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Chimeric antigen receptors targeting CD70

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CHIMERIC ANTIGEN RECEPTORS TARGETING CD70

ABSTRACT

The disclosure provides CARs (CARs) that specifically bind to CD70. The disclosure further relates to engineered immune cells comprising such CARs, CAR-encoding nucleic acids, and methods of making such CARs, engineered immune cells, and nucleic acids. The disclosure further relates to therapeutic methods for use of these CARs and engineered immune cells comprising these CARs for the treatment of a condition associated with malignant cells expressing CD70 (*e.g.*, cancer).

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CHIMERIC ANTIGEN RECEPTORS TARGETING CD70

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a divisional of Australian patent application number 2019216420, which is the Australian national phase of PCT/US2019/016189, which claims priority to U.S. Provisional Patent Appl. No. 62/775,246, filed December 4, 2018, U.S. Provisional Patent Appl. No. 62/641,869, filed March 12, 2018, U.S. Provisional Patent Appl. No. 62/641,873, filed March 12, 2018, U.S. Provisional Patent Appl. No. 62/625,009, filed February 1, 2018, and U.S. Provisional Patent Appl. No. 62/625,019, filed February 1, 2018, each of which is incorporated herein by reference in its entirety.

FIELD

[0002] The disclosure relates to chimeric antigen receptors (CAR). CARs are able to redirect immune cell specificity and reactivity toward a selected target exploiting the ligand-binding domain properties. In particular, the disclosure relates to CARs that specifically bind to Cluster of Differentiation 70 (CD70-specific CARs). The disclosure further relates to polynucleotides encoding CD70-specific CARs and isolated cells expressing CD70-specific CARs at their surface. The disclosure further relates to methods for engineering immune cells expressing CD70-specific CARs at their surface. The disclosure is particularly useful for the treatment of cancer such as lymphoma, leukemia, glioma or Renal Cell Carcinoma (RCC). The disclosure further relates to immune cells comprising the CD70-specific CARs (CD70-specific CAR-T cells), compositions comprising the CD70-specific CAR-T cells, and methods of using the CD70-specific CAR-T cells for treating conditions associated with malignant cells expressing CD70 (*e.g.*, cancer).

BACKGROUND

[0003] Adoptive transfer of immune cells genetically modified to recognize malignancy-associated antigens is showing promise as a new approach to treating cancer (see, *e.g.*, Brenner et al., Current Opinion in Immunology, 22(2): 251-257 (2010); Rosenberg et al., Nature Reviews Cancer, 8(4): 299-308 (2008)). T cells can be genetically modified to express chimeric antigen receptors (CARs), fusion proteins comprised of an antigen

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recognition moiety and T cell activation domains (see, *e.g.*, Eshhar et al., Proc. Natl. Acad. Sci. USA, 90(2): 720-724 (1993), and Sadelain et al., Curr. Opin. Immunol, 21(2): 215-223 (2009)).

[0004] Cluster of Differentiation 70 (CD70, CD27LG or TNFSF7) is a member of the tumor necrosis factor (TNF) superfamily and the ligand for CD27, a TNF superfamily receptor. The transient interaction between CD27 and CD70 provides T cell costimulation complementary to that provided by CD28. CD70 is expressed on hematological cancers such as Non-Hodgkin's Lymphoma and Hodgkin's disease as well as on solid tumors such as Glioblastoma and Renal Cell Carcinoma; with its expression on ccRCC being nearly uniform (see *e.g.*, Grewal I., et al., Expert Opinion on Therapeutic Targets, 12(3): 341-351 (2008)). Adoptive transfer of T cells genetically modified to recognize malignancy-associated antigens is showing promise as a new approach to treating cancer (see, *e.g.*, Brenner et al., Current Opinion in Immunology, 22(2): 251-257 (2010); Rosenberg et al., Nature Reviews Cancer, 8(4): 299-308 (2008)). T cells can be genetically modified to express chimeric antigen receptors (CARs), which are fusion proteins comprised of an antigen recognition moiety and T cell activation domains (see, *e.g.*, Eshhar et al., Proc. Natl. Acad. Sci. USA, 90(2): 720-724 (1993), and Sadelain et al., Current Opinion in Immunology, 21(2): 215-223 (2009)). Expression of CD70 on normal tissues is limited to activated T cells, B cells, NK cells, and dendritic cells. However, CD70 expression on activated T cells may pose a concern for production of CAR T cells due to potential target-driven T cell differentiation, exhaustion, and fratricide during the production process.

