aggattctgg agtttatttc tgtgccagca gccaagcgga ttcaccctc
360

c a c t t t g g g a a t g g g a c c a g g c t c a c t g t g a c a
393

<210> 152
<211> 393
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 152

atggctctcca ggctgctctc cctcgtgagc ctgtgtctcc tgggagccaa gcacattgag
60

gccggcgtga cccaattccc cagccacagc gtgattgaga agggacagac cgtcaccctg
120

aggtgtgac ctatcagcgg ccacgacaac ctctactggt ataggagagt catgggcaag
180

gaaattaaat ttctgctgca tttcgtgaaa gagtccaaac aggacgaaag cggcatgccc
240

aataataggt tcctcgccga gaggaccggc ggcacatatt ccaccctgaa ggtccagccc
300

gctgagctcg aagactccgg cgtctatttc tgtgcctcca gccaggctga ctcccctctc
360

c a t t t c g g a a a c g g c a c c a g g c t c a c c g t g a c c
393

<210> 153

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153

Met Val Ser Arg Leu Leu Ser Leu Val Ser Leu Cys Leu Leu Gly Ala
1 5 10 15

Lys His Ile Glu Ala Gly Val Thr Gln Phe Pro Ser His Ser Val Ile
20 25 30

Glu Lys Gly Gln Thr Val Thr Leu Arg Cys Asp Pro Ile Ser Gly His
35 40 45

Asp Asn Leu Tyr Trp Tyr Arg Arg Val Met Gly Lys Glu Ile Lys Phe
50 55 60

Leu Leu His Phe Val Lys Glu Ser Lys Gln Asp Glu Ser Gly Met Pro
65 70 75 80

Asn Asn Arg Phe Leu Ala Glu Arg Thr Gly Gly Thr Tyr Ser Thr Leu
85 90 95

Lys Val Gln Pro Ala Glu Leu Glu Asp Ser Gly Val Tyr Phe Cys Ala
100 105 110

Ser Ser Gln Ala Asp Ser Pro Leu His Phe Gly Asn Gly Thr Arg Leu
115 120 125

Thr Val Thr
130

<210> 154

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 154

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val

1		5						10						15			
Val	Ser	Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser		
			20					25					30				
Val	Val	Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg		
		35					40					45					
Asp	Thr	Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu		
	50					55					60						
Leu	Val	Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile		
65					70					75					80		
Ser	Gly	Arg	Tyr	Ser	Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	Asn		
				85					90					95			
Phe	Thr	Ile	Thr	Ala	Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	Phe	Cys		
			100					105					110				
Ala	Leu	Ser	Glu	Ala	Arg	Val	Phe	Asn	Gly	Ala	Asn	Ser	Lys	Leu	Thr		
		115					120					125					
Phe	Gly	Lys	Gly	Ile	Thr	Leu	Ser	Val	Arg	Pro	Asp	Ile	Gln	Asn	Pro		
	130					135					140						
Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser		
145					150					155					160		
Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser		
				165					170					175			
Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg		
			180					185					190				

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
195 200 205

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
210 215 220

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu
225 230 235 240

Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val
245 250 255

Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
260 265 270

Met Thr Leu Arg Leu Trp Ser Ser
275 280

<210> 155

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 155

Met Val Ser Arg Leu Leu Ser Leu Val Ser Leu Cys Leu Leu Gly Ala
1 5 10 15

Lys His Ile Glu Ala Gly Val Thr Gln Phe Pro Ser His Ser Val Ile
20 25 30

Glu Lys Gly Gln Thr Val Thr Leu Arg Cys Asp Pro Ile Ser Gly His

35

40

45

Asp Asn Leu Tyr Trp Tyr Arg Arg Val Met Gly Lys Glu Ile Lys Phe
50 55 60

Leu Leu His Phe Val Lys Glu Ser Lys Gln Asp Glu Ser Gly Met Pro
65 70 75 80

Asn Asn Arg Phe Leu Ala Glu Arg Thr Gly Gly Thr Tyr Ser Thr Leu
85 90 95

Lys Val Gln Pro Ala Glu Leu Glu Asp Ser Gly Val Tyr Phe Cys Ala
100 105 110

Ser Ser Gln Ala Asp Ser Pro Leu His Phe Gly Asn Gly Thr Arg Leu
115 120 125

Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val
130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Phe
305

<210> 156

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 156

Ala Leu Asn Ser Glu Ala Leu Ser Val
1 5

<210> 157

<211> 201

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 157

Met Arg Arg Leu Ser Ala Ala Arg Arg Ala Gly Thr Ser Cys Ala Asn
1 5 10 15

Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Asn Gly Asp
20 25 30

Pro Val Cys Asn Ala Cys Gly Leu Tyr Tyr Lys Leu His Asn Ile Asn
35 40 45

Arg Pro Leu Thr Met Lys Lys Glu Gly Ile Gln Thr Arg Asn Arg Lys
50 55 60

Met Ser Ser Lys Ser Lys Lys Cys Lys Lys Val His Asp Ser Leu Glu
65 70 75 80

Asp Phe Pro Lys Asn Ser Ser Phe Pro Gly Arg Pro Leu Gln Thr His
85 90 95

Val Leu Pro Glu Pro His Leu Ala Leu Gln Pro Leu Gln Pro His Ala
100 105 110

Asp His Ala His Ala Asp Ala Pro Ala Ile Gln Pro Val Leu Trp Thr
115 120 125

Thr Pro Pro Leu Gln His Gly His Arg His Gly Leu Glu Pro Cys Ser
130 135 140

Met Leu Thr Gly Pro Pro Ala Arg Val Pro Ala Val Pro Phe Asp Leu
145 150 155 160

His Phe Cys Arg Ser Ser Ile Met Lys Pro Lys Arg Asp Gly Tyr Met
165 170 175

Phe Leu Lys Ala Glu Ser Lys Ile Met Phe Ala Thr Leu Gln Arg Ser
180 185 190

Ser Leu Trp Cys Leu Cys Ser Asn His
195 200

<210> 158

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 158

Pro Gly Arg Pro Leu Gln Thr His Val Leu Pro Glu Pro His Leu Ala
1 5 10 15

Leu Gln Pro Leu Gln Pro His Ala Asp His Ala His Ala Asp Ala Pro
20 25 30

Ala Ile Gln Pro Val Leu Trp Thr Thr Pro Pro Leu Gln His Gly His
35 40 45

Arg His Gly Leu Glu Pro Cys Ser Met Leu Thr Gly Pro Pro Ala Arg
50 55 60

Val Pro Ala Val Pro Phe Asp Leu His Phe Cys Arg Ser Ser Ile Met
65 70 75 80

Lys Pro Lys Arg Asp Gly Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile
85 90 95

Met Phe Ala Thr Leu Gln Arg Ser Ser Leu Trp Cys Leu Cys Ser Asn
100 105 110

His

<210> 159

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 159

Asp Arg Gly Ser Gln Ser
1 5

<210> 160

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 160

Ile Tyr Ser Asn Gly Asp
1 5

<210> 161

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 161

Ala Val Asn Asp Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe
1 5 10

<210> 162

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 162

Ser Glu His Asn Arg
1 5

<210> 163

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 163

Phe Gln Asn Glu Ala Gln
1 5

<210> 164

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 164

Ala Ser Ser Phe Gly Pro Asp Glu Lys Leu Phe Phe

<210> 165

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 165

atgatgaaat ccttgagagt tttactagtg atcctgtggc ttcagttgag ctggggttgg
60

agccaacaga aggaggtgga gcagaattct ggacccctca gtgttccaga gggagccatt
120

gcctctctca actgcactta cagtgaccga ggttcccagt ccttcttctg gtacagacaa
180

tattctggga aaagccctga gttgataatg ttcataact ccaatgggtga caaagaagat
240

ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac
300

tcccagccca gtgattcagc cacctacctc tgtgccgtga acgattatgg aggaagccaa
360

ggaaatctca tctttggaaa aggcactaaa ctctctgtta aacca
405

<210> 166

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 166

atgatgaaga gcctgcgggt gctgctggtc atcctgtggc tgcagctgtc ttgggtgtgg
60

agccagcaga aggaggtgga gcagaactcc ggaccactgt ctgtgcctga gggagccatc
120

gccagcctga attgcaccta ctccgacaga ggctcccagt ctttcttttg gtacaggcag
180

tatagcggca agtcccccgga gctgatcatg ttcattctact ccaacggcga caaggaggat
240

ggccgcttta cagcccagct gaataaggcc agccagtacg tgagcctgct gatccgggac
300

tctcagccaa gcgattccgc cacctacctg tgcgccgtga acgattatgg cggcagccag
360

ggcaatctga tcttttgcaa gggcacaaag ctgtccgtga agccc
405

<210> 167

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 167

Met	Met	Lys	Ser	Leu	Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	

Ser	Trp	Val	Trp	Ser	Gln	Gln	Lys	Glu	Val	Glu	Gln	Asn	Ser	Gly	Pro
			20					25					30		

Leu	Ser	Val	Pro	Glu	Gly	Ala	Ile	Ala	Ser	Leu	Asn	Cys	Thr	Tyr	Ser
		35					40					45			

Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys

50

55

60

Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
65 70 75 80

Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu
85 90 95

Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala
100 105 110

Val Asn Asp Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe Gly Lys Gly
115 120 125

Thr Lys Leu Ser Val Lys Pro
130 135

<210> 168

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 168

atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat
60

actggagtct cccagaaccc cagacacaag atcacaaaga ggggacagaa tgtaactttc
120

aggtgtgatc caatttctga acacaaccgc ctttattggt accgacagac cctggggcag
180

ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc
240

agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc
300

acagagcagg gggactcggc catgtatctc tgtgccagca gcttcggacc tgatgaaaaa
360

ctgttttttg gcagtggaac ccagctctct gtcttg
396

<210> 169

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 169

atgggcacct ctctgctgtg ctggatggca ctgtgcctgc tgggagcaga ccacgcagat
60

acaggcgtga gccagaaccc acgccacaag atcaccaagc ggggccagaa tgtgacattc
120

agatgcgacc ccatcagcga gcacaacagg ctgtactggg ataggcagac cctgggacag
180

ggaccagagt tcctgacata ctttcagaat gagggcccagc tggagaagtc tcggctgctg
240

agcgatagat tctccgccga gaggcctaag ggctcctttt ctaccctgga gatccagagg
300

acagagcagg gcgactccgc catgtatctg tgcgccagct ccttcggccc tgatgagaag
360

ctgtttctttg gctctggcac ccagctgagc gtgctg
396

<210> 170

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 170

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Phe Gly Pro Asp Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln
115 120 125

Leu Ser Val Leu
130

<210> 171

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 171

Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro
20 25 30

Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
35 40 45

Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys
50 55 60

Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
65 70 75 80

Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu
85 90 95

Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala
100 105 110

Val Asn Asp Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe Gly Lys Gly
115 120 125

Thr Lys Leu Ser Val Lys Pro Asp Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe

145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
180 185 190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
275

<210> 172

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 172

Met	Gly	Thr	Ser	Leu	Leu	Cys	Trp	Met	Ala	Leu	Cys	Leu	Leu	Gly	Ala	1	5	10	15
Asp	His	Ala	Asp	Thr	Gly	Val	Ser	Gln	Asn	Pro	Arg	His	Lys	Ile	Thr	20	25	30	
Lys	Arg	Gly	Gln	Asn	Val	Thr	Phe	Arg	Cys	Asp	Pro	Ile	Ser	Glu	His	35	40	45	
Asn	Arg	Leu	Tyr	Trp	Tyr	Arg	Gln	Thr	Leu	Gly	Gln	Gly	Pro	Glu	Phe	50	55	60	
Leu	Thr	Tyr	Phe	Gln	Asn	Glu	Ala	Gln	Leu	Glu	Lys	Ser	Arg	Leu	Leu	65	70	75	80
Ser	Asp	Arg	Phe	Ser	Ala	Glu	Arg	Pro	Lys	Gly	Ser	Phe	Ser	Thr	Leu	85	90	95	
Glu	Ile	Gln	Arg	Thr	Glu	Gln	Gly	Asp	Ser	Ala	Met	Tyr	Leu	Cys	Ala	100	105	110	
Ser	Ser	Phe	Gly	Pro	Asp	Glu	Lys	Leu	Phe	Phe	Gly	Ser	Gly	Thr	Gln	115	120	125	
Leu	Ser	Val	Leu	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	130	135	140	
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	145	150	155	160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	165	170	175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro				

180

185

190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Phe
305

<210> 173

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 173

Ser Leu Leu Asn Tyr Leu Arg Glu Met
1 5

<210> 174

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 174

Asp Arg Gly Ser Gln Ser

1 5

<210> 175

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 175

Ile Tyr Ser Asn Gly Asp

1 5

<210> 176

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 176

Ala Val Asn Glu Gly Asp Ser Ser Tyr Lys Leu Ile

1 5 10

<210> 177
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 177
Ser Gly Asp Leu Ser
1 5

<210> 178
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 178
Tyr Tyr Asn Gly Glu Glu
1 5

<210> 179
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 179
Ala Ser Ser Pro Gly Ala Asn Glu Lys Leu Phe
1 5 10

<210> 180
<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 180

atgatgaaat ccttgagagt tttactagt atcctgtggc ttcagttgag ctgggtttgg
60

agccaacaga aggaggtgga gcagaattct ggaccctca gtgttccaga gggagccatt
120

gcctctctca actgcactta cagtgaccga ggttcccagt ccttcttctg gtacagacaa
180

tattctggga aaagccctga gttgataatg ttcataact ccaatgggtga caaagaagat
240

ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac
300

tcccagccca gtgattcagc cacctacctc tgtgccgtga acgaggggga tagcagctat
360

aaattgatct tcgggagtg gaccagactg ctgggtcaggc ct
402

<210> 181

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 181

atgatgaaga gcctgcgggt gctgctggtc atcctgtggc tgcagctgag ctgggtgtgg
60

tcccagcaga aggaggtgga gcagaactct ggaccactga gcgtgcctga gggagccatc
120

gcctccctga attgcaccta ctctgacaga ggcagccagt ccttcttttg gtacaggcag
180

tattccggca agtctcccga gctgatcatg ttcatctaca gcaacggcga caaggaggat
240

ggccgcttta cagcccagct gaataaggcc tcccagtagc tgagcctgct gatccgggac
300

tctcagccat ctgatagcgc cacctacctg tgcgccgtga acgagggcga tagctcctat
360

aagctgatct ttggcagcgg cacaagactg ctggtgaggc cc
402

<210> 182

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 182

Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro
20 25 30

Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
35 40 45

Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys
50 55 60

Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
65 70 75 80

Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu
85 90 95

Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala
100 105 110

Val Asn Glu Gly Asp Ser Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr
115 120 125

Arg Leu Leu Val Arg Pro
130

<210> 183

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 183

atgggcttca ggctcctctg ctgtgtggcc ttttgtctcc tgggagcagg cccagtggat
60

tctggagtca cacaaccccc aaagcacctg atcacagcaa ctggacagcg agtgacgctg
120

agatgctccc ctaggtcttg agacctctct gtgtactggt accaacagag cctggaccag
180

ggcctccagt tcctcattca gtattataat ggagaagaga gagcaaaaagg aacattctt
240

gaacgattct ccgcacaaca gttccctgac ttgcactctg aactaaacct gagctctctg
300

gagctggggg actcagcttt gtatttctgt gccagcagcc cgggggctaa tgaaaaactg
360

t t t t t g g c a g t g g a a c c c a g c t c t c t g t c t t g
393

<210> 184

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 184

atgggcttcc ggctgctgtg ctgctgtgga ttttgccctgc tgggagcagg accagtggac
60

tccggcgtga cccagacacc caagcacctg atcaccgcaa caggacagag ggtgaccctg
120

agatgttccc ctaggtctgg cgacctgagc gtgtactggt atcagcagtc cctggatcag
180

ggcctgcagt tcctgatcca gtactataac ggcgaggagc gcgccaaggg caatatcctg
240

gagcggttct ccgcccagca gtttcccgac ctgcactctg agctgaacct gagctccctg
300

gagctgggcg atagcgccct gtacttctgc gcctctagcc ctggcgccaa tgagaagctg
360

t t c t t t g g c a g c g g c a c c c a g c t g t c c g t g c t g
393

<210> 185

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 185

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

Ala Thr Gly Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Pro Gly Ala Asn Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln Leu
115 120 125

Ser Val Leu
130

<210> 186

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 186

Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro
20 25 30

Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
35 40 45

Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys
50 55 60

Ser Pro Glu Leu Ile Met Phe Ile Tyr Ser Asn Gly Asp Lys Glu Asp
65 70 75 80

Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu
85 90 95

Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala
100 105 110

Val Asn Glu Gly Asp Ser Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr
115 120 125

Arg Leu Leu Val Arg Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175

Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240

Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
245 250 255

Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
260 265 270

Trp Ser Ser
275

<210> 187

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 187

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr

20

25

30

Ala Thr Gly Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
 65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
 85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
 100 105 110

Ser Pro Gly Ala Asn Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln Leu
 115 120 125

Ser Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val
 130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
 145 150 155 160

Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
 165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
 180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
 195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Phe
305