[0005] Renal Cell Carcinoma (RCC) is a cancer that originates in the renal cortex and accounts for about 90% of cancers in the kidney. Based on histology, RCC can be classified into several sub-types, of which Clear Cell Renal Cell Carcinoma (ccRCC) is the most common and leads to the most deaths. Each year, over 320,000 cases of RCC are reported worldwide leading to roughly 140,000 deaths. The incidence of RCC has risen steadily over the last 10 years and accounts for 2-3% of all adult malignancies. Patients with early stage localized tumors can opt for surgical resection; however, localized disease can undergo early hematogenous dissemination leading to metastasis. Sites of early metastases include lungs, lymph nodes, liver, bone, and brain; less commonly the adrenal glands, and the contralateral kidney. Patients with advanced disease face high morbidity rates with a 5-year median survival rate of 53% for stage III disease and only 8% for metastatic disease. Current first-

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line treatment options for advanced disease include small molecule Tyrosine Kinase Inhibitors (TKIs) such as sunitinib and pazopanib that target Vascular Endothelial Growth Factor (VEGF) receptor, monoclonal antibody targeting VEGF such as bevacizumab, mammalian target of Rapamycin (mTOR) inhibitor temsirolimus, as well as high dose IL-2. Although these VEGF-targeted therapies have improved over-all survival, long-term drug resistance leads to disease relapse and treatment for advanced disease still remains an unmet need (see, e.g., Zarrabi, K. et al., Journal of Hematology and Oncology, 10:38 (2017)).

[0006] Accordingly, there is a need for alternative treatments for cancer and in particular malignancies involving aberrant expression of CD70. Novel immunotherapies, such as CAR T therapy, have the potential to significantly improve the outcome for patients with cancer where CD70 is expressed, for example in mRCC. Accordingly, treatment to a cancer (such as, e.g., mRCC) using CD70-specific CARs and CD70-specific CAR-T cells would make a promising therapeutic agent. Provided herein are methods and compositions addressing this need.

[0007] Any reference to or discussion of any document, act or item of knowledge in this specification is included solely for the purpose of providing a context for the present invention. It is not suggested or represented that any of these matters or any combination thereof formed at the priority date part of the common general knowledge, or was known to be relevant to an attempt to solve any problem with which this specification is concerned.

[0008] It is to be noted that, throughout the description and claims of this specification, the word 'comprise' and variations of the word, such as 'comprising' and 'comprises', is not intended to exclude other variants or additional components, integers or steps. Modifications and improvements to the invention will be readily apparent to those skilled in the art. Such modifications and improvements are intended to be within the scope of this invention.

SUMMARY

[0009] In a first aspect, the invention relates to a method for treating a CD70-mediated condition in a subject, the method comprising:

(i) administering to the subject engineered immune cells expressing at their cell surface CD70-specific CARs and

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(ii) subsequently depleting the engineered immune cells from the subject by administering one or more monoclonal antibodies specific for the epitope to the subject wherein:

the CAR comprises an extracellular ligand-binding domain, a first transmembrane domain, and an intracellular signaling domain, wherein the extracellular ligand-binding domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70, and

the CAR further comprises one or more epitopes specific for one or more monoclonal antibodies;

or the method comprising:

(iii) in a subject to whom have been administered engineered immune cells expressing at cell surface CD70-specific CARs, depleting the engineered immune cells from the subject by administering one or more monoclonal antibodies specific for the epitope to the subject; wherein:

the CAR comprises an extracellular ligand-binding domain, a first transmembrane domain, and an intracellular signaling domain, wherein the extracellular ligand-binding domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70, and

the CAR further comprises one or more epitopes specific for one or more monoclonal antibodies;

and further wherein the scFv comprises:

(a) a heavy chain variable (VH) region comprising three CDRs from the VH region shown in SEQ ID NO: 18 and a light chain variable (VL) region comprising three CDRs from the VL region shown in SEQ ID NO: 17; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, a combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(b) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 371; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 370; wherein each CDR is defined in accordance with the Kabat definition, the

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Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(c) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 339; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 338; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(d) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 343; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 342; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(e) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 345; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 344; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(f) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 349; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 348; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(g) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 351; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 350; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(h) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 355; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 354; wherein each CDR is defined in accordance with the Kabat definition, the

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Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(i) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 357; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 356; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(j) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 359; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 358; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(k) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 361; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 360; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(l) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 365; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 364; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR.

[0010] Chimeric antigen receptors (CARs) that bind to CD70 are provided herein, as well as methods of making and methods of using the same. Also provided herein are immune cells, e.g. T-cells comprising such CD70 CARs. It is demonstrated that certain CD70-specific CARs are effective when expressed in T cells to activate T cells upon contact with CD70. Advantageously, the CD70-specific CARs provided herein bind human CD70. Also advantageously, the CD70-specific CAR-T cells provided herein exhibit cytotoxic activity upon contact with CD70-expressing cells. Also provided herein are antibodies that bind to CD70, as well as methods of making and methods of using the same. CD70-specific antibodies provided herein bind human CD70.

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[0011] In one aspect, the disclosure provides Cluster of Differentiation 70 (CD70) specific chimeric antigen receptor (CAR) comprising an extracellular ligand-binding domain, a first transmembrane domain, and an intracellular signaling domain, wherein the extracellular domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70.

[0012] In some embodiments, the disclosure provides a CD70-specific CAR wherein the extracellular domain of a CAR provided herein comprises a scFv comprising a heavy chain variable (VH) region comprising three CDRs from the VH region comprising the sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379 or 381; and a light chain variable (VL) region comprising three CDRs from the VL region shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378 or 380. In some embodiments, the VH region comprises the sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379 or 381, or a variant thereof with one or several conservative amino acid substitutions in residues that are not within a CDR and/or the VL region comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378 or 380 or a variant thereof with one or several amino acid substitutions in amino acids that are not within a CDR.

[0013] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 49, 50, or 51; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 52 or 53; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 54; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 193; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 194; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 195.

[0014] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 2 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 1.

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[0015] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 55, 56, or 57; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 58 or 59 ; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 60; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 196; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 197; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 198.

[0016] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 4 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 3.

[0017] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 61, 62, or 63; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 64 or 65; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 66; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 199; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 200; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 201.

[0018] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 6 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 5.

[0019] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 67, 68, or 69; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 70 or 71; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 72; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 202; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 203; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 204.

[0020] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 8 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 7.

[0021] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 73, 74, or 75; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 76 or 77; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 78; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 205; a VL CDR2 comprising the amino acid

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sequence shown in SEQ ID NO: 206; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 207.

[0022] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 10 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 9

[0023] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 79, 80, or 81; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 82 or 83; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 84; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 208; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 209; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 210.

[0024] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 12 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 11.

[0025] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 85, 86, or 87; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 88 or 89; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 90; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 211; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 212; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 213.

In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 14 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 13.

[0026] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 91, 92, or 93; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 94 or 95; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 96; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 214; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 215; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 216.

[0027] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 16 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 15.

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[0028] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 97, 98, or 99; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 100 or 101; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 102; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 217; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 218; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 219.

[0029] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 18 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 17.

[0030] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 103, 104, or 105; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 106 or 107; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 108; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 220; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 221; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 222.

[0031] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 20 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 19.

[0032] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 109, 110, or 111; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 112 or 113; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 114; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 223; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 224; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 225.

[0033] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 22 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 21.

[0034] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 115, 116, or 117; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 118 or 119; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 120; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 226; a VL CDR2 comprising the amino acid

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sequence shown in SEQ ID NO: 227; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 228.

[0035] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 24 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 23.

[0036] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 121, 122, or 123; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 124 or 125; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 126; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 229; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 230; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 231.

[0037] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 26 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 25.

[0038] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 127, 128, or 129; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 130 or 131; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 132; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 232; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 233; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 234.

[0039] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 28 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 27.

[0040] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 133, 134, or 135; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 136 or 137; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 138; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 235; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 236; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 237.

[0041] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 30 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 29.

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[0042] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 139, 140, or 141; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 142 or 143; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 144; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 238; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 239; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 240.

[0043] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 32 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 31.

[0044] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 145, 146, or 147; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 148 or 149; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 150; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 241; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 242; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 243.

[0045] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 34 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 33.