<210> 188

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 188

Ser Leu Leu Asn Tyr Leu Arg Glu Met
1 5

<210> 189

<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 189

Asn Ser Met Phe Asp Tyr
1 5

<210> 190

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 190

Ile Ser Ser Ile Lys Asp Lys
1 5

<210> 191

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 191

Ala Ala Ser Ala Ser Asn Asn Asp Met Arg
1 5 10

<210> 192

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 192

Ser Glu His Asn Arg
1 5

<210> 193

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 193

Phe Gln Asn Glu Ala Gln
1 5

<210> 194

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 194

Ala Ser Ser Gln Ser Gly Gln Gly Pro Tyr Glu Gln Tyr
1 5 10

<210> 195

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 195

atggccatgc tcctgggggc atcagtgctg attctgtggc ttcagccaga ctgggtaaac
60

agtcaacaga agaatgatga ccagcaagtt aagcaaaatt caccatccct gagcgtccag
120

gaaggaagaa tttctattct gaactgtgac tataactaaca gcatgtttga ttatttccta
180

tggtacaaaa aataccctgc tgaaggctct acattcctga tatctataag ttccattaag
240

gataaaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct
300

ctgcacattg tgccctccca gcctggagac tctgcagtgt acttctgtgc agcaagcgcg
360

tcaaacaatg acatgcgctt tggagcaggg accagactga cagtaaaacc a
411

<210> 196

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 196

atggcaatgc tgctgggagc ctctgtgctg atcctgtggc tgcagccaga ttgggtgaac
60

tcccagcaga agaatgacga tcagcaggtg aagcagaata gcccctccct gtctgtgcag
120

gagggcagaa tcagcatcct gaactgcgac tacaccaatt ccatgttcga ttatittctg
180

tggtacaaga agtatccagc cgagggcccc acctttctga tcagcatctc ctctatcaag
240

gacaagaacg aggatggcag gttcacagtg tttctgaata agtctgccaa gcacctgagc
300

ctgcacatcg tgccatccca gcctggcgac tctgccgtgt acttctgtgc cgccagcgcc
360

tccaacaatg atatgagatt tggcgccggc accaggctga cagtgaagcc c
411

<210> 197

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 197

Met	Ala	Met	Leu	Leu	Gly	Ala	Ser	Val	Leu	Ile	Leu	Trp	Leu	Gln	Pro
1			5					10					15		

Asp	Trp	Val	Asn	Ser	Gln	Gln	Lys	Asn	Asp	Asp	Gln	Gln	Val	Lys	Gln
		20					25						30		

Asn	Ser	Pro	Ser	Leu	Ser	Val	Gln	Glu	Gly	Arg	Ile	Ser	Ile	Leu	Asn
		35				40					45				

Cys	Asp	Tyr	Thr	Asn	Ser	Met	Phe	Asp	Tyr	Phe	Leu	Trp	Tyr	Lys	Lys
50						55					60				

Tyr	Pro	Ala	Glu	Gly	Pro	Thr	Phe	Leu	Ile	Ser	Ile	Ser	Ser	Ile	Lys
65					70					75				80	

Asp	Lys	Asn	Glu	Asp	Gly	Arg	Phe	Thr	Val	Phe	Leu	Asn	Lys	Ser	Ala
			85						90					95	

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Ala Ser Asn Asn Asp Met Arg Phe Gly
115 120 125

Ala Gly Thr Arg Leu Thr Val Lys Pro
130 135

<210> 198

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 198

atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat
60

actggagtct cccaggaccc cagacacaag atcacaaga ggggacagaa tgtaactttc
120

aggtgtgatc caatttctga acacaaccgc ctttattggt accgacagac cctggggcag
180

ggcccagagt ttctgactta ctccagaat gaagctcaac tagaaaaatc aaggctgctc
240

agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc
300

acagagcagg gggactcggc catgtatctc tgtgccagca gccaatcggg acaggggccc
360

tacgagcagt acttcggggc gggcaccagg ctcacgggtca cagag
405

<210> 199

<211> 405
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 199

atgggacacct ctctgctgtg ctggatggca ctgtgcctgc tgggagcaga ccacgcagat
60

acaggcgtga gccaggaccc ccgccacaag atcaccaagc ggggccagaa cgtgacattc
120

agatgcgatc ctatctccga gcacaatagg ctgtactggt ataggcagac cctgggacag
180

ggaccagagt tcctgacata ctttcagaac gaggcccagc tggagaagag ccggctgctg
240

tccgacagat tctctgccga gaggcctaag ggcagctttt ccaccctgga gatccagagg
300

acagagcagg gcgattctgc catgtatctg tgcgccagct cccagagcgg acagggacct
360

tacgagcagt atttcggacc aggaaccagg ctgaccgtga cagag
405

<210> 200

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 200

Met	Gly	Thr	Ser	Leu	Leu	Cys	Trp	Met	Ala	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	

Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Gln Ser Gly Gln Gly Pro Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr Glu
130 135

<210> 201

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 201

Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro
1 5 10 15

Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln
20 25 30

Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn
35 40 45

Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys
50 55 60

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Ala Ser Asn Asn Asp Met Arg Phe Gly
115 120 125

Ala Gly Thr Arg Leu Thr Val Lys Pro Asp Ile Gln Asn Pro Asp Pro
130 135 140

Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys
145 150 155 160

Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp
165 170 175

Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met
180 185 190

Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe
 195 200 205

Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe
 210 215 220

Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser
 225 230 235 240

Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly
 245 250 255

Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr
 260 265 270

Leu Arg Leu Trp Ser Ser
 275

<210> 202
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 202
 Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
 20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
 35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Gln Ser Gly Gln Gly Pro Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr Glu Glu Asp Leu Asn Lys Val Phe Pro Pro
130 135 140

Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
260 265 270

Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 203

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 203

Lys Pro Lys Arg Asp Gly Tyr Met Phe
1 5

<210> 204

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

peptide

<400> 204

Tyr Gly Gly Thr Val Asn

1 5

<210> 205

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 205

Tyr Phe Ser Gly Asp Pro Leu Val

1 5

<210> 206

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 206

Ala Val Ile Ser Val Thr Gly Asn Asn Arg Lys Leu Ile

1 5 10

<210> 207

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 207

Leu Asn His Asp Ala
1 5

<210> 208
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 208
Ser Gln Ile Val Asn Asp
1 5

<210> 209
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 209
Ala Ser Ser Arg Thr Ala Met Asn Thr Glu Ala Phe
1 5 10

<210> 210
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 210
atgctcctgt tgctcatacc agtgctgggg atgatttttg ccctgagaga tgccagagcc
60

cagtctgtga gccagcataa ccaccacgta attctctctg aagcagcctc actggagttg
120

ggatgcaact attcctatgg tggaactggt aatctcttct ggtatgtcca gtaccctggg
180

caacaccttc agcttctcct caagtacttt tcaggggatc cactgggttaa aggcatacaag
240

ggctttgagg ctgaatttat aaagagtaaa ttctccttta atctgaggaa accctctgtg
300

cagtggagtg acacagctga gtacttctgt gccgtgatct ccgtgactgg caacaaccgt
360

aagctgattt ggggattggg aacaagcctg gcagtaaata cg
402

<210> 211
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 211
atgctgctgc tgctgatccc tgtgctgggc atgatctttg cactgaggga cgcaagagca
60

cagtccgtgt ctcagcacia ccaccacgtg atcctgagcg aggcagcctc cctggagctg
120

ggctgcaact actcttatgg cggcacagtg aatctgttct ggtacgtgca gtatccaggc
180

cagcacctgc agctgctgct gaagtacttt agcggcgacc ccctgggtgaa gggcatcaag
240

ggcttcgagg ccgagtttat caagtccaag ttctctttta acctgcggaa gccatctgtg
300

cagtggagcg ataccgccga gtatttctgt gccgtgatca gcgtgacagg caacaataga
360

Ser Leu Ala Val Asn Pro
130

<210> 213
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 213
atgagcaacc aggtgctctg ctgtgtggtc ctttgtctcc tgggagcaaa caccgtggat
60

ggtggaatca ctcagtcccc gaagtacctg ttcagaaagg aaggacagaa tgtgaccctg
120

agttgtgaac agaatttgaa ccacgatgcc atgtactggg accgacagga cccagggcaa
180

gggctgagat tgatctacta ctcacagata gtaaattgact ttcagaaagg agatatagct
240

gaaggggtaca gcgtctctcg ggagaagaag gaatcctttc ctctcactgt gacatcggcc
300

caaaagaacc cgacagcttt ctatctctgt gccagtagtc ggactgcaat gaacactgaa
360

g c t t t c t t t g g a c a a g g c a c c a g a c t c a c a g t t g t a
396

<210> 214
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 214

atgtccaacc aggtgctgtg ctgctggtg ctgtgcctgc tgggagcaaa taccgtggac
60

ggagggcatca cacagtcccc caagtacctg ttcaggaagg agggccagaa cgtgaccctg
120

tcttgtgagc agaacctgaa tcacgacgcc atgtactggg ataggcagga ccccggacag
180

ggactgagac tgatctacta tagccagatc gtgaatgact ttcagaaggc cgacatcgcc
240

gagggctact ccgtgtctag ggagaagaag gagagcttcc ccctgaccgt gacatccgcc
300

cagaagaacc ctacagcctt ttatctgtgc gccagctccc gcaccgccat gaatacagag
360

g c c t t c t t t g g c c a g g g c a c c a g g c t g a c a g t g g t g
396

<210> 215

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 215

Met Ser Asn Gln Val Leu Cys Cys Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Asn Thr Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg
20 25 30

Lys Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His
35 40 45

Asp Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr
85 90 95

Val Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser
100 105 110

Ser Arg Thr Ala Met Asn Thr Glu Ala Phe Phe Gly Gln Gly Thr Arg
115 120 125

Leu Thr Val Val
130

<210> 216

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 216

Met Leu Leu Leu Leu Ile Pro Val Leu Gly Met Ile Phe Ala Leu Arg
1 5 10 15

Asp Ala Arg Ala Gln Ser Val Ser Gln His Asn His His Val Ile Leu
20 25 30

Ser Glu Ala Ala Ser Leu Glu Leu Gly Cys Asn Tyr Ser Tyr Gly Gly

35

40

45

Thr Val Asn Leu Phe Trp Tyr Val Gln Tyr Pro Gly Gln His Leu Gln
50 55 60

Leu Leu Leu Lys Tyr Phe Ser Gly Asp Pro Leu Val Lys Gly Ile Lys
65 70 75 80

Gly Phe Glu Ala Glu Phe Ile Lys Ser Lys Phe Ser Phe Asn Leu Arg
85 90 95

Lys Pro Ser Val Gln Trp Ser Asp Thr Ala Glu Tyr Phe Cys Ala Val
100 105 110

Ile Ser Val Thr Gly Asn Asn Arg Lys Leu Ile Trp Gly Leu Gly Thr
115 120 125

Ser Leu Ala Val Asn Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175

Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240

Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
245 250 255

Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
260 265 270

Trp Ser Ser
275

<210> 217

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 217

Met Ser Asn Gln Val Leu Cys Cys Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Asn Thr Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg
20 25 30

Lys Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His
35 40 45

Asp Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala

65					70					75					80
Glu	Gly	Tyr	Ser	Val	Ser	Arg	Glu	Lys	Lys	Glu	Ser	Phe	Pro	Leu	Thr
				85					90					95	
Val	Thr	Ser	Ala	Gln	Lys	Asn	Pro	Thr	Ala	Phe	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Arg	Thr	Ala	Met	Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Val	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
	130					135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro
			180					185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
	210					215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225					230					235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
				245					250					255	

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Phe
305

<210> 218
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 218
Glu Ser Lys Ile Met Phe Ala Thr Leu
1 5

<210> 219
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 219
Lys Leu Val Val Val Gly Ala Asp Gly Val
1 5 10

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 220
Leu Val Val Val Gly Ala Asp Gly Val
1 5

<210> 221
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 221
Lys Leu Val Val Val Gly Ala Val Gly Val
1 5 10

<210> 222
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 222
Leu Val Val Val Gly Ala Val Gly Val
1 5

<210> 223

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<210> 238

<400> 238

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<210> 239

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 239

Ser Val Phe Ser Ser

1 5

<210> 240

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 240

Val Val Thr Gly Gly Glu Val

1 5

<210> 241

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 241

Ala Gly Gly Pro Asn Thr Gly Asn Gln Phe Tyr

1 5 10

<210> 242
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 242
Ser Gly His Asn Thr
1 5

<210> 243
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 243
Tyr Tyr Arg Glu Glu Glu
1 5

<210> 244
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 244
Ala Ser Ser Thr Ser Phe Trp Glu Val Asn Thr Glu Ala Phe
1 5 10

<210> 245
<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 245

atgggtcctga aattctccgt gtccattctt tggattcagt tggcatgggt gagcaccag
60

ctgctggagc agagccctca gtttctaagc atccaagagg gagaaaatct cactgtgtac
120

tgcaactcct caagtgtttt ttccagctta caatgggtaca gacaggagcc tggggaaggt
180

cctgtcctcc tggtgacagt agttacgggt ggagaagtga agaagctgaa gagactaacc
240

tttcagtttg gtgatgcaag aaaggacagt tctctccaca tcactgcggc ccagcctggt
300

gatacaggcc tctacctctg tgcaggaggg ccgaacaccg gtaaccagtt ctattttggg
360

a c a g g g a c a a
390

g t t t g a c g g t

c a t t c c a a a t

<210> 246

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 246

atgggtgctga agttttccgt gtctatcctg tggattcagc tggcctgggt gtctaccag
60

ctgctggagc agagccccc a gttcctgtcc atccaggagg gcgagaacct gacagtgtac
120

tgcaattcta gctccgtggt ttctagcctg cagtgggtata ggcaggagcc aggagagggga
180

cccgtgctgc tgggtgaccgt ggtgacaggc ggcgaggtga agaagctgaa gagactgacc
240

ttccagtttg gcgacgccag gaaggattcc tctctgcaca tcaccgcagc acagcctggc
300

gatacaggac tgtacctgtg cgcaggagga ccaaacaccg gcaatcagtt ctattttggc
360

a c c g g c a c a t c c c t g a c a g t g a t c c c t a a t
390

<210> 247

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 247

Met Val Leu Lys Phe Ser Val Ser Ile Leu Trp Ile Gln Leu Ala Trp
1 5 10 15

Val Ser Thr Gln Leu Leu Glu Gln Ser Pro Gln Phe Leu Ser Ile Gln
20 25 30

Glu Gly Glu Asn Leu Thr Val Tyr Cys Asn Ser Ser Ser Val Phe Ser
35 40 45

Ser Leu Gln Trp Tyr Arg Gln Glu Pro Gly Glu Gly Pro Val Leu Leu
50 55 60

Val Thr Val Val Thr Gly Gly Glu Val Lys Lys Leu Lys Arg Leu Thr
65 70 75 80

Phe Gln Phe Gly Asp Ala Arg Lys Asp Ser Ser Leu His Ile Thr Ala
85 90 95

Ala Gln Pro Gly Asp Thr Gly Leu Tyr Leu Cys Ala Gly Gly Pro Asn
100 105 110

Thr Gly Asn Gln Phe Tyr Phe Gly Thr Gly Thr Ser Leu Thr Val Ile
115 120 125

Pro Asn
130

<210> 248

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 248

atggggccctg ggctcctctg ctgggtgctg ctttgtctcc tgggagcagg ctcagtggag
60

actggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg
120

agatgctctt ctcagtctgg gcacaacact gtgtcctggt accaacaggc cctggggtcag
180

gggccccagt ttatctttca gtattatagg gaggaagaga atggcagagg aaacttcct
240

cctagattct cagggtctcca gttccctaata tatagctctg agctgaatgt gaacgccttg
300

gagctggacg actcggccct gtatctctgt gccagcagca catctttttg ggagggtgaac
360

actgaagctt tcttttgaca aggcaccaga ctcacagttg ta
402

<210> 249

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 249

atgggaccag gactgctgtg ctgggtgctg ctgtgcctgc tgggagcagg ctccgtggag
60

accggcgtga cacagtctcc caccacctg atcaagacaa gaggccagca ggtgaccctg
120

agggtcagct cccagtctgg ccacaacaca gtgagctggt accagcaggc cctgggacag
180

ggacctcagt tcattctttca gtactatagg gaggaggaga acggccgcgg caatttcccc
240

cctcggttta gcggcctgca gttcccaaac tactctagcg agctgaacgt gaatgccctg
300

gagctggacg atagcgccct gtatctgtgc gcctcctcta cctccttttg ggaagtgaat
360

acagaggcct tcttttgcca gggcaccgc ctgacagtgg tg
402

<210> 250

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 250

Met Gly Pro Gly Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Ser Val Glu Thr Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Ser Gln Ser Gly His
35 40 45

Asn Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Arg Glu Glu Glu Asn Gly Arg Gly Asn Phe Pro
65 70 75 80

Pro Arg Phe Ser Gly Leu Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Glu Leu Asp Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Thr Ser Phe Trp Glu Val Asn Thr Glu Ala Phe Phe Gly Gln Gly
115 120 125