[0046] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 151, 152, or 153; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 154 or 155; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 156; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 244; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 245; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 246.

[0047] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 36 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 35.

[0048] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 157, 158, or 159; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 160 or 161; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 162; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 247; a VL CDR2 comprising the amino acid

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sequence shown in SEQ ID NO: 248; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 249.

[0049] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 38 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 37.

[0050] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 163, 164, or 165; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 166 or 167; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 168; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 250; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 251; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 252.

[0051] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 40 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 39.

[0052] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 169, 170, or 171; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 172 or 173; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 174; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 253; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 254; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 255.

[0053] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 42 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 41.

[0054] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 175, 176, or 177; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 178 or 179; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 180; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 256; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 257; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 258.

[0055] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 44 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 43.

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[0056] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 181, 182, or 183; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 184 or 185; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 186; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 259; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 260; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 261.

[0057] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 46 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 45.

[0058] In some embodiments, the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 187, 188, or 189; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 190 or 191; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 192; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 262; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 263; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 264.

[0059] In some embodiments, the VH region comprises the amino acid sequence shown in SEQ ID NO: 48 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 47.

[0060] In some embodiments, each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR.

[0061] In some embodiments, each CDR is defined in accordance with the Kabat definition, the Chothia definition, the extended definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, the contact definition, and/or the conformational definition of CDRs.

[0062] In some embodiments, the intracellular signaling domain comprises a CD3ζ signalling domain. In some embodiments, the intracellular signaling domain comprises a 4-1BB domain. In some embodiments, the CAR further comprises a second intracellular signaling domain. In some embodiments, the second intracellular signaling domain comprises a 4-1BB domain. In some embodiments, the CAR comprises a first CD3ζ intracellular signaling domain and a second 4-1BB intracellular signaling domain.

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[0063] In some embodiments, the intracellular signaling domain comprises a CD3ζ signalling domain. In some embodiments, the intracellular signaling domain comprises a 4-1BB domain. In some embodiments, the CAR further comprises two intracellular signaling domains. In some embodiments, the CAR further comprises 3, 4, 5, or 6 intracellular signaling domains. In some embodiments, the CAR comprises a first intracellular signaling domain and a second intracellular signatling domain, wherein the second intracellular signaling domain comprises a 4-1BB domain. In some embodiments, the CAR comprises an CD3ζ intracellular signaling domain and a 4-1BB intracellular signaling domain.

[0064] In some embodiments, the CAR can comprise a stalk domain between the extracellular ligand-binding domain and the first transmembrane domain. In some embodiments, the stalk domain is selected from the group consisting of: a human CD8α hinge, an IgG1 hinge, and an FcγRIIIα hinge. In some embodiments, the stalk domain is a human CD8α hinge, a human IgG1 hinge, or a human FcγRIIIα hinge.

[0065] In some embodiments, the CAR can comprise a CD20 epitope. In some embodiments, the CD20 epitope comprises the amino acid sequence shown in SEQ ID NO: 293 or SEQ ID NO: 294 or SEQ ID NO: 609.

[0066] In some embodiments, the CAR can comprise the amino acid sequence shown in SEQ ID NO: 311 to 334 listed in Table 5. In some embodiments, the CAR can comprise the amino acid sequence shown in SEQ ID NO: 319 or 327.

[0067] In some embodiments, the first transmembrane domain comprises a CD8α chain transmembrane domain.

[0068] In some embodiments, the CAR can comprise another extracellular ligand-binding domain which is not specific for CD70.

[0069] In some embodiments, the extracellular ligand-binding domain(s), the first transmembrane domain, and intracellular signaling domain(s) are on a single polypeptide.

[0070] In some embodiments, the CAR can comprise a second transmembrane domain, wherein the first transmembrane domain and the extracellular ligand-binding domain(s) are on a first polypeptide, and wherein the second transmembrane domain and the intracellular signaling domain(s) are on a second polypeptide, wherein the first transmembrane domain comprises a transmembrane domain from the α chain of the high-affinity IgE receptor (FcεRI) and the second transmembrane domain comprises a transmembrane domain from the γ or β chain of FcεRI.

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[0071] In some embodiments, the CAR can comprise a third polypeptide comprising a third transmembrane domain fused to an intracellular signaling domain from a co-stimulatory molecule, wherein the third transmembrane domain comprises a transmembrane domain from the γ or β chain of FcεRI.