Thr Arg Leu Thr Val Val
130

<210> 251

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 251

Met Val Leu Lys Phe Ser Val Ser Ile Leu Trp Ile Gln Leu Ala Trp
1 5 10 15

Val Ser Thr Gln Leu Leu Glu Gln Ser Pro Gln Phe Leu Ser Ile Gln
20 25 30

Glu Gly Glu Asn Leu Thr Val Tyr Cys Asn Ser Ser Ser Val Phe Ser
35 40 45

Ser Leu Gln Trp Tyr Arg Gln Glu Pro Gly Glu Gly Pro Val Leu Leu
50 55 60

Val Thr Val Val Thr Gly Gly Glu Val Lys Lys Leu Lys Arg Leu Thr
65 70 75 80

Phe Gln Phe Gly Asp Ala Arg Lys Asp Ser Ser Leu His Ile Thr Ala
85 90 95

Ala Gln Pro Gly Asp Thr Gly Leu Tyr Leu Cys Ala Gly Gly Pro Asn
100 105 110

Thr Gly Asn Gln Phe Tyr Phe Gly Thr Gly Thr Ser Leu Thr Val Ile
115 120 125

Pro Asn Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
130 135 140

Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
145 150 155 160

Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
165 170 175

Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
180 185 190

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
195 200 205

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
210 215 220

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
225 230 235 240

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
245 250 255

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 252

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 252

Met Gly Pro Gly Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Ser Val Glu Thr Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Ser Gln Ser Gly His

35

40

45

Asn Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Arg Glu Glu Glu Asn Gly Arg Gly Asn Phe Pro
65 70 75 80

Pro Arg Phe Ser Gly Leu Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Glu Leu Asp Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Thr Ser Phe Trp Glu Val Asn Thr Glu Ala Phe Phe Gly Gln Gly
115 120 125

Thr Arg Leu Thr Val Val Lys Asp Leu Arg Asn Val Thr Pro Pro Lys
130 135 140

Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser
195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe
210 215 220

Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro
225 230 235 240

Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp
245 250 255

Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val
260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
275 280 285

Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys
290 295 300

Lys Asn Ser
305

<210> 253
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 253
Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 254
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 254

Val	Val	Val	Gly	Ala	Cys	Gly	Val	Gly	Lys
1				5					10

<210> 255

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 255

Thr	Ser	Gly	Phe	Asn	Gly
1				5	

<210> 256

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 256

Asn	Val	Leu	Asp	Gly	Leu
1				5	

<210> 257

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 257

Ala	Val	Arg	Glu	Glu	Val	Leu	Tyr	Asn	Gln	Gly	Gly	Lys	Leu	Ile
1				5				10					15	

<210> 258

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 258

Leu	Asn	His	Asp	Ala
1			5	

<210> 259

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 259

Ser	Gln	Ile	Val	Asn	Asp
1				5	

<210> 260

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 260

Ala Ser Ser Lys Arg Gly Trp Pro Tyr Glu Gln Tyr

<210> 261

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 261

atgtggggag ttttccttct ttatgtttcc atgaagatgg gaggcactac aggacaaaac
60

attgaccagc ccactgagat gacagctacg gaaggtgcca ttgtccagat caactgcacg
120

taccagacat ctgggttcaa cgggctgttc tggtaccagc aacatgctgg cgaagcacc
180

acatttctgt cttacaatgt tctggatggt ttggaggaga aaggctgttt ttcttcattc
240

cttagtcggt ctaaagggtta cagttacctc cttttgaagg agctccagat gaaagactct
300

gcctcttacc tctgtgctgt gagagaggag gtcctttata accagggagg aaagcttatt
360

t t c g g a c a g g g a a c g g a g t t a t c t g t g a a a c c c
393

<210> 262

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 262

atgtggggcg tgtttctgct gtacgtgagc atgaagatgg gcggcaccac aggccagaac
60

atcgaccagc caaccgagat gaccgccaca gagggcgcca tcgtgcagat caactgcacc
120

taccagacaa gcggcttcaa tggcctgttt tggtatcagc agcacgcagg agaggcaccc
180

acattcctgt cctataatgt gctggacggc ctggaggaga agggcagggtt ctccctctttt
240

ctgagccgct ccaagggcta ctcctatctg ctgctgaagg agctgcagat gaaggattct
300

gccagctacc tgtgcgccgt gcgggaggag gtgctgtata atcagggcgg caagctgata
360

t t t g g c c a g g g c a c c g a g c t g a g c g t g a a g c c t
393

<210> 263

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 263

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser

50

55

60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Val Arg Glu Glu Val Leu
100 105 110

Tyr Asn Gln Gly Gly Lys Leu Ile Phe Gly Gln Gly Thr Glu Leu Ser
115 120 125

Val Lys Pro
130

<210> 264

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 264

atgagcaacc aggtgctctg ctgtgtggtc ctttgtctcc tgggagcaaa caccgtggat
60

ggtggaatca ctcagtcccc gaagtacctg ttcagaaagg aaggacagaa tgtgaccctg
120

agttgtgaac agaatttgaa ccacgatgcc atgtactggt accgacagga cccagggcaa
180

gggctgagat tgatctacta ctcacagata gtaaatgact ttcagaaagg agatatagct
240

gaagggtaca gcgtctctcg ggagaagaag gaatcctttc ctctcactgt gacatcggcc
300

caaaagaacc cgacagcttt ctatctctgt gccagtagta aaaggggatg gccctacgag
360

c a g t a c t t c g g g c c g g g c a c c a g g c t c a c g g t c a c a
396

<210> 265

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 265

atgtccaacc aggtgctgtg ctgctgtggtg ctgtgcctgc tgggagcaaa taccgtggac
60

ggaggcatca cacagtcccc caagtacctg ttccggaagg agggccagaa cgtgaccctg
120

tcttgtgagc agaacctgaa tcacgacgcc atgtactggt ataggcagga ccccggacag
180

ggactgagac tgatctacta tagccagatc gtgaacgact ttcagaaggg cgacatcgcc
240

gagggctaca gcgtgtcccg ggagaagaag gagtccttcc cactgaccgt gacatctgcc
300

cagaagaatc ccaccgcctt ttatctgtgc gccagctcca agagaggctg gccctacgag
360

c a g t a t t t c g g c c c t g g c a c c a g g c t g a c c g t g a c a
396

<210> 266

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 266

Met Ser Asn Gln Val Leu Cys Cys Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Asn Thr Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg
20 25 30

Lys Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His
35 40 45

Asp Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr
85 90 95

Val Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser
100 105 110

Ser Lys Arg Gly Trp Pro Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Thr Val Thr
130

<210> 267

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 267

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Val Arg Glu Glu Val Leu
100 105 110

Tyr Asn Gln Gly Gly Lys Leu Ile Phe Gly Gln Gly Thr Glu Leu Ser
115 120 125

Val Lys Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys
130 135 140

Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp

Asn	Thr	Val	Asp	Gly	Gly	Ile	Thr	Gln	Ser	Pro	Lys	Tyr	Leu	Phe	Arg			
			20					25					30					
Lys	Glu	Gly	Gln	Asn	Val	Thr	Leu	Ser	Cys	Glu	Gln	Asn	Leu	Asn	His			
		35					40					45						
Asp	Ala	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Gln	Gly	Leu	Arg	Leu			
	50					55					60							
Ile	Tyr	Tyr	Ser	Gln	Ile	Val	Asn	Asp	Phe	Gln	Lys	Gly	Asp	Ile	Ala			
65					70					75					80			
Glu	Gly	Tyr	Ser	Val	Ser	Arg	Glu	Lys	Lys	Glu	Ser	Phe	Pro	Leu	Thr			
				85					90					95				
Val	Thr	Ser	Ala	Gln	Lys	Asn	Pro	Thr	Ala	Phe	Tyr	Leu	Cys	Ala	Ser			
			100					105					110					
Ser	Lys	Arg	Gly	Trp	Pro	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg			
		115					120					125						
Leu	Thr	Val	Thr	Lys	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val	Ser			
	130					135					140							
Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr			
145					150					155					160			
Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser			
				165					170					175				
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro			
			180					185					190					
Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu			

195

200

205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
 210 215 220

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
 225 230 235 240

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
 245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
 260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
 275 280 285

Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn
 290 295 300

Ser
 305

<210> 269

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 269

Val Val Gly Ala Cys Gly Val Gly Lys
 1 5

<210> 270
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 270
Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10

<210> 271
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 271
Thr Ser Ile Asn Asn
1 5

<210> 272
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 272
Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 273
<211> 12
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 273

Ala Thr Asp Arg Gln Ser Ser Gly Asp Lys Leu Thr
1 5 10

<210> 274

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 274

Ser Gly His Ala Thr
1 5

<210> 275

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 275

Phe Gln Asn Asn Gly Val
1 5

<210> 276

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 276

Ala Ser Ser Leu Ala Asp Ile Tyr Glu Gln Tyr
1 5 10

<210> 277

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 277

atggaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggaggggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaat tttaatacgt tcaaataaaa gagagaaaca cagtggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acggaccgtc aaagcagcgg agacaagctg
360

a c t t t t g g g a c c g g g a c t c g t t t a g c a g t t a g g c c c
396

<210> 278

<211> 396

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic polynucleotide

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Arg Gln Ser Ser Gly Asp Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Ala Val Arg Pro
130

<210> 280

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 280

atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa
60

gctggagttg ccagtcctcc cagatataag attatagaga aaaggcagag tgtggctttt
120

tggtgcaatc ctatatctgg ccatgctacc ctttactggt accagcagat cctgggacag
180

ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct
240

aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct
300

gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gcttagccga catctacgag
360

c a g t a c t t c g g g c c g g g c a c c a g g c t c a c g g t c a c a
396

<210> 281

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 281

atgggaacaa ggctgctgtg ctgggccgcc ctgtgcctgc tgggagcaga gctgaccgag
60

gccggcgtgg cccagagccc ccggtacaag atcatcgaga agagacagag cgtggccttc
120

tgggtgaacc ctatctccgg ccacgccaca ctgtactggg atcagcagat cctgggccag
180

ggcccaaagc tgctgatcca gttccagaac aatggcgtgg tggacgattc ccagctgccc
240

aaggaccggt tttctgccga gagactgaag ggcgtggatt ccaccctgaa gatccagccc
300

gccaagctgg aggactctgc cgtgtatctg tgcgccagct ccctggccga catctacgag
360

c a g t a t t t c g g c c c t g g c a c a a g g c t g a c c g t g a c a
396

<210> 282
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 282
Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Leu Ala Asp Ile Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Thr Val Thr
130

<210> 283
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 283
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Arg Gln Ser Ser Gly Asp Lys Leu Thr Phe Gly Thr Gly Thr Arg Leu
115 120 125

Ala Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu

130

135

140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala
245 250 255

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 284

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 284

Met	Gly	Thr	Arg	Leu	Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala	1	5	10	15
Glu	Leu	Thr	Glu	Ala	Gly	Val	Ala	Gln	Ser	Pro	Arg	Tyr	Lys	Ile	Ile	20	25	30	
Glu	Lys	Arg	Gln	Ser	Val	Ala	Phe	Trp	Cys	Asn	Pro	Ile	Ser	Gly	His	35	40	45	
Ala	Thr	Leu	Tyr	Trp	Tyr	Gln	Gln	Ile	Leu	Gly	Gln	Gly	Pro	Lys	Leu	50	55	60	
Leu	Ile	Gln	Phe	Gln	Asn	Asn	Gly	Val	Val	Asp	Asp	Ser	Gln	Leu	Pro	65	70	75	80
Lys	Asp	Arg	Phe	Ser	Ala	Glu	Arg	Leu	Lys	Gly	Val	Asp	Ser	Thr	Leu	85	90	95	
Lys	Ile	Gln	Pro	Ala	Lys	Leu	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	100	105	110	
Ser	Ser	Leu	Ala	Asp	Ile	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	115	120	125	
Leu	Thr	Val	Thr	Lys	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val	Ser	130	135	140	
Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr	145	150	155	160
Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	165	170	175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro				

180

185

190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
210 215 220

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
275 280 285

Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn
290 295 300

Ser
305

<210> 285

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 285

Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 286

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 286

Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10

<210> 287

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 287

Thr Ser Glu Ser Asp Tyr Tyr
1 5

<210> 288

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 288

Gln Glu Ala Tyr Lys Gln Gln Asn
1 5

<210> 289
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 289
Ala Leu Tyr Ile Tyr Gly Gly Ser Gln Gly Asn Leu Ile
1 5 10

<210> 290
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 290
Ser Glu His Asn Arg
1 5

<210> 291
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 291
Phe Gln Asn Glu Ala Gln
1 5

<210> 292
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 292
Ala Ser Ser Ser Thr Asp Arg Ile Glu Ala Phe
1 5 10

<210> 293
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 293
atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga atttagcatg
60

gctcagacag tcactcagtc tcaaccagag atgtctgtgc aggaggcaga gaccgtgacc
120

ctgagctgca catatgacac cagtgagagt gattattatt tattctggta caagcagcct
180

cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaaca
240

gagaatcggt tctctgtgaa cttccagaaa gcagccaaat ccttcagtct caagatctca
300

gactcacagc tgggggatgc cgcgatgtat ttctgtgctc tctatattta tggaggaagc
360

caaggaaatc tcatcttttg aaaaggcact aaactctctg ttaaacca
408

<210> 294

<211> 408
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 294

atggcatgcc caggcttcct gtgggcactg gtcatcagca catgtctgga gttttctatg
60

gcccagaccg tgacacagtc tcagcctgag atgagcgtgc aggaggccga gaccgtgaca
120

ctgagctgca cctacgacac atctgagagc gattactatc tgttctggta taagcagcca
180

ccctccagac agatgatacct ggtcatcagg caggaggcct acaagcagca gaacgccacc
240

gagaatcggg tctccgtgaa ctttcagaag gccgccaagt ctttttctct gaagatcagc
300

gactcccagc tgggcgatgc cgccatgtat ttctgtgccc tgtacatcta tggcggctct
360

cagggcaatc tgatctttgg caagggcacc aagctgagcg tgaagcct
408

<210> 295

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 295

Met	Ala	Cys	Pro	Gly	Phe	Leu	Trp	Ala	Leu	Val	Ile	Ser	Thr	Cys	Leu
1				5				10						15	

Glu Phe Ser Met Ala Gln Thr Val Thr Gln Ser Gln Pro Glu Met Ser
20 25 30

Val Gln Glu Ala Glu Thr Val Thr Leu Ser Cys Thr Tyr Asp Thr Ser
35 40 45

Glu Ser Asp Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Arg Gln
50 55 60

Met Ile Leu Val Ile Arg Gln Glu Ala Tyr Lys Gln Gln Asn Ala Thr
65 70 75 80

Glu Asn Arg Phe Ser Val Asn Phe Gln Lys Ala Ala Lys Ser Phe Ser
85 90 95

Leu Lys Ile Ser Asp Ser Gln Leu Gly Asp Ala Ala Met Tyr Phe Cys
100 105 110

Ala Leu Tyr Ile Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe Gly Lys
115 120 125

Gly Thr Lys Leu Ser Val Lys Pro
130 135

<210> 296

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 296

atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat
60

actggagtct cccaggaccc cagacacaag atcacaaaga ggggacagaa tgtaactttc
120

aggtgtgatc caatttctga acacaaccgc ctttattggg accgacagac cctggggcag
180

ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc
240

agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc
300

acagagcagg gggactcggc catgtatctc tgtgccagca gctccaccga caggattgaa
360

g c t t t c t t t g g a c a a g g c a c c a g a c t c a c a g t t g t a
396

<210> 297

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 297

atgggcacct ccctgctgtg ctggatggca ctgtgcctgc tgggagcaga ccacgcagat
60

acaggcgtgt ctcaggaccc acgccacaag atcaccaagc ggggccagaa cgtgacattc
120

agatgcgatc ccattctccga gcacaatagg ctgtactggg ataggcagac cctggggacag
180

ggaccagagt tcctgacata ctttcagaac gagggcccagc tggagaagag ccggctgctg
240

tccgacagat tctctgccga gagggccaag ggctctttta gcaccctgga gatccagaga
300

acagagcagg gcgacagcgc catgtatctg tgcgccagct cctctaccga taggatcgag
360

g t g g t g

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic polypeptide

Ser Ser Ser Thr Asp Arg Ile Glu Ala Phe Phe Gly Gln Gly Thr Arg
115 120 125

Leu Thr Val Val
130

<210> 299

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 299

Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu
1 5 10 15

Glu Phe Ser Met Ala Gln Thr Val Thr Gln Ser Gln Pro Glu Met Ser
20 25 30

Val Gln Glu Ala Glu Thr Val Thr Leu Ser Cys Thr Tyr Asp Thr Ser
35 40 45

Glu Ser Asp Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Arg Gln
50 55 60

Met Ile Leu Val Ile Arg Gln Glu Ala Tyr Lys Gln Gln Asn Ala Thr
65 70 75 80

Glu Asn Arg Phe Ser Val Asn Phe Gln Lys Ala Ala Lys Ser Phe Ser
85 90 95

Leu Lys Ile Ser Asp Ser Gln Leu Gly Asp Ala Ala Met Tyr Phe Cys
100 105 110

Ala Leu Tyr Ile Tyr Gly Gly Ser Gln Gly Asn Leu Ile Phe Gly Lys

115

120

125

Gly Thr Lys Leu Ser Val Lys Pro Asp Ile Gln Asn Pro Glu Pro Ala
 130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
 145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
 165 170 175

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
 180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
 195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
 210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
 225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu
 245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
 260 265 270

Ser

<210> 300

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 300

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Ser Thr Asp Arg Ile Glu Ala Phe Phe Gly Gln Gly Thr Arg
115 120 125

Leu Thr Val Val Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser
130 135 140

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr

145 150 155 160

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
210 215 220

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
275 280 285

Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn
290 295 300

Ser
305

<210> 301
<211> 9

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 301
Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 302
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 302
Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 303
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 303
Val Ser Asn Ala Tyr Asn
1 5

<210> 304
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 304

Gly Ser Lys Pro

1

<210> 305

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 305

Ala Thr Tyr Asn Phe Asn Lys Phe Tyr

1

5

<210> 306

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 306

Ser Gly His Thr Ser

1

5

<210> 307

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 307

Tyr Asp Glu Gly Glu Glu
1 5

<210> 308

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 308

Ala Ser Thr Thr Phe Lys Thr Gly Arg Ala Ile Glu Lys Leu Phe
1 5 10 15

<210> 309

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 309

atggccttgc agagcactct gggggcggtg tggctagggc ttctcctcaa ctctctctgg
60

aagggttgcag aaagcaagga ccaagtgttt cagccttcca cagtggcatc ttcagagggga
120

gctgtggtgg aaatcttctg taatcactct gtgtccaatg cttacaactt cttctggtac
180

cttcacttcc cgggatgtgc accaagactc cttgttaaag gctcaaagcc ttctcagcag
240

ggacgataca acatgaccta tgaacgggtc tcttcacgc tgctcatcct ccagggtgcgg
300

gaggcagatg ctgctgttta ctactgtgct acgtacaact tcaacaaatt ttactttgga
360

t c t g g g a c c a a a c t c a a t g t a a a a c c a
387

<210> 310

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 310

atggccctgc agtctacact gggagccgtg tggctgggac tgctgctgaa ctctctgtgg
60

aagggtggccg agagcaagga ccagggtgttc cagcctagca ccgtggcctc ctctgagggg
120

gcagtgggtgg agatcttttg caatcactcc gtgtctaacg cctacaattt cttttggtat
180

ctgcactttc caggatgtgc accaaggctg ctggtgaagg gcagcaagcc atcccagcag
240

ggccggtaca acatgaccta tgagagattc agctcctctc tgctgatacct gcagggtgaga
300

gaggccgatg ccgccgtgta ctattgtgcc acctacaact ttaataagtt ctattttggc
360

t c c g g c a c a a a g c t g a a t g t g a a g c c t
387

<210> 311

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 311

Met	Ala	Leu	Gln	Ser	Thr	Leu	Gly	Ala	Val	Trp	Leu	Gly	Leu	Leu	Leu
1				5					10					15	

Asn	Ser	Leu	Trp	Lys	Val	Ala	Glu	Ser	Lys	Asp	Gln	Val	Phe	Gln	Pro
		20						25					30		

Ser	Thr	Val	Ala	Ser	Ser	Glu	Gly	Ala	Val	Val	Glu	Ile	Phe	Cys	Asn
		35					40					45			

His	Ser	Val	Ser	Asn	Ala	Tyr	Asn	Phe	Phe	Trp	Tyr	Leu	His	Phe	Pro
	50					55					60				

Gly	Cys	Ala	Pro	Arg	Leu	Leu	Val	Lys	Gly	Ser	Lys	Pro	Ser	Gln	Gln
65					70					75					80

Gly	Arg	Tyr	Asn	Met	Thr	Tyr	Glu	Arg	Phe	Ser	Ser	Ser	Leu	Leu	Ile
				85					90					95	

Leu	Gln	Val	Arg	Glu	Ala	Asp	Ala	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr
			100					105					110		

Asn	Phe	Asn	Lys	Phe	Tyr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Asn	Val	Lys
		115					120					125			

Pro

<210> 312

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 312

atgggaccca ggctcctctt ctgggcactg ctttgtctcc tcggaacagg cccagtggag
60

gctggagtca cacaagttcc cacacacctg atcaaaacga gaggacagca agcgactctg
120

agatgctctc ctatctctgg gcacaccagt gtgtactggg accaacaggc cctgggtctg
180

ggcctccagt tcctcctttg gtatgacgag ggtgaagaga gaaacagagg aaacttcct
240

cctagatttt caggtcgcca gttccctaata tatagctctg agctgaatgt gaacgccttg
300

gagctggagg actcggccct gtatctctgt gccagcacca cttttaagac gggacgggca
360

attgaaaaac tgttttttgg cagtgggaacc cagctctctg tcttg
405

<210> 313

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 313

atgggaccaa ggctgctgtt ctgggcactg ctgtgcctgc tgggaaccgg acctgtggag
60

gccggcgtga cccagtctcc aacacacctg atcaagacca ggggacagca ggccacactg
120

agggtgtagcc ccatctccgg ccacacaagc gtgtactggg atcagcaggc cctgggactg
180

ggactgcagt tcctgctgtg gtacgacgag ggcgaggaga ggaaccgcgg caatttccca
240

cctcggttca gcggccggca gtttcccaac tacagctccg agctgaacgt gaatgccctg
300

gagctggagg acagcgcctt gtatctgtgc gcctccacca cattcaagac cggcagggcc
360

atcgagaagc tgttctttgg ctctggcacc cagctgagcg tgctg
405

<210> 314

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 314

Met	Gly	Pro	Arg	Leu	Leu	Phe	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Thr
1				5				10						15	

Gly	Pro	Val	Glu	Ala	Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys
		20					25						30		

Thr	Arg	Gly	Gln	Gln	Ala	Thr	Leu	Arg	Cys	Ser	Pro	Ile	Ser	Gly	His
		35				40						45			

Thr	Ser	Val	Tyr	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Leu	Gly	Leu	Gln	Phe
	50					55				60					

Leu	Leu	Trp	Tyr	Asp	Glu	Gly	Glu	Glu	Arg	Asn	Arg	Gly	Asn	Phe	Pro
65					70				75					80	

Pro Arg Phe Ser Gly Arg Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn

85

90

95

Val Asn Ala Leu Glu Leu Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Thr Thr Phe Lys Thr Gly Arg Ala Ile Glu Lys Leu Phe Phe Gly Ser
115 120 125

Gly Thr Gln Leu Ser Val Leu
130 135

<210> 315

<211> 266

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 315

Met Ala Leu Gln Ser Thr Leu Gly Ala Val Trp Leu Gly Leu Leu Leu
1 5 10 15

Asn Ser Leu Trp Lys Val Ala Glu Ser Lys Asp Gln Val Phe Gln Pro
20 25 30

Ser Thr Val Ala Ser Ser Glu Gly Ala Val Val Glu Ile Phe Cys Asn
35 40 45

His Ser Val Ser Asn Ala Tyr Asn Phe Phe Trp Tyr Leu His Phe Pro
50 55 60

Gly Cys Ala Pro Arg Leu Leu Val Lys Gly Ser Lys Pro Ser Gln Gln
65 70 75 80

Gly Arg Tyr Asn Met Thr Tyr Glu Arg Phe Ser Ser Ser Leu Leu Ile
85 90 95

Leu Gln Val Arg Glu Ala Asp Ala Ala Val Tyr Tyr Cys Ala Thr Tyr
100 105 110

Asn Phe Asn Lys Phe Tyr Phe Gly Ser Gly Thr Lys Leu Asn Val Lys
115 120 125

Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
130 135 140

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
145 150 155 160

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser

<210> 316

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 316

Met Gly Pro Arg Leu Leu Phe Trp Ala Leu Leu Cys Leu Leu Gly Thr
1 5 10 15

Gly Pro Val Glu Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Ala Thr Leu Arg Cys Ser Pro Ile Ser Gly His
35 40 45

Thr Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Leu Gly Leu Gln Phe
50 55 60

Leu Leu Trp Tyr Asp Glu Gly Glu Glu Arg Asn Arg Gly Asn Phe Pro
65 70 75 80

Pro Arg Phe Ser Gly Arg Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Glu Leu Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Thr Thr Phe Lys Thr Gly Arg Ala Ile Glu Lys Leu Phe Phe Gly Ser
115 120 125

Gly Thr Gln Leu Ser Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro
130 135 140

Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp
225 230 235 240

Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys
290 295 300

Lys Lys Asn Ser

<210> 317

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 317

Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 318

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 318

Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 319

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 319

Thr Ser Gly Phe Asn Gly
1 5

<210> 320
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 320
Asn Val Leu Asp Gly Leu
1 5

<210> 321
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 321
Ala Val Arg Asp Arg Gly Gly Ser Tyr Ile Pro Thr
1 5 10

<210> 322
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 322
Met Asn His Glu Tyr
1 5

<210> 323
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 323

Ser Met Asn Val Glu Val
1 5

<210> 324

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 324

Ala Ser Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe
1 5 10

<210> 325

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 325

atgtggggag ttttccttct ttatgtttcc atgaagatgg gaggcactac aggacaaaac
60

attgaccagc cactgagat gacagctacg gaagggtgcca ttgtccagat caactgcacg
120

taccagacat ctgggttcaa cgggctgttc tggtaccagc aacatgctgg cgaagcaccc
180

acatttctgt cttacaatgt tctggatggt ttggaggaga aaggtcgttt ttcttcattc
240

cttagtcggt ctaaagggt cagttacctc cttttgaagg agctccagat gaaagactct
300

gcctcttacc tctgtgctgt gagagatcga ggaggaagct acatacctac atttggaaga
360

g g a a c c a g c c t t a t t g t t c a t c c g
384

<210> 326

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 326

atgtggggcg tgtttctgct gtacgtgtct atgaagatgg gcggcaccac aggccagaac
60

atcgaccagc ctaccgagat gaccgccaca gagggcgcca tcgtgcagat caactgcacc
120

taccagacat ctggcttcaa tggcctgttt tggatatcagc agcacgccgg cgaggcccca
180

acattcctgt cctataatgt gctggatggc ctggaggaga agggcagggt ctctagcttt
240

ctgtcccgt ctaagggtta cagctatctg ctgctgaagg agctgcagat gaaggacagc
300

gcctcctacc tgtgcgccgt gcgggataga ggaggctcct atatccctac ctttggccgg
360

g g c a c a t c t c t g a t c g t g c a c c c a
384

<210> 327

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 327

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Val Arg Asp Arg Gly Gly
100 105 110

Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro
115 120 125

<210> 328

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 328

atgggcccc agctccttgg ctatgtggtc ctttgccttc taggagcagg ccccttgga
60

gccaagtga ccagaaccc aagatacctc atcacagtga ctggaaagaa gttaacagt
120

acttgttctc agaatatgaa ccatgagtat atgtcctggc atcgacaaga ccaggggct
180

ggcttaaggc agatctacta ttcaatgaat gttgagggtga ctgataaggg agatgttcct
240

gaagggtaca aagtctctcg aaaagagaag aggaatttcc ccctgaccc ggagtcgccc
300

agccccaacc agacctctct gtacttctgt gccagcagtt ccagggggca ttcgggcact
360

gaagccttctc ttggacaagg caccagactc acagttgta
399

<210> 329

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 329

atgggaccac agctgctggg atacgtgggtg ctgtgcctgc tgggagcagg accactggag
60

gcacaggtga ccagaaccc acggtatctg atcacctgta caggcaagaa gctgaccgtg
120

acatgttctc agaacatgaa tcacgagtac atgagctggc ataggcagga ccctggactg
180

ggactgagac agatctacta tagcatgaat gtggaggtga cgcacaaggg cgatgtgccc
240

gagggctaca aggtgtccag gaaggagaag cgcaacttcc ctctgatcct ggagtcccca
300

tctcccaatc agaccagcct gtatTTTTgc gccagctcct ctagggggaca ctccggaaca
360

gaggccttct ttggccaggg caccaggctg acagtgggtg
399

<210> 330

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 330

Met	Gly	Pro	Gln	Leu	Leu	Gly	Tyr	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	

Gly	Pro	Leu	Glu	Ala	Gln	Val	Thr	Gln	Asn	Pro	Arg	Tyr	Leu	Ile	Thr
			20					25					30		

Val	Thr	Gly	Lys	Lys	Leu	Thr	Val	Thr	Cys	Ser	Gln	Asn	Met	Asn	His
		35					40					45			

Glu	Tyr	Met	Ser	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Gln
	50					55					60				

Ile	Tyr	Tyr	Ser	Met	Asn	Val	Glu	Val	Thr	Asp	Lys	Gly	Asp	Val	Pro
65					70					75				80	

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile

85

90

95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
 100 105 110

Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr
 115 120 125

Arg Leu Thr Val Val
 130

<210> 331

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 331

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
 1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly
 20 25 30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
 35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
 50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
 65 70 75 80

Leu	Ser	Arg	Ser	Lys	Gly	Tyr	Ser	Tyr	Leu	Leu	Leu	Lys	Glu	Leu	Gln			
				85					90					95				
Met	Lys	Asp	Ser	Ala	Ser	Tyr	Leu	Cys	Ala	Val	Arg	Asp	Arg	Gly	Gly			
			100					105					110					
Ser	Tyr	Ile	Pro	Thr	Phe	Gly	Arg	Gly	Thr	Ser	Leu	Ile	Val	His	Pro			
		115					120					125						
Asp	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg			
	130					135					140							
Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile			
145					150					155					160			
Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Thr			
				165					170					175				
Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala			
			180					185					190					
Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr			
		195					200					205						
Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr			
	210					215					220							
Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser			
225					230					235					240			
Val	Met	Gly	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu			
				245					250					255				
Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser										

<210> 332

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 332

Met Gly Pro Gln Leu Leu Gly Tyr Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Leu Glu Ala Gln Val Thr Gln Asn Pro Arg Tyr Leu Ile Thr
20 25 30

Val Thr Gly Lys Lys Leu Thr Val Thr Cys Ser Gln Asn Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Gln
50 55 60

Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp Lys Gly Asp Val Pro
65 70 75 80

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
85 90 95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr
115 120 125

[illegible]

<210> 333

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 333

Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 334

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 334

Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 335

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 335

Thr Ser Ile Asn Asn
1 5

<210> 336
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 336
Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 337
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 337
Ala Gly Leu Tyr Ser Ser Ala Ser Lys Ile Ile
1 5 10

<210> 338
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 338
Met Asn His Glu Tyr
1 5

<210> 339
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 339

Ser Met Asn Val Glu Val
1 5

<210> 340

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 340

Ala Ser Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe
1 5 10

<210> 341

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 341

atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggaggggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaatt ttaatacgt tcaaatgaaa gagagaaaca cagtggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct gggctgtaca gcagtgcttc caagataatc
360

t t t g g a t c a g g g a c c a g a c t c a g c a t c c g g c c a
393

<210> 342

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 342

atggagacac tgctgggcgt gtccctggtc atcctgtggc tgcagctggc cagagtgaac
60

agccagcagg gagaggagga ccctcaggcc ctgagcatcc aggagggcga gaacgccacc
120

atgaattgct cttacaagac aagcatcaac aatctgcagt ggtataggca gaactccggc
180

cgcggaactgg tgcacctgat cctgatcagg tctaattgagc gcgagaagca cagcggccgg
240

ctgagagtga ccctggacac aagcaagaag tctagctccc tgctgatcac cgcctccaga
300

gcagcagata cagcctctta cttctgtgcc ggcctgtatt ctagcgcctc caagatcatc
360

t t t g g c a g c g g c a c c c g g c t g t c c a t c a g a c c c
393

<210> 343

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 343

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Gly Leu
100 105 110

Tyr Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
115 120 125

Ile Arg Pro
130

<210> 344

<211> 399
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 344

atgggcccc agctccttgg ctatgtggtc ctttgccttc taggagcagg ccccttgaa
60

gcccaagtga cccagaaccc aagatacctc atcacagtga ctggaaagaa gttaacagtg
120

acttgttctc agaatatgaa ccatgagtat atgtcctggg atcgacaaga cccagggctg
180

ggcttaaggc agatctacta ttcaatgaat gttgagggtga ctgataaggg agatgttcct
240

gaagggtaca aagtctctcg aaaagagaag aggaatttcc ccctgatcct ggagtcgccc
300

agccccaacc agacctctct gtacttctgt gccagcagtt ccagggggca ttcgggcact
360

gaagctttct ttggacaagg caccagactc acagttgta
399

<210> 345

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 345

atgggcccac agctgctggg ctacgtggtg ctgtgcctgc tgggagcagg accactggag
60

gcacaggtga cccagaaccc caggtatctg atcaccgtga caggcaagaa gctgaccgtg
120

acatgtagcc agaacatgaa tcacgagtag atgtcctggt ataggcagga ccccgactg
180

ggactgagac agatctacta ttccatgaat gtggaggtga cgcacaaggg cgatgtgcct
240

gagggctaca aggtgtctag gaaggagaag cgcaacttcc cactgacccct ggagtcacca
300

tctcccaatc agacctccct gtatTTTTgc gccagctcct ctaggggcca ctctggcaca
360

gaggccttct ttggccaggg caccaggctg acagtgggtg
399

<210> 346

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 346

Met	Gly	Pro	Gln	Leu	Leu	Gly	Tyr	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	

Gly	Pro	Leu	Glu	Ala	Gln	Val	Thr	Gln	Asn	Pro	Arg	Tyr	Leu	Ile	Thr
			20					25					30		

Val	Thr	Gly	Lys	Lys	Leu	Thr	Val	Thr	Cys	Ser	Gln	Asn	Met	Asn	His
		35					40					45			

Glu	Tyr	Met	Ser	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Gln
	50					55					60				

Ile	Tyr	Tyr	Ser	Met	Asn	Val	Glu	Val	Thr	Asp	Lys	Gly	Asp	Val	Pro
65					70					75				80	

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
85 90 95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr
115 120 125

Arg Leu Thr Val Val
130

<210> 347

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 347

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg

65

70

75

80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Gly Leu
100 105 110

Tyr Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
115 120 125

Ile Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys
130 135 140

Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp
145 150 155 160

Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr
165 170 175

Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly
180 185 190

Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe
195 200 205

Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala
210 215 220

Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln
225 230 235 240

Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly
245 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 348

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 348

Met Gly Pro Gln Leu Leu Gly Tyr Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Leu Glu Ala Gln Val Thr Gln Asn Pro Arg Tyr Leu Ile Thr
20 25 30

Val Thr Gly Lys Lys Leu Thr Val Thr Cys Ser Gln Asn Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Gln
50 55 60

Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp Lys Gly Asp Val Pro
65 70 75 80

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
85 90 95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Ser Arg Gly His Ser Gly Thr Glu Ala Phe Phe Gly Gln Gly Thr

115

120

125

Arg Leu Thr Val Val Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val
 130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
 145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
 165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
 180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
 210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
 225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
 245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
 260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
 290 295 300

Asn Ser
305

<210> 349
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 349
Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 350
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 350
Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 351
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 351
Asn Ile Ala Thr Asn Asp Tyr

1

5

<210> 352

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 352

Gly Tyr Lys Thr Lys

1

5

<210> 353

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 353

Leu Ala Asn Thr Gly Gly Phe Lys Thr Ile

1

5

10

<210> 354

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 354

Ser Gly His Val Ser

1

5

<210> 355
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 355
Phe Gln Asn Glu Ala Gln
1 5

<210> 356
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 356
Ala Thr Tyr Lys Val Gly Asp Glu Gln Phe
1 5 10

<210> 357
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 357
atgaggcaag tggcgagagt gatcgtgttc ctgaccctga gtactttgag ccttgctaag
60

accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc
120

cacaacaaca ttgctacaaa tgattatatc acgtggtacc aacagtttcc cagccaagga
180

ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt
240

atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact
300

gctgtgtact actgcctcgc taatactgga ggcttcaaaa ctatctttgg agcaggaaca
360

a g a c t a t t t g t t a a a g c a
378

<210> 358

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 358

atgaggcagg tggcacgcgt gatcgtgttt ctgaccctga gcacactgtc cctggccaag
60

accacacagc ctatctctat ggacagctac gagggccagg aggtgaacat cacctgctct
120

cacaacaata tcgccaccaa tgattacatc acatgggtatc agcagttccc cagccagggc
180

cctcggttta tcatccaggg ctataagacc aaggtgacaa acgaggtggc cagcctgttc
240

atccctgccg acaggaagtc tagcaccctg tccctgccac gcgtgagcct gtccgataca
300

gccgtgtact attgtctggc caataccggc ggcttcaaga caatctttgg cgccggcacc
360

a g a c t g t t t g t g a a g g c c
378

<210> 359
<211> 126
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 359

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
65 70 75 80

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Ala Asn Thr Gly Gly Phe
100 105 110

Lys Thr Ile Phe Gly Ala Gly Thr Arg Leu Phe Val Lys Ala
115 120 125

<210> 360

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 360

atgggacacca ggctcctctg ctgggtggtc ctgggtttcc tagggacaga tcacacaggt
60

gctggagtct cccagtcctc taggtacaaa gtcgcaaaga gaggacagga tgtagctctc
120

aggtgtgatc caatttcggg tcatgtatcc cttttttggt accaacaggc cctggggcag
180

gggccagagt ttctgactta tttccagaat gaagctcaac tagacaaatc ggggctgccc
240

agtgatcgct tctttgcaga aaggcctgag ggatccgtct ccactctgaa gatccagcgc
300

acacagcagg aggactccgc cgtgtatctc tgtgccacct ataaggtcgg ggatgagcag
360

t t c t t c g g g c c a g g g a c a c g g c t c a c c g t g c t a
393

<210> 361

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 361

atgggaacca ggctgctgtg ctgggtgggtg ctgggcttcc tgggaaaccga ccacacagga
60

gcaggcgtgt cccagtctcc aagggtacaag gtggcaaaga ggggacagga cgtggccctg
120

Ser Asp Arg Phe Phe Ala Glu Arg Pro Glu Gly Ser Val Ser Thr Leu
85 90 95

Lys Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Thr Tyr Lys Val Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Leu
130

<210> 363

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 363

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe

65

70

75

80

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Ala Asn Thr Gly Gly Phe
100 105 110

Lys Thr Ile Phe Gly Ala Gly Thr Arg Leu Phe Val Lys Ala Asp Ile
115 120 125

Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln
130 135 140

Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val
145 150 155 160

Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu
165 170 175

Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser
180 185 190

Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala
195 200 205

Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys
210 215 220

Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met
225 230 235 240

Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
245 250 255

Thr Leu Arg Leu Trp Ser Ser
260

<210> 364

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 364

Met Gly Thr Arg Leu Leu Cys Trp Val Val Leu Gly Phe Leu Gly Thr
1 5 10 15

Asp His Thr Gly Ala Gly Val Ser Gln Ser Pro Arg Tyr Lys Val Ala
20 25 30

Lys Arg Gly Gln Asp Val Ala Leu Arg Cys Asp Pro Ile Ser Gly His
35 40 45

Val Ser Leu Phe Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Asp Lys Ser Gly Leu Pro
65 70 75 80

Ser Asp Arg Phe Phe Ala Glu Arg Pro Glu Gly Ser Val Ser Thr Leu
85 90 95

Lys Ile Gln Arg Thr Gln Gln Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Thr Tyr Lys Val Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu

115

120

125

Thr Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu
 130 135 140

Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu
 145 150 155 160

Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
 165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
 180 185 190

Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg
 195 200 205

Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln
 210 215 220

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
 225 230 235 240

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
 245 250 255

Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala
 260 265 270

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
 275 280 285

Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
 290 295 300

<210> 365
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 365
Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 366
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 366
Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 367
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 367
Asp Ser Ala Ser Asn Tyr
1 5

<210> 368

<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 368
Ile Arg Ser Asn Val Gly Glu
1 5

<210> 369
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 369
Ala Glu Thr Gly Phe Gln Lys Leu Val
1 5

<210> 370
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 370
Met Asp His Glu Asn
1 5

<210> 371
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 371

Ser Tyr Asp Val Lys Met
1 5

<210> 372

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 372

Ala Ser Ser Asp Trp Leu Ala Gly Ala Lys Asp Glu Gln Tyr
1 5 10

<210> 373

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 373

atgacatcca ttcgagctgt atttatatc ctgtggctgc agctggactt ggtgaatgga
60

gagaatgtgg agcagcatcc ttcaaccctg agtgtccagg agggagacag cgctgttatc
120

aagtgtactt attcagacag tgccctcaaac tacttccctt ggtataagca agaacttgga
180

aaaagacctc agcttattat agacattcgt tcaaattgtgg gcgaaaagaa agaccaacga
240

attgctgtta cattgaacaa gacagccaaa catttctccc tgcacatcac agagacccaa
300

cctgaagact cggctgtcta cttctgtgca gaaacaggct ttcagaaact tgtatttgga
360

a c t g g c a c c c g a c t t c t g g t c a g t c c a
387

<210> 374

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 374

atgacatcta tccgcgccgt gttcatcttt ctgtggctgc agctggacct ggtgaacggc
60

gagaatgtgg agcagcaccc aagcaccctg tccgtgcagg agggcgacag cgccgtgatc
120

aagtgcacat actctgatag cgcctccaac tactttccct ggtataagca ggagctgggc
180

aagcggcctc agctgatcat cgacatcaga tccaacgtgg gcgagaagaa ggatcagcgg
240

atcgccgtga ccctgaataa gacagccaag cacttcagcc tgcacatcac cgagacacag
300

cccgaggatt ccgccgtgta tttttgtgcc gagaccggct tccagaagct ggtgtttggc
360

a c c g g c a c a a g a c t g c t g g t g t c c c c t
387

<210> 375

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 375

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser Asp Ser Ala
35 40 45

Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys Arg Pro Gln
50 55 60

Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys Asp Gln Arg
65 70 75 80

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Glu Thr
100 105 110

Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu Leu Val Ser
115 120 125

Pro

<210> 376

<211> 402
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 376

atggggaatca ggctcctctg tcgtgtggcc ttttgtttcc tggctgtagg cctcgtagat
60

gtgaaagtaa cccagagctc gagatatcta gtcaaaagga cgggagagaa agtttttctg
120

gaatgtgtcc aggatatgga ccatgaaaat atgttctggg atcgacaaga cccaggtctg
180

gggctacggc tgatctatct ctcatatgat gttaaaatga aagaaaaagg agatattcct
240

gaggggtaca gtgtctctag agagaagaag gagcgcttct ccctgattct ggagtcgcc
300

agcaccaacc agacatctat gtacctctgt gccagcagtg actggctagc gggagcgaag
360

gacgagcagt acttcgggcc gggcaccagg ctcacgggtca ca
402

<210> 377

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 377

atgggcatcc ggctgctgtg cagagtggcc ttctgttttc tggccgtggg cctgggtggac
60

gtgaagggtga cccagagctc ccggtacctg gtgaagagaa caggcgagaa ggtgttcctg
120

gagtgcgtgc aggacatgga tcacgagaac atgttttggg ataggcagga ccccgactg
180

ggactgagac tgatctactt cagctatgac gtgaagatga aggagaaggg cgacatccca
240

gagggctaca gcgtgtccag ggagaagaag gagcgggtca gcctgacccg ggagtctgcc
300

agcaccaatc agacaagcat gtacctgtgc gcctctagcg actggctggc cggagcaaag
360

gatgagcagt atttcggccc aggcaccagg ctgaccgtga ca
402

<210> 378

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 378

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
20 25 30

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Asp Trp Leu Ala Gly Ala Lys Asp Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr
130

<210> 379

<211> 266

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 379

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser Asp Ser Ala
35 40 45

Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys Arg Pro Gln
50 55 60

Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys Asp Gln Arg

65

70

75

80

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Glu Thr
100 105 110

Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu Leu Val Ser
115 120 125

Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
130 135 140

Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
145 150 155 160

Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
165 170 175

Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
180 185 190

Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
195 200 205

Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
210 215 220

Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
225 230 235 240

Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
245 250 255

Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 380

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 380

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
20 25 30

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Asp Trp Leu Ala Gly Ala Lys Asp Glu Gln Tyr Phe Gly Pro Gly

115

120

125

Thr Arg Leu Thr Val Thr Lys Asp Leu Arg Asn Val Thr Pro Pro Lys
 130 135 140

Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys
 145 150 155 160

Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu
 165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 180 185 190

Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser
 195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe
 210 215 220

Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro
 225 230 235 240

Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp
 245 250 255

Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val
 260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
 275 280 285

Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys
 290 295 300

Lys Asn Ser
305

<210> 381
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 381
Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 382
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 382
Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

<210> 383
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 383
Thr Ser Ile Asn Asn

1

5

<210> 384

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 384

Ile Arg Ser Asn Glu Arg Glu

1

5

<210> 385

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 385

Ala Thr Asp Pro Leu Asp Tyr Lys Leu Ser

1

5

10

<210> 386

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 386

Met Asn His Glu Tyr

1

5

<210> 387
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 387
Ser Met Asn Val Glu Val
1 5

<210> 388
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 388
Ala Ser Ser Leu Val Ala Ser Asn Glu Gln Phe
1 5 10

<210> 389
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 389
atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaattttaatacgt tcaaatagaaa gagagaaaca cagtggaaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acggaccct tagactacaa gctcagcttt
360

g g a g c c g g a a c c a c a g t a a c t g t a a g a g c a
390

<210> 390

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 390

atggagaccc tgctgggcgt gtctctggtc atcctgtggc tgcagctggc cagagtgaac
60

tctcagcagg gagaggagga ccctcaggcc ctgagcatcc aggagggcga gaacgccacc
120

atgaattgct cttacaagac aagcatcaac aatctgcagt ggtatcggca gaactccggc
180

agaggcctgg tgcacctgat cctgatcagg agcaatgagc gcgagaagca ctccggccgg
240

ctgagagtga ccctggacac atctaagaag tcctctagcc tgctgatcac cgctctagg
300

gcagcagata cagccagcta cttctgtgcc accgaccac tggattataa gctgtccttt
360

g g c g c c g g c a c c a c a g t g a c c g t g c g c g c c
390

<210> 391
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 391
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Pro Leu Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr Val
115 120 125

Arg Ala
130

<210> 392
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 392
atgggcccc agctccttgg ctatgtggtc ctttgccttc taggagcagg cccctggaa
60
gcccaagtga cccagaaccc aagatacctc atcacagtga ctggaaagaa gttaacagtg
120
acttgttctc agaatatgaa ccatgagtat atgtcctggg atcgacaaga ccagggctg
180
ggcttaaggc agatctacta ttcaatgaat gttgaggtga ctgataaggg agatgttcct
240
gaagggtaca aagtctctcg aaaagagaag aggaatttcc ccctgacctt ggagtcgccc
300
agccccaacc agacctctct gtacttctgt gccagcagtt tggaggctag caatgagcag
360
t t c t t c g g g c c a g g g a c a c g g c t c a c c g t g c t a
393

<210> 393
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 393
atgggcccac agctgctggg ctacgtgggt ctgtgcctgc tgggagcagg accactggag
60

Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp Lys Gly Asp Val Pro
65 70 75 80

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
85 90 95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Leu Val Ala Ser Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Leu
130

<210> 395

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 395

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
100 105 110

Pro Leu Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr Val
115 120 125

Arg Ala Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
130 135 140

Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
145 150 155 160

Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
165 170 175

Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
180 185 190

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
195 200 205

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
210 215 220

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
225 230 235 240

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
245 250 255

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 396

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 396

Met Gly Pro Gln Leu Leu Gly Tyr Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Leu Glu Ala Gln Val Thr Gln Asn Pro Arg Tyr Leu Ile Thr
20 25 30

Val Thr Gly Lys Lys Leu Thr Val Thr Cys Ser Gln Asn Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Gln
50 55 60

Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp Lys Gly Asp Val Pro
65 70 75 80

Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys Arg Asn Phe Pro Leu Ile
85 90 95

Leu Glu Ser Pro Ser Pro Asn Gln Thr Ser Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Leu Val Ala Ser Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu
130 135 140

Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg
195 200 205

Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln
210 215 220

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
225 230 235 240

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
245 250 255

Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala
260 265 270

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
275 280 285

Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
290 295 300

<210> 397

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 397

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 398

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 398

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 399

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 399

Thr Ser Glu Ser Asp Tyr Tyr
1 5

<210> 400
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 400
Gln Glu Ala Tyr Lys Gln Gln Asn
1 5

<210> 401
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 401
Ala Cys Gln Gly Gly Ser Glu Lys Leu Val
1 5 10

<210> 402
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 402
Ser Gly His Asn Thr
1 5

<210> 403

<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 403

Tyr Tyr Arg Glu Glu Glu
1 5

<210> 404

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 404

Ala Ser Ser Leu Gly Leu Leu Leu Tyr Asn Glu Gln Phe
1 5 10

<210> 405

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 405

atggcatgcc ctggcttcct gtgggcactt gtgatctcca cctgtcttga atttagcatg
60

gctcagacag tcaactcagtc tcaaccagag atgtctgtgc aggaggcaga gaccgtgacc
120

ctgagctgca catatgacac cagtgagagt gattattatt tattctggta caagcagcct
180

cccagcaggc agatgattct cgttattcgc caagaagctt ataagcaaca gaatgcaaca
240

gagaatcggt tctctgtgaa cttccagaaa gcagccaaat ccttcagtct caagatctca
300

gactcacagc tgggggatgc cgcgatgtat ttctgtgctt gtcagggcgg atctgaaaag
360

ctgggtctttg gaaagggaac gaaactgaca gtaaaccca
399

<210> 406

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 406

atggcatgcc caggcttcct gtgggcactg gtcatcagca cctgtctgga gttttctatg
60

gccagaccg tgacacagag ccagccagag atgtccgtgc aggaggcaga gaccgtgaca
120

ctgtcctgta cctacgacac aagcgagtcc gattactatc tgttctggta taagcagcct
180

ccatctcgcc agatgatacct ggtcatccgg caggaggcct acaagcagca gaacgccacc
240

gagaatcggt tctctgtgaa ttttcagaag gccgccaagt cttttagcct gaagatctcc
300

gactctcagc tgggcgatgc cgccatgtat ttctgcgcat gtcagggagg cagcgagaag
360

ctgggtgtttg gcaagggcac caagctgaca gtgaaccct
399

<210> 407
<211> 133
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 407

Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu
1 5 10 15

Glu Phe Ser Met Ala Gln Thr Val Thr Gln Ser Gln Pro Glu Met Ser
20 25 30

Val Gln Glu Ala Glu Thr Val Thr Leu Ser Cys Thr Tyr Asp Thr Ser
35 40 45

Glu Ser Asp Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Arg Gln
50 55 60

Met Ile Leu Val Ile Arg Gln Glu Ala Tyr Lys Gln Gln Asn Ala Thr
65 70 75 80

Glu Asn Arg Phe Ser Val Asn Phe Gln Lys Ala Ala Lys Ser Phe Ser
85 90 95

Leu Lys Ile Ser Asp Ser Gln Leu Gly Asp Ala Ala Met Tyr Phe Cys
100 105 110

Ala Cys Gln Gly Gly Ser Glu Lys Leu Val Phe Gly Lys Gly Thr Lys
115 120 125

Leu Thr Val Asn Pro
130

<210> 408
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 408
atggggccctg ggctcctctg ctgggtgctg ctttgtctcc tgggagcagg ctcagtggag
60

actggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg
120

agatgctctt ctcagtctgg gcacaacact gtgtcctggg accaacaggc cctgggtcag
180

gggccccagt ttatctttca gtattatagg gaggaagaga atggcagagg aaacttcct
240

cctagattct caggtctcca gttccctaata tatagctctg agctgaatgt gaacgccttg
300

gagctggacg actcggccct gtatctctgt gccagcagct tgggactcct cctctacaat
360

gagcagttct tcggggccagg gacacggctc accgtgcta
399

<210> 409
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 409
atgggaccag gactgctgtg ctgggtgctg ctgtgcctgc tgggagcagg cagcgtggag
60

accggcgtga cacagtcccc taccacctg atcaagacaa gaggccagca ggtgaccctg
120

aggtgcagct cccagtctgg ccacaataca gtgagctggt accagcaggc cctgggacag
180

ggacctcagt tcatctttca gtactatagg gaggaggaga acggccgcgg caatttcccc
240

cctcggttta gcggcctgca gttcccaaac tattctagcg agctgaacgt gaatgccctg
300

gagctggacg attccgccct gtacctgtgc gcctcctctc tgggcctgct gctgtataac
360

gagcagttct ttggccccgg caccagactg acagtgctg
399

<210> 410

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 410

Met Gly Pro Gly Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Ser Val Glu Thr Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Ser Gln Ser Gly His
35 40 45

Asn Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Arg Glu Glu Glu Asn Gly Arg Gly Asn Phe Pro
65 70 75 80

Pro Arg Phe Ser Gly Leu Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Glu Leu Asp Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Leu Gly Leu Leu Leu Tyr Asn Glu Gln Phe Phe Gly Pro Gly Thr
115 120 125

Arg Leu Thr Val Leu
130

<210> 411

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 411

Met Ala Cys Pro Gly Phe Leu Trp Ala Leu Val Ile Ser Thr Cys Leu
1 5 10 15

Glu Phe Ser Met Ala Gln Thr Val Thr Gln Ser Gln Pro Glu Met Ser
20 25 30

Val Gln Glu Ala Glu Thr Val Thr Leu Ser Cys Thr Tyr Asp Thr Ser
35 40 45

Glu Ser Asp Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Arg Gln
50 55 60

Met Ile Leu Val Ile Arg Gln Glu Ala Tyr Lys Gln Gln Asn Ala Thr
65 70 75 80

Glu Asn Arg Phe Ser Val Asn Phe Gln Lys Ala Ala Lys Ser Phe Ser
85 90 95

Leu Lys Ile Ser Asp Ser Gln Leu Gly Asp Ala Ala Met Tyr Phe Cys
100 105 110

Ala Cys Gln Gly Gly Ser Glu Lys Leu Val Phe Gly Lys Gly Thr Lys
115 120 125

Leu Thr Val Asn Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln
130 135 140

Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp
145 150 155 160

Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe
165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser
180 185 190

Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp
195 200 205

Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys
210 215 220

Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn
225 230 235 240

Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val
245 250 255

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265 270

<210> 412

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 412

Met Gly Pro Gly Leu Leu Cys Trp Val Leu Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Ser Val Glu Thr Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
20 25 30

Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Ser Gln Ser Gly His
35 40 45

Asn Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
50 55 60

Ile Phe Gln Tyr Tyr Arg Glu Glu Glu Asn Gly Arg Gly Asn Phe Pro
65 70 75 80

Pro Arg Phe Ser Gly Leu Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
85 90 95

Val Asn Ala Leu Glu Leu Asp Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser Leu Gly Leu Leu Leu Tyr Asn Glu Gln Phe Phe Gly Pro Gly Thr
115 120 125

Arg Leu Thr Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val
130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 413
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 413
Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 414
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 414
Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 415
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 415
Thr Ser Ile Asn Asn
1 5

<210> 416
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 416
Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 417
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 417
Ala Thr Asp Ala Gln Thr Gly Ala Asn Asn Leu Phe
1 5 10

<210> 418
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 418
Ser Gly His Ala Thr

1

5

<210> 419

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 419

Phe Gln Asn Asn Gly Val

1

5

<210> 420

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 420

Ala Ser Ser Leu Gly Asp Ser Tyr Glu Gln Tyr Phe

1

5

10

<210> 421

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 421

atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60

agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggaggggtga aaatgccacc
120

atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
180

agaggccttg tccacctaata ttttaatacgt tcaaatagaaa gagagaaaca cagtggaga
240

ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
300

gcagcagaca ctgcttctta cttctgtgct acggacgctc aaactggggc aaacaacctc
360

t t c t t t g g g a c t g g a a c g a g a c t c a c c g t t a t t c c c
396

<210> 422

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 422

atggagacac tgctgggagcgt gtctctgggc atcctgtggc tgcagctggc cagagtgaat
60

agccagcagg gagaggagga cccccaggcc ctgtccatcc aggagggcga gaacgccacc
120

atgaattgca gctacaagac atccatcaac aatctgcagt ggtatcggca gaactctggc
180

agaggcctgg tgcacctgat cctgatccgg tccaatgaga gagagaagca ctctggccgg
240

ctgagagtga ccctggatac atccaagaag tcctctagcc tgctgatcac cgccagccgg
300

gcagcagaca cagcctccta tttttgtgcc accgatgccc agacaggcgc caacaatctg
360

Thr Val Ile Pro
130

<210> 424
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 424
atgggcacca ggctcctctg ctgggcggcc ctctgtctcc tgggagcaga actcacagaa
60

gctggagttg cccagtctcc cagatataag attatagaga aaaggcagag tgtggctttt
120

tggtgcaatc ctatatctgg ccatgctacc ctttactggt accagcagat cctgggacag
180

ggcccaaagc ttctgattca gtttcagaat aacgggtgtag tggatgattc acagttgcct
240

aaggatcgat tttctgcaga gaggctcaaa ggagtagact ccactctcaa gatccagcct
300

gcaaagcttg aggactcggc cgtgtatctc tgtgccagca gctta
345

<210> 425
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 425
atgggcacca ggctgctgtg ctgggccggc ctgtgcctgc tgggagcaga gctgacagag
60

gcaggagtgg cccagagccc caggtacaag atcatcgaga agcgccagtc cgtggccttc
120

tggtgcaacc ctatctctgg ccacgccacc ctgtactggg atcagcagat cctgggccag
180

ggcccaaagc tgctgatcca gttccagaac aatggcgtgg tggacgattc tcagctgccc
240

aaggacaggt ttagcgccga gcgccctgaag ggcgtggatt ctaccctgaa gatccagcca
300

gcaaagctgg aggacagcgc cgtgtacctg tgcgccagct ccctg
345

<210> 426

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 426

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Leu
115

<210> 427

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 427

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15

Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30

Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45

Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60

His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80

Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile

85

90

95

Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asp
 100 105 110

Ala Gln Thr Gly Ala Asn Asn Leu Phe Phe Gly Thr Gly Thr Arg Leu
 115 120 125

Thr Val Ile Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
 130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
 145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
 165 170 175

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
 180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
 195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
 210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
 225 230 235 240

Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala
 245 250 255

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 260 265

<210> 428
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 428
Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Glu Leu Thr Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile
20 25 30

Glu Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His
35 40 45

Ala Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu
50 55 60

Leu Ile Gln Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro
65 70 75 80

Lys Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu
85 90 95

Lys Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala
100 105 110

Ser Ser Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu
115 120 125

Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu

130

135

140

Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
145 150 155 160

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
165 170 175

Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg
180 185 190

Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln
195 200 205

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
210 215 220

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
225 230 235 240

Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala
245 250 255

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
260 265 270

Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
275 280 285

<210> 429

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 429

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 430

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 430

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 431

<400> 431

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<210> 432

<400> 432

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<210> 433

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<210> 446

<400> 446
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<210> 447
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 447
Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 448
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 448

Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 449

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 449

Ala Leu Lys Gly Ala Asn Thr Gly Phe Gln Lys Leu Val
1 5 10

<210> 450

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 450

Ser Gly His Asp Tyr
1 5

<210> 451

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 451

Phe Asn Asn Asn Val Pro
1 5

<210> 452

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 452

Ala Ser Gly Gly Gly Leu Gly Leu Phe Glu Thr Gln Tyr
1 5 10

<210> 453

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 453

atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg
60

gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc
120

ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca
180

ccaagtggag aattgggttt ccttattcgt cggaactctt ttgatgagca aaatgaaata
240

agtggtcggt attcttgga cttccagaaa tccaccagtt ccttcaactt caccatcaca
300

gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgaaaggggc gaacacaggc
360

tttcagaaac ttgtatttgg aactggcacc cgacttctgg tcagtcca
408

<210> 454

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 454

atgctgacag cctccctgct gagggccgtg atcgccctcta tctgcgtggg gtctagcatg
60

gcccagaagg tgaccacaggc ccagacagag atcagcgtgg tggagaagga ggacgtgacc
120

ctggattgcg tgtacgagac acgggacacc acatactatc tgttttggta taagcagcca
180

cccagcggcg agctggtggt cctgatcagg cgcaattcct ttgatgagca gaacgagatc
240

tccggcagat actcttggaa tttccagaag tccacctcct ctttcaactt taccatcaca
300

gcctcccagg tgggtggactc tgccgtgtat ttttgtgccc tgaagggcgc caacacaggc
360

ttccagaagc tgggtgtttgg caccggcaca agactgctgg tgagccct
408

<210> 455

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 455

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val
1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu
50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Lys Gly Ala Asn Thr Gly Phe Gln Lys Leu Val Phe Gly Thr
115 120 125

Gly Thr Arg Leu Leu Val Ser Pro
130 135

<210> 456

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 456

atggactcct ggaccctctg ctgtgtgtcc ctttgcaccc tggtagcaaa gcacacagat
60

gctggagtta tccagtcacc ccggcacgag gtgacagaga tgggacaaga agtgactctg
120

agatgtaaac caatttcagg acacgactac cttttctggt acagacagac catgatgcgg
180

ggactggagt tgctcattta ctttaacaac aacgttccga tagatgattc agggatgccc
240

gaggatcgat tctcagctaa gatgcctaata gcatcattct ccactctgaa gatccagccc
300

tcagaaccca gggactcagc tgtgtacttc tgtgccagcg gagggggact aggtctatatt
360

gagacccagt acttcggggcc aggcacgcgg ctccctgggtgc tc
402

<210> 457

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 457

atggacagct ggaccctgtg ctgcgtgagc ctgtgcaccc tgggtggccaa gcacacagat
60

gcaggcgtga tccagtcacc aaggcacgag gtgaccgaga tgggacagga ggtgacactg
120

aggtgtaagc ctatctctgg ccacgactac ctgttctggt atcggcagac catgatgaga
180

ggcctggagc tgctgatcta ctttaacaat aacgtgccta tcgacgattc tggcatgcca
240

gaggacaggt tcagcgccaa gatgcctaata gccagctttt ccaccctgaa gatccagcca
300

agcgagccaa gggattccgc cgtgtacttc tgcgcctccg gaggaggact gggactgttc
360

gagacccagt attttggccc aggcacaagg ctgctgggtgc tg
402

<210> 458

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 458

Met	Asp	Ser	Trp	Thr	Leu	Cys	Cys	Val	Ser	Leu	Cys	Ile	Leu	Val	Ala
1				5					10					15	

Lys	His	Thr	Asp	Ala	Gly	Val	Ile	Gln	Ser	Pro	Arg	His	Glu	Val	Thr
			20					25					30		

Glu	Met	Gly	Gln	Glu	Val	Thr	Leu	Arg	Cys	Lys	Pro	Ile	Ser	Gly	His
		35					40					45			

Asp	Tyr	Leu	Phe	Trp	Tyr	Arg	Gln	Thr	Met	Met	Arg	Gly	Leu	Glu	Leu
	50					55					60				

Leu	Ile	Tyr	Phe	Asn	Asn	Asn	Val	Pro	Ile	Asp	Asp	Ser	Gly	Met	Pro
65					70					75				80	

Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu

85

90

95

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
100 105 110

Ser Gly Gly Gly Leu Gly Leu Phe Glu Thr Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Leu Val Leu
130

<210> 459

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 459

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val
1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu
50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Lys Gly Ala Asn Thr Gly Phe Gln Lys Leu Val Phe Gly Thr
115 120 125

Gly Thr Arg Leu Leu Val Ser Pro Asp Ile Gln Asn Pro Glu Pro Ala
130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
165 170 175

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser

260

265

270

Ser

<210> 460

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 460

Met	Asp	Ser	Trp	Thr	Leu	Cys	Cys	Val	Ser	Leu	Cys	Ile	Leu	Val	Ala
1				5					10					15	

Lys	His	Thr	Asp	Ala	Gly	Val	Ile	Gln	Ser	Pro	Arg	His	Glu	Val	Thr
			20					25					30		

Glu	Met	Gly	Gln	Glu	Val	Thr	Leu	Arg	Cys	Lys	Pro	Ile	Ser	Gly	His
		35					40					45			

Asp	Tyr	Leu	Phe	Trp	Tyr	Arg	Gln	Thr	Met	Met	Arg	Gly	Leu	Glu	Leu
	50					55					60				

Leu	Ile	Tyr	Phe	Asn	Asn	Asn	Val	Pro	Ile	Asp	Asp	Ser	Gly	Met	Pro
65					70					75				80	

Glu	Asp	Arg	Phe	Ser	Ala	Lys	Met	Pro	Asn	Ala	Ser	Phe	Ser	Thr	Leu
				85					90					95	

Lys	Ile	Gln	Pro	Ser	Glu	Pro	Arg	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala
			100					105					110		

Ser Gly Gly Gly Leu Gly Leu Phe Glu Thr Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Leu Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys
130 135 140

Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser
195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe
210 215 220

Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro
225 230 235 240

Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp
245 250 255

Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val
260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
275 280 285

Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys

290

295

300

Lys Asn Ser
305

<210> 461
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 461
Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 462
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 462
Leu Ile Met Gln Leu Met Pro Phe Gly Cys
1 5 10

<210> 463
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 463

Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 464

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 464

Asp Ser Ser Ser Thr Tyr

1 5

<210> 465

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 465

Ile Phe Ser Asn Met Asp Met

1 5

<210> 466

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 466

Ala Glu Trp Ala Asn Thr Asp Lys Leu Ile

1 5 10

<210> 467
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 467
Asp Phe Gln Ala Thr Thr
1 5

<210> 468
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 468
Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 469
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 469
Ser Ala Arg Arg Arg Glu Gly Glu Ile Glu Gln Tyr
1 5 10

<210> 470
<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 470

atgaagacat ttgctggatt ttcgttcctg tttttgtggc tgcagctgga ctgtatgagt
60

agaggagagg atgtggagca gagtcttttc ctgagtgtcc gagagggaga cagctccgtt
120

ataaactgca cttacacaga cagctcctcc acctacttat actggtataa gcaagaacct
180

ggagcaggtc tccagttgct gacgtatatt ttttcaaata tggacatgaa acaagaccaa
240

agactcactg ttctattgaa taaaaaggat aaacatctgt ctctgcgcat tgcagacacc
300

cagactgggg actcagctat ctacttctgt gcagagtggg ctaacaccga caagctcatc
360

t t t g g g a c t g g g a c c a g a t t a c a a g t c t t t c c a
393

<210> 471

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 471

atgaagacct tcgccggcct ctcctttctg ttcctgtggc tgcagctgga ctgcatgagc
60

cggggagagg atgtggagca gtccctgttc ctgtctgtga gggagggcga ctcctctgtg
120

atcaactgta catataccga tagctcctct acctacctgt attggtacaa gcaggagcca
180

ggagcaggac tgcagctgct gacatacatc tttagcaaca tggacatgaa gcaggatcag
240

cgcttgaccg tgctgctgaa taagaaggac aagcacctgt ctctgcggat cgccgacaca
300

cagaccggcg atagcgccat ctacttctgt gccgagtggg ccaataccga taagctgac
360

t t t g g c a c a g g c a c c c g g c t g c a g g t g t t c c c t
393

<210> 472

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 472

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
100 105 110

Trp Ala Asn Thr Asp Lys Leu Ile Phe Gly Thr Gly Thr Arg Leu Gln
115 120 125

Val Phe Pro
130

<210> 473

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 473

atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa
60

catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccttg
120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg
180

atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag
240

tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct
300

gaagacagca gcttctacat ctgcagtgct agaaggcggg agggggagat cgagcagtac
360

t t c g g g c c g g
390

g c a c c a g g c t

c a c g g t c a c a

<210> 474

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 474

atgttattac tgctgctgct gctgggacca ggctccggac tgggagccgt ggtgtcccag
60

cacccttctt gggtcattctg caagtccggc acatctgtga agatcgagtg tcgctctctg
120

gactttcagg ccaccacaat gttttggtat cggcagttcc ccaagcagag cctgatgctg
180

atggccacaa gcaacgaggg ctccaaggcc acctacgagc agggcgtgga gaaggacaag
240

ttcctgatca atcacgcctc tctgaccctg agcaccctga cagtgcctc cgcccaccct
300

gaggatagct cctttttatat ctgctctgcc cggagaaggg agggcgagat cgagcagtac
360

t t c g g c c c a g
390

g c a c a a g a c t

g a c a g t g a c c

<210> 475

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 475

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Arg
100 105 110

Arg Glu Gly Glu Ile Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

Val Thr
130

<210> 476

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 476

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
100 105 110

Trp Ala Asn Thr Asp Lys Leu Ile Phe Gly Thr Gly Thr Arg Leu Gln
115 120 125

Val Phe Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys
130 135 140

Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp
145 150 155 160

Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr
165 170 175

Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly
180 185 190

Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe
195 200 205

Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala
210 215 220

Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln
225 230 235 240

Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly
245 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 477

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 477

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe

35

40

45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Arg
100 105 110

Arg Glu Gly Glu Ile Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

Val Thr Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe
130 135 140

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
145 150 155 160

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala
180 185 190

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
195 200 205

Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val
210 215 220

Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro
225 230 235 240

Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp
245 250 255

Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr
260 265 270

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
275 280 285

Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
290 295 300

<210> 478

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 478

Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 479

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 479

Leu Ile Met Gln Leu Met Pro Phe Gly Cys
1 5 10

<210> 480

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 480

Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 481

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 481

Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 482

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 482

Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 483
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 483
Ala Leu Thr Pro Phe Pro Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu
1 5 10 15

Thr

<210> 484
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 484
Ser Gly His Asn Ser
1 5

<210> 485
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 485
Phe Asn Asn Asn Val Pro

1

5

<210> 486

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 486

Ala Ser Ser Leu Ala Tyr Leu Thr Gly Arg Val Glu Ala Phe
1 5 10

<210> 487

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 487

atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg
60

gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc
120

ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca
180

ccaagtggag aattggtttt ccttattcgt cggaactctt ttgatgagca aaatgaaata
240

agtggtcggt attcttgga cttccagaaa tccaccagtt ccttcaactt caccatcaca
300

gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgactccctt cccaatgct
360

ggtggtacta gctatggaaa gctgacattt ggacaaggga ccatcttgac tgtccatcca
420

<210> 488

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 488

atgctgacag cctctctgct gagggccgtg atcgccagca tctgcgtggt gtcctctatg
60

gcccagaagg tgacccaggc ccagacagag atcagcgtgg tggagaagga ggacgtgacc
120

ctggattgcg tgtacgagac acgggacacc acatactatc tgttctggta taagcagcca
180

ccctccggcg agctggtggt cctgatcagg cgcaattctt ttgatgagca gaacgagatc
240

tctggcagat acagctggaa ttttcagaag tctaccagct ctttcaactt taccatcaca
300

gcctctcagg tgggtggatag cgccgtgtac ttctgtgccc tgacaccatt tcccaatgcc
360

ggcggcacca gctatggcaa gctgacattc ggccagggca ccatcctgac agtgcaccct
420

<210> 489

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 489

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val
1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu
50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Thr Pro Phe Pro Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu
115 120 125

Thr Phe Gly Gln Gly Thr Ile Leu Thr Val His Pro
130 135 140

<210> 490

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 490

atggactcct ggaccttctg ctgtgtgtcc ctttgcattc tggtagcgaa gcatacagat
60

gctggagtta tccagtcacc ccgccatgag gtgacagaga tgggacaaga agtgactctg
120

agatgtaaac caatttcagg ccacaactcc cttttctggt acagacagac catgatgcgg
180

ggactggagt tgctcattta ctttaacaac aacgttccga tagatgattc agggatgccc
240

gaggatcgat tctcagctaa gatgcctaata gcatcattct ccactctgaa gatccagccc
300

tcagaaccca gggactcagc tgtgtacttc tgtgccagca gtttagccta cctgacaggg
360

aggggttgaag ctttctttgg acaaggcacc agactcacag ttgta
405

<210> 491

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 491

atggactcct ggaccttctg ctgcgtgagc ctgtgcattc tgggtggccaa gcacacagat
60

gcaggcgtga tccagtcacc aaggcacgag gtgaccgaga tgggacagga ggtgacactg
120

aggtgtaagc ccatcagcgg ccacaattcc ctgttctggt accggcagac catgatgaga
180

ggcctggagc tgctgatcta cttcaacaat aacgtgccc tgcacgatag cggcatgcct
240

gaggaccggt tctccgccaa gatgcccaac gcctctttta gcaccctgaa gatccagcct
300

tccgagccaa gggattctgc cgtgtacttc tgcgccagct ccctggccta tctgaccgga
360

aggggtggagg ccttcttttg acaggggcacc aggctgacag tgggtg
405

<210> 492

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 492

Met	Asp	Ser	Trp	Thr	Phe	Cys	Cys	Val	Ser	Leu	Cys	Ile	Leu	Val	Ala
1				5					10					15	

Lys	His	Thr	Asp	Ala	Gly	Val	Ile	Gln	Ser	Pro	Arg	His	Glu	Val	Thr
			20					25					30		

Glu	Met	Gly	Gln	Glu	Val	Thr	Leu	Arg	Cys	Lys	Pro	Ile	Ser	Gly	His
		35					40						45		

Asn	Ser	Leu	Phe	Trp	Tyr	Arg	Gln	Thr	Met	Met	Arg	Gly	Leu	Glu	Leu
	50					55					60				

Leu	Ile	Tyr	Phe	Asn	Asn	Asn	Val	Pro	Ile	Asp	Asp	Ser	Gly	Met	Pro
65					70					75				80	

Glu	Asp	Arg	Phe	Ser	Ala	Lys	Met	Pro	Asn	Ala	Ser	Phe	Ser	Thr	Leu
				85					90					95	

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
 100 105 110

Ser Ser Leu Ala Tyr Leu Thr Gly Arg Val Glu Ala Phe Phe Gly Gln
 115 120 125

Gly Thr Arg Leu Thr Val Val
 130 135

<210> 493
 <211> 277
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 493
 Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val
 1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
 20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
 35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu
 50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
 65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
 85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Thr Pro Phe Pro Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu
115 120 125

Thr Phe Gly Gln Gly Thr Ile Leu Thr Val His Pro Asp Ile Gln Asn
130 135 140

Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser
145 150 155 160

Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys
165 170 175

Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met
180 185 190

Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln
195 200 205

Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr
210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe
225 230 235 240

Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
275

<210> 494

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 494

Met	Asp	Ser	Trp	Thr	Phe	Cys	Cys	Val	Ser	Leu	Cys	Ile	Leu	Val	Ala
1				5					10					15	

Lys	His	Thr	Asp	Ala	Gly	Val	Ile	Gln	Ser	Pro	Arg	His	Glu	Val	Thr
			20					25					30		

Glu	Met	Gly	Gln	Glu	Val	Thr	Leu	Arg	Cys	Lys	Pro	Ile	Ser	Gly	His
		35					40					45			

Asn	Ser	Leu	Phe	Trp	Tyr	Arg	Gln	Thr	Met	Met	Arg	Gly	Leu	Glu	Leu
	50					55					60				

Leu	Ile	Tyr	Phe	Asn	Asn	Asn	Val	Pro	Ile	Asp	Asp	Ser	Gly	Met	Pro
65					70					75					80

Glu	Asp	Arg	Phe	Ser	Ala	Lys	Met	Pro	Asn	Ala	Ser	Phe	Ser	Thr	Leu
				85					90					95	

Lys	Ile	Gln	Pro	Ser	Glu	Pro	Arg	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala
			100					105					110		

Ser	Ser	Leu	Ala	Tyr	Leu	Thr	Gly	Arg	Val	Glu	Ala	Phe	Phe	Gly	Gln
		115					120					125			

Gly Thr Arg Leu Thr Val Val Lys Asp Leu Arg Asn Val Thr Pro Pro
130 135 140

Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp
225 230 235 240

Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys
290 295 300

Lys Lys Asn Ser
305

<210> 495
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 495
Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 496
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 496
Leu Ile Met Gln Leu Met Pro Phe Gly Cys
1 5 10

<210> 497
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 497
Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 498
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 498
Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 499
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 499
Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 500
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 500
Ala Leu Ile Arg Gly Ser Tyr Gln Leu Ile
1 5 10

<210> 501
<211> 6

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 501

Asp Phe Gln Ala Thr Thr
1 5

<210> 502

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 502

Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 503

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 503

Ser Ala Gln Gly Ser Ser Gly Arg Ile Glu Gln Phe
1 5 10

<210> 504

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 504

atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg
60

gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc
120

ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca
180

ccaagtggag aattgggttt ccttattcgt cggaactctt ttgatgagca aaatgaaata
240

agtggtcggt attcttgga cttccagaaa tccaccagtt cttcaactt caccatcaca
300

gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgattcgagg gagctatcag
360

ttaatctggg gcgctgggac caagctaatt ataaagcca
399

<210> 505

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 505

atgctgaccg cctctctgct gagggccgtg atcgccagca tctgcgtggt gagctccatg
60

gcccagaagg tgacacaggc ccagaccgag atcagcgtgg tggagaagga ggacgtgaca
120

ctggattgcg tgtacgagac ccgcgacacc acatactatc tgttttggta taagcagcca
180

ccctccggcg agctggtggt cctgatcagg cgcaactctt ttgatgagca gaatgagatc
240

tctggccggt acagctggaa cttccagaag agcacatcta gcttcaactt caccatcacc
300

gccagccagg tgggtggactc cgccgtgtac ttttgtgccc tgatcagagg ctctatcag
360

ctgatctggg gcgccggcac caagctgac atcaagccc
399

<210> 506

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 506

Met	Leu	Thr	Ala	Ser	Leu	Leu	Arg	Ala	Val	Ile	Ala	Ser	Ile	Cys	Val
1				5					10					15	

Val	Ser	Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser
			20					25					30		

Val	Val	Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg
		35					40					45			

Asp	Thr	Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu
	50					55					60				

Leu	Val	Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile
65					70					75					80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn

85

90

95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Ile Arg Gly Ser Tyr Gln Leu Ile Trp Gly Ala Gly Thr Lys
115 120 125

Leu Ile Ile Lys Pro
130

<210> 507

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 507

atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa
60

catccgagca gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccttg
120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg
180

atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag
240

tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct
300

gaagacagca gcttctacat ctgcagcgcc caggggagta gcgggaggat tgagcagttc
360

t t c g g g c c a g g g a c a c g g c t c a c c g t g c t a
390

<210> 508
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 508
atgttattac tgctgctgct gctgggacca ggctccggac tgggagcagt ggtgtctcag
60
cacccaagca gagtgatctg caagtctggc accagcgtga agatcgagtg taggtccctg
120
gacttccagg ccaccacaat gttctggtac cgccagtttc caaagcagtc tctgatgctg
180
atggccacat ccaacgaggg ctctaaggcc acctatgagc agggcgtgga gaaggacaag
240
ttcctgatca atcacgccag cctgaccctg tccaccctga cagtgaccag cgcccaccca
300
gaggatagct cctttttacat ctgctccgcc cagggtctta gcggccggat cgagcagttc
360
t t t g g c c c t g g c a c a c g g c t g a c c g t g c t g
390

<210> 509
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 509
Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala

1	5	10	15
Val Val Ser Gln His Pro Ser Arg Val Ile Cys Lys Ser Gly Thr Ser			
20	25	30	
Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe			
35	40	45	
Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser			
50	55	60	
Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys			
65	70	75	80
Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr			
85	90	95	
Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Gln Gly			
100	105	110	
Ser Ser Gly Arg Ile Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr			
115	120	125	
Val Leu			
130			

<210> 510

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 510

Met 1	Leu	Thr	Ala	Ser 5	Leu	Leu	Arg	Ala	Val 10	Ile	Ala	Ser	Ile	Cys 15	Val
Val	Ser	Ser	Met 20	Ala	Gln	Lys	Val	Thr 25	Gln	Ala	Gln	Thr	Glu 30	Ile	Ser
Val	Val	Glu 35	Lys	Glu	Asp	Val	Thr 40	Leu	Asp	Cys	Val	Tyr 45	Glu	Thr	Arg
Asp 50	Thr	Thr	Tyr	Tyr	Leu	Phe 55	Trp	Tyr	Lys	Gln	Pro 60	Pro	Ser	Gly	Glu
Leu 65	Val	Phe	Leu	Ile	Arg 70	Arg	Asn	Ser	Phe	Asp 75	Glu	Gln	Asn	Glu	Ile 80
Ser	Gly	Arg	Tyr	Ser 85	Trp	Asn	Phe	Gln	Lys 90	Ser	Thr	Ser	Ser	Phe 95	Asn
Phe	Thr	Ile	Thr 100	Ala	Ser	Gln	Val	Val 105	Asp	Ser	Ala	Val	Tyr 110	Phe	Cys
Ala	Leu	Ile 115	Arg	Gly	Ser	Tyr	Gln 120	Leu	Ile	Trp	Gly	Ala 125	Gly	Thr	Lys
Leu 130	Ile	Ile	Lys	Pro	Asp	Ile 135	Gln	Asn	Pro	Glu	Pro 140	Ala	Val	Tyr	Gln
Leu 145	Lys	Asp	Pro	Arg	Ser 150	Gln	Asp	Ser	Thr	Leu 155	Cys	Leu	Phe	Thr	Asp 160
Phe	Asp	Ser	Gln	Ile 165	Asn	Val	Pro	Lys	Thr 170	Met	Glu	Ser	Gly	Thr 175	Phe
Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser

180

185

190

Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp
 195 200 205

Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys
 210 215 220

Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn
 225 230 235 240

Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val
 245 250 255

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 260 265 270

<210> 511

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 511

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
 1 5 10 15

Val Val Ser Gln His Pro Ser Arg Val Ile Cys Lys Ser Gly Thr Ser
 20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
 35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Gln Gly
100 105 110

Ser Ser Gly Arg Ile Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe
130 135 140

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
145 150 155 160

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala
180 185 190

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
195 200 205

Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val
210 215 220

Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro

240

Leu Ile Met Gln Leu Met Pro Phe Gly Cys
1 5 10

10

<210> 514
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 514
Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 515
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 515
Asp Ser Val Asn Asn
1 5

<210> 516
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 516
Ile Pro Ser Gly Thr
1 5

<210> 517

<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 517

Ala Val Met Asp Ser Ser Tyr Lys Leu Ile
1 5 10

<210> 518

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 518

Asp Phe Gln Ala Thr Thr
1 5

<210> 519

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 519

Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 520

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 520

Ser Ala Leu Pro Gly Phe Ser Tyr Glu Gln Tyr
1 5 10

<210> 521

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 521

atgaagagga tattgggagc tctgctgggg ctcttgagtg cccagggttg ctgtgtgaga
60

ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg
120

ctgcggtgca atttttctga ctctgtgaac aatttgcagt ggtttcatca aaacccttgg
180

ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc
240

gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca
300

gactcaggcg tttattttctg tgctgtgatg gatagcagct ataaattgat cttcgggagt
360

g g g a c c a g a c
384

t g c t g g t c a g

g c c t

<210> 522

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 522

atgaagagaa tcctgggCGc cctgctggga ctgctgtccg cccaggtgtg ctgcgtgcgg
60

ggcatccagg tggagcagag cccaccagac ctgatacctgc aggagggagc caactccacc
120

ctgagatgca atttctccga ttctgtgaac aatctgcagt ggtttcacca gaacccttgg
180

ggccagctga tcaatctggt ttacatccca tccggcacia agcagaacgg caggctgtct
240

gccaccacag tggccaccga gcggtactct ctgctgtata tctcctctag ccagaccaca
300

gacagcggcg tgtacttctg tgccgtgatg gattcctctt ataagctgat ctttggcagc
360

g g c a c c a g g c t g c t g g t g c g c c c t
384

<210> 523

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 523

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Met Asp Ser
100 105 110

Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr Arg Leu Leu Val Arg Pro
115 120 125

<210> 524

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 524

atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa
60

catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttcctg
120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg
180

atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag
240

tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct
300

gaagacagca gcttctacat ctgcagtgtc ctgcccggat tctcctacga gcagtacttc
360

g g g c c g g g c a c c a g g c t c a c g g t c a c a
387

<210> 525

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 525

atgttattac tgctgctgct gctgggacca ggcagcggac tgggagcagt ggtgagccag
60

cacccttcct gggtcattctg caagagcggc acatccgtga agatcgagtg tcggtctctg
120

gacttccagg ccaccacaat gttctgggtac agacagtttc ctaagcagtc cctgatgctg
180

atggccacat ctaacgaggg cagcaaggcc acctatgagc agggcggtgga gaaggacaag
240

ttcctgatca atcacgcctc cctgaccctg tctaccctga cagtgacctc cgcccaccca
300

gaggatagct cctttttacat ctgctctgcc ctgccaggct tcagctacga gcagtatttt
360

g g c c c c g g c a c a c g g c t g a c a g t g a c c
387

<210> 526
<211> 129
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 526

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Leu Pro
100 105 110

Gly Phe Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val
115 120 125

Thr

<210> 527
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 527
Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Met Asp Ser
100 105 110

Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr Arg Leu Leu Val Arg Pro
115 120 125

Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg
130 135 140

Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile
145 150 155 160

Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr
165 170 175

Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala
180 185 190

Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr
195 200 205

Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr
210 215 220

Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser
225 230 235 240

Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
245 250 255

Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 528

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 528

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala

1		5						10					15			
Val	Val	Ser	Gln	His	Pro	Ser	Trp	Val	Ile	Cys	Lys	Ser	Gly	Thr	Ser	
			20					25					30			
Val	Lys	Ile	Glu	Cys	Arg	Ser	Leu	Asp	Phe	Gln	Ala	Thr	Thr	Met	Phe	
		35					40					45				
Trp	Tyr	Arg	Gln	Phe	Pro	Lys	Gln	Ser	Leu	Met	Leu	Met	Ala	Thr	Ser	
	50					55					60					
Asn	Glu	Gly	Ser	Lys	Ala	Thr	Tyr	Glu	Gln	Gly	Val	Glu	Lys	Asp	Lys	
65					70					75					80	
Phe	Leu	Ile	Asn	His	Ala	Ser	Leu	Thr	Leu	Ser	Thr	Leu	Thr	Val	Thr	
				85					90					95		
Ser	Ala	His	Pro	Glu	Asp	Ser	Ser	Phe	Tyr	Ile	Cys	Ser	Ala	Leu	Pro	
			100					105					110			
Gly	Phe	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	
		115					120					125				
Thr	Lys	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val	Ser	Leu	Phe	Glu	
	130					135					140					
Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr	Leu	Val	Cys	
145					150					155					160	
Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	
				165					170					175		
Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Ala	Tyr	
			180					185					190			

Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
195 200 205

Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
210 215 220

Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys
225 230 235 240

Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
245 250 255

Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile
260 265 270

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
275 280 285

Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
290 295 300

<210> 529

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 529

Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 530

<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 530

Leu Ile Met Gln Leu Met Pro Phe Gly Cys
1 5 10

<210> 531

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 531

Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 532

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 532

Asn Ser Met Phe Asp Tyr
1 5

<210> 533

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 533

Ile Ser Ser Ile Lys Asp Lys
1 5

<210> 534

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 534

Ala Ala Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu Thr
1 5 10

<210> 535

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 535

Ser Asn His Leu Tyr
1 5

<210> 536

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

peptide

<400> 536

Phe Tyr Asn Asn Glu Ile

1

5

<210> 537

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 537

Ala Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe

1

5

10

<210> 538

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 538

atggccatgc tcctgggggc atcagtgtg attctgtggc ttcagccaga ctgggtaaac
60

agtcaacaga agaatgatga ccagcaagtt aagcaaaatt caccatccct gagcgtccag
120

gaaggaagaa tttctattct gaactgtgac tataactaaca gcatgtttga ttatttccta
180

tggtacaaaa aataccctgc tgaaggctcct acattcctga tatctataag ttccattaag
240

gataaaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct
300

ctgcacattg tggcctccca gcctggagac tctgcagtgt acttctgtgc agcaaagtct
360

ggtaggtacta gctatggaaa gctgacattt ggacaaggga ccatcttgac tgtccatcca
420

a
421

<210> 539

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 539

Met	Ala	Met	Leu	Leu	Gly	Ala	Ser	Val	Leu	Ile	Leu	Trp	Leu	Gln	Pro
1			5						10					15	

Asp	Trp	Val	Asn	Ser	Gln	Gln	Lys	Asn	Asp	Asp	Gln	Gln	Val	Lys	Gln
			20					25					30		

Asn	Ser	Pro	Ser	Leu	Ser	Val	Gln	Glu	Gly	Arg	Ile	Ser	Ile	Leu	Asn
		35					40					45			

Cys	Asp	Tyr	Thr	Asn	Ser	Met	Phe	Asp	Tyr	Phe	Leu	Trp	Tyr	Lys	Lys
50						55					60				

Tyr	Pro	Ala	Glu	Gly	Pro	Thr	Phe	Leu	Ile	Ser	Ile	Ser	Ser	Ile	Lys
65					70					75				80	

Asp	Lys	Asn	Glu	Asp	Gly	Arg	Phe	Thr	Val	Phe	Leu	Asn	Lys	Ser	Ala
				85					90					95	

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu
115 120 125

Thr Phe Gly Gln Gly Thr Ile Leu Thr Val His Pro
130 135 140

<210> 540

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 540

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa
60

cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg
120

cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttggggcag
180

aaagtcgagt ttctgggttc cttttataat aatgaaatct cagagaagtc tgaaatattc
240

gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccggtcc
300

acaaagctgg aggactcagc catgtacttc tgtgccagca gtgaatgggg aagcaccggg
360

gagctgtttt ttggagaagg ctctaggctg accgtactgg
400

<210> 541

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 541

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
1 5 10 15

Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
20 25 30

Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
35 40 45

Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
50 55 60

Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
65 70 75 80

Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
85 90 95

Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
100 105 110

Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu
130

<210> 542
<211> 277
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 542

Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro
1 5 10 15

Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln
20 25 30

Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn
35 40 45

Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys
50 55 60

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu
115 120 125

Thr Phe Gly Gln Gly Thr Ile Leu Thr Val His Pro Asp Ile Gln Asn
130 135 140

Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser
145 150 155 160

Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys
165 170 175

Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met
180 185 190

Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln
195 200 205

Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr
210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe
225 230 235 240

Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
275

<210> 543

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 543

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
1 5 10 15

Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
20 25 30

Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
35 40 45

Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
50 55 60

Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
65 70 75 80

Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
85 90 95

Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
100 105 110

Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val
130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 544

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 544
Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 545
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 545
Thr Thr Ser Asp Arg
1 5

<210> 546
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 546
Leu Leu Ser Asn Gly Ala Val
1 5

<210> 547
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 547
Ala Val Asp Ile Ile Gly Gly Lys Ser Thr

1 5 10

<210> 548
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 548
Ser Asn His Leu Tyr
1 5

<210> 549
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 549
Phe Tyr Asn Asn Glu Ile
1 5

<210> 550
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 550
Ala Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe
1 5 10

<210> 551
<211> 385
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 551
atgaagaagc tactagcaat gattctgtgg cttcaactag accggttaag tggagagctg
60
aaagtggaac aaaaccctct gttcctgagc atgcaggagg gaaaaaacta taccatctac
120
tgcaattatt caaccacttc agacagactg tattggtaca ggcaggatcc tgggaaaagt
180
ctggaatctc tgtttgtgtt gctatcaaat ggagcagtga agcaggaggg acgattaatg
240
gcctcacttg ataccaaagc ccgtctcagc accctccaca tcacagctgc cgtgcatgac
300
ctctctgcca cctacttctg tgccgtggac atcatcggag gcaaataaac ctttggggat
360
g g g a c t a c g c t c a c t g t g a a g c c a a
385

<210> 552
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 552
Met Lys Lys Leu Leu Ala Met Ile Leu Trp Leu Gln Leu Asp Arg Leu
1 5 10 15

Ser Gly Glu Leu Lys Val Glu Gln Asn Pro Leu Phe Leu Ser Met Gln
20 25 30

Glu Gly Lys Asn Tyr Thr Ile Tyr Cys Asn Tyr Ser Thr Thr Ser Asp
35 40 45

Arg Leu Tyr Trp Tyr Arg Gln Asp Pro Gly Lys Ser Leu Glu Ser Leu
50 55 60

Phe Val Leu Leu Ser Asn Gly Ala Val Lys Gln Glu Gly Arg Leu Met
65 70 75 80

Ala Ser Leu Asp Thr Lys Ala Arg Leu Ser Thr Leu His Ile Thr Ala
85 90 95

Ala Val His Asp Leu Ser Ala Thr Tyr Phe Cys Ala Val Asp Ile Ile
100 105 110

Gly Gly Lys Ser Thr Phe Gly Asp Gly Thr Thr Leu Thr Val Lys Pro
115 120 125

<210> 553

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 553

atggatacct ggctcgtatg ctgggcaatt tttagtctct tgaaagcagg actcacagaa
60

cctgaagtca cccagactcc cagccatcag gtcacacaga tgggacagga agtgatcttg
120

cgctgtgtcc ccattctctaa tcacttatac ttctattggt acagacaaat cttggggcag
180

aaagtcgagt ttctgggttc cttttataat aatgaaatct cagagaagtc tgaaatattc
240

gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccgggtcc
300

acaaagctgg aggactcagc catgtacttc tgtgccagca gtgaatgggg aagcaccggg
360

gagctgtttt ttggagaagg ctctaggctg accgtactgg
400

<210> 554

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 554

Met	Asp	Thr	Trp	Leu	Val	Cys	Trp	Ala	Ile	Phe	Ser	Leu	Leu	Lys	Ala
1				5				10						15	

Gly	Leu	Thr	Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr
			20					25					30		

Gln	Met	Gly	Gln	Glu	Val	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His
		35					40					45			

Leu	Tyr	Phe	Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe
	50					55					60				

Leu	Val	Ser	Phe	Tyr	Asn	Asn	Glu	Ile	Ser	Glu	Lys	Ser	Glu	Ile	Phe
65					70					75				80	

Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
85 90 95

Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
100 105 110

Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu
130

<210> 555

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 555

Met Lys Lys Leu Leu Ala Met Ile Leu Trp Leu Gln Leu Asp Arg Leu
1 5 10 15

Ser Gly Glu Leu Lys Val Glu Gln Asn Pro Leu Phe Leu Ser Met Gln
20 25 30

Glu Gly Lys Asn Tyr Thr Ile Tyr Cys Asn Tyr Ser Thr Thr Ser Asp
35 40 45

Arg Leu Tyr Trp Tyr Arg Gln Asp Pro Gly Lys Ser Leu Glu Ser Leu
50 55 60

Phe Val Leu Leu Ser Asn Gly Ala Val Lys Gln Glu Gly Arg Leu Met
65 70 75 80

Ala Ser Leu Asp Thr Lys Ala Arg Leu Ser Thr Leu His Ile Thr Ala
85 90 95

Ala Val His Asp Leu Ser Ala Thr Tyr Phe Cys Ala Val Asp Ile Ile
100 105 110

Gly Gly Lys Ser Thr Phe Gly Asp Gly Thr Thr Leu Thr Val Lys Pro
115 120 125

Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg
130 135 140

Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile
145 150 155 160

Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr
165 170 175

Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala
180 185 190

Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr
195 200 205

Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr
210 215 220

Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser
225 230 235 240

Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
245 250 255

Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 556

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 556

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
1 5 10 15

Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
20 25 30

Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
35 40 45

Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
50 55 60

Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
65 70 75 80

Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
85 90 95

Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
100 105 110

Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser
115 120 125

Arg Leu Thr Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val
130 135 140

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 557
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 557
Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 558
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 558
Asn Ser Met Phe Asp Tyr
1 5

<210> 559
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 559
Ile Ser Ser Ile Lys Asp Lys
1 5

<210> 560
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 560
Ala Ala Ser Ala Val Gly Gln Glu Tyr Gly Asn Lys Leu Val
1 5 10

<210> 561
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 561
Ser Glu His Asn Arg
1 5

<210> 562
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 562
Phe Gln Asn Glu Ala Gln
1 5

<210> 563

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 563
Ala Ser Ser Glu Tyr Thr Met Gly Thr Gln Tyr
1 5 10

<210> 564
<211> 424
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 564
atggccatgc tcctgggggc atcagtgctg attctgtggc ttcagccaga ctgggtaaac
60
agtcaacaga agaatgatga ccagcaagtt aagcaaaatt caccatccct gagcgtccag
120
gaaggaagaa tttctattct gaactgtgac tataactaaca gcatgtttga ttatttccta
180
tggtacaaaa aataccctgc tgaaggtcct acattcctga tatctataag ttccattaag
240
gataaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct
300
ctgcacattg tgccctccca gcctggagac tctgcagtgt acttctgtgc agcaagcgca
360
gtaggtcagg aatatggaaa caagctggtc tttggcgcag gaaccattct gagagtcaag
420
t c c t
424

<210> 565
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 565
Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro
1 5 10 15

Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln
20 25 30

Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn
35 40 45

Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys
50 55 60

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Ala Val Gly Gln Glu Tyr Gly Asn Lys
115 120 125

Leu Val Phe Gly Ala Gly Thr Ile Leu Arg Val Lys Ser

130

135

140

<210> 566

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 566

atgggacacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat
60

actggagtct cccagaacct cagacacaag atcacaaaga ggggacagaa tgtaactttc
120

aggtgtgatc caatttctga acacaaccgc ctttattggg accgacagac cctggggcag
180

ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc
240

agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc
300

acagagcagg gggactcggc catgtatctc tgtgccagca gtgaatatac tatggggacc
360

c a g t a c t t c g g g c c a g g c a c g c g g c t c c t g g t g c t c g
397

<210> 567

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 567

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Glu Tyr Thr Met Gly Thr Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Leu Val Leu
130

<210> 568

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 568

Met Ala Met Leu Leu Gly Ala Ser Val Leu Ile Leu Trp Leu Gln Pro
1 5 10 15

Asp Trp Val Asn Ser Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln
20 25 30

Asn Ser Pro Ser Leu Ser Val Gln Glu Gly Arg Ile Ser Ile Leu Asn
35 40 45

Cys Asp Tyr Thr Asn Ser Met Phe Asp Tyr Phe Leu Trp Tyr Lys Lys
50 55 60

Tyr Pro Ala Glu Gly Pro Thr Phe Leu Ile Ser Ile Ser Ser Ile Lys
65 70 75 80

Asp Lys Asn Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Ala
85 90 95

Lys His Leu Ser Leu His Ile Val Pro Ser Gln Pro Gly Asp Ser Ala
100 105 110

Val Tyr Phe Cys Ala Ala Ser Ala Val Gly Gln Glu Tyr Gly Asn Lys
115 120 125

Leu Val Phe Gly Ala Gly Thr Ile Leu Arg Val Lys Ser Asp Ile Gln
130 135 140

Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp
145 150 155 160

Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro
165 170 175

Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp
180 185 190

Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn
195 200 205

Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr
210 215 220

Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser
225 230 235 240

Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly
245 250 255

Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr
260 265 270

Leu Arg Leu Trp Ser Ser
275

<210> 569

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 569

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Glu Tyr Thr Met Gly Thr Gln Tyr Phe Gly Pro Gly Thr Arg
115 120 125

Leu Leu Val Leu Lys Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser
130 135 140

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
210 215 220

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
275 280 285

Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn
290 295 300

Ser
305

<210> 570

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<210> 600
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 600
Val Val Gly Ala Val Gly Val Gly Lys
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<210> 601
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 601

Ser Gly Ser Gly

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<210> 602

<211> 8

<212> PRT

<213> Influenza virus

<400> 602

Gly Ile Leu Gly Phe Val Thr Leu

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5

<210> 603

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 603

Cys Ala Val Lys Gly Gly Gly Ser Gly Thr Tyr Lys Tyr Ile Phe

1

5

10

15

<210> 604

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 604

Cys Ala Val Gly Asn Asn Gln Gly Gly Lys Leu Ile Phe
1 5 10

<210> 605

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 605

Cys Ala Gly Pro Asn Thr Asn Ala Gly Lys Ser Thr Phe
1 5 10

<210> 606

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 606

Cys Ala Ala Ser Ile Ala Asp Gly Gln Lys Leu Leu Phe
1 5 10

<210> 607

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 607

Cys Ala Tyr Ile Asp Ala Gly Asn Gln Phe Tyr Phe
1 5 10

<210> 608
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 608
Cys Ala Val Arg Gly Asp Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe
1 5 10 15

<210> 609
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 609
Cys Ala Val Asp Ile Ile Gly Gly Lys Ser Thr Phe
1 5 10

<210> 610
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 610
Cys Ala Ala Asn Ala Gly Gly Thr Ser Tyr Gly Lys Leu Thr Phe
1 5 10 15

<210> 611
<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 611

Cys	Ala	Ser	Ser	Phe	Phe	Pro	Thr	Ser	Thr	Gly	Arg	Thr	Asp	Thr	Gln
1				5					10					15	

Tyr Phe

<210> 612

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 612

Cys	Ala	Ser	Ser	Gly	Pro	Gly	Pro	Arg	Gly	Phe	Asn	Glu	Gln	Phe	Phe
1				5					10					15	

<210> 613

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 613

Cys	Ala	Ser	Ser	Leu	Gly	Gln	Asp	Thr	Glu	Ala	Phe	Phe
1				5					10			

<210> 614

<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 614

Cys Ala Ser Ser Glu Ser Gly Ser Gly Glu Lys Leu Phe Phe
1 5 10

<210> 615

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 615

Cys Ala Ser Ile Thr Pro Arg Asp Glu Gln Phe Phe
1 5 10

<210> 616

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 616

Cys Ala Ser Ser Glu Trp Gly Ser Thr Gly Glu Leu Phe Phe
1 5 10

<210> 617

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 617

Cys	Ala	Met	Arg	Glu	Gly	Arg	Gly	Ala	Gly	Asn	Asn	Arg	Lys	Leu	Ile
1				5					10					15	

Trp

<210> 618

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 618

Cys	Ala	Leu	Ser	Glu	Ala	Gly	Leu	Gly	Gly	Gly	Lys	Leu	Ile	Phe
1				5					10					15

<210> 619

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 619

Cys	Ala	Ala	Ser	Ala	Val	Gly	Gln	Glu	Tyr	Gly	Asn	Lys	Leu	Val	Phe
1				5					10					15	

<210> 620

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 620

Cys	Ala	Ser	Ser	Gln	Asp	Arg	Leu	Ala	Gly	Asp	Tyr	Glu	Gln	Tyr	Phe
1				5					10					15	

<210> 621

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 621

Cys	Ala	Ser	Ser	Glu	Tyr	Thr	Met	Gly	Thr	Gln	Tyr	Phe
1				5					10			