[0072] In another aspect, the disclosure provides an isolated polynucleotide comprising a nucleic acid sequence encoding the CD70-specific CAR described herein.

[0073] In another aspect, the disclosure provides an expression vector comprising the polynucleotide encoding the CD70-specific CAR described herein.

[0074] In another aspect, the disclosure provides an engineered immune cell expressing at its cell-surface membrane a CD70-specific CAR described herein. In some embodiments, the engineered immune cell can comprise another CAR which is not specific for CD70. In some embodiments, the engineered immune cell can comprise a polynucleotide encoding a suicide polypeptide. In some embodiments, the suicide polypeptide is RQR8.

[0075] In some embodiments, the engineered immune is derived from an inflammatory T-lymphocyte, a cytotoxic T-lymphocyte, a regulatory T-lymphocyte, or a helper T-lymphocyte.

[0076] In some embodiments, the engineered immune cell can comprise a disruption one or more endogenous genes, wherein the endogenous gene encodes TCRα, TCRβ, CD52, glucocorticoid receptor (GR), deoxycytidine kinase (dCK), CD70 or an immune checkpoint protein such as for example programmed death-1 (PD-1).

[0077] In some embodiments, the engineered immune cell is obtained from a healthy donor. In some embodiments, the engineered immune cell is obtained from a patient.

[0078] In another aspect, the disclosure provides an engineered immune cell expressing at its cell-surface membrane a CD70-specific CAR as described herein for use as a medicament. In some embodiments, the medicament is for use in treatment of a cancer. In some embodiments, the medicament is for treatment of Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom's macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

[0079] In another aspect, the disclosure provides a method of engineering an immune cell comprising: providing an immune cell; and expressing at the surface of the cell at least one CD70-specific CAR as described herein. In some embodiments, the method comprises:

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providing an immune cell; introducing into the cell at least one polynucleotide encoding said CD70-specific CAR; and expressing said polynucleotide into the cell.

[0080] In some embodiments, the method comprises providing an immune cell; introducing into the cell at least one polynucleotide encoding said CD70-specific CAR; and introducing at least one other CAR which is not specific for CD70.

[0081] In another aspect, the disclosure provides a method of treating a subject suffering from a condition associated with malignant cells, the method comprising: providing a immune cell expressing at the surface a CD70-specific CAR as described herein; and administering said immune cells to said patient.

[0082] In another aspect, the disclosure provides a pharmaceutical composition comprising an engineered immune cell as described herein.

[0083] In another aspect, the disclosure provides a method of treating a condition associated with malignant cells expressing CD70 in a subject comprising administering to a subject in need thereof an effective amount of the pharmaceutical composition comprising an engineered immune cell as described herein. In some embodiments, the condition is a cancer. In some embodiments, the cancer is a Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom's macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

[0084] In another aspect, the disclosure provides a method of inhibiting tumor growth or progression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition comprising an engineered immune cell as described herein to the subject.

[0085] In another aspect, the disclosure provides a method of inhibiting metastasis of malignant cells expressing CD70 in a subject, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition comprising an engineered immune cell as described herein to the subject.

[0086] In another aspect, the disclosure provides a method of inducing tumor regression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition comprising an engineered immune cell as described herein to the subject.

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[0087] In some embodiments, any of the above methods further comprises administering one or more additional therapies, such as for example, a monoclonal antibody and/or a chemotherapeutic. In some embodiments, the monoclonal antibody can be, for example, an antibody that binds to a checkpoint inhibitor such as, for example, an anti-PD-1 antibody or an anti-PD-L1 antibody. In some embodiments, any of the above methods further comprises administering a Receptor Tyrosine Kinase inhibitor such as sunitinib or axitinib.

[0088] In some embodiments, the disclosure provides a CD70-specific CAR comprising an extracellular ligand-binding domain, a transmembrane domain, and an intracellular signaling domain, wherein the extracellular domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70 having a heavy chain variable (VH) region and a light chain variable (VL) region; wherein the VH region comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 18 and the VL region comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 17; or the VH region comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 34 and the VL region comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 33.

[0089] In some embodiments, the extracellular domain comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 319. In some embodiments, the extracellular domain comprises an amino acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 327.

[0090] In some embodiments, the disclosure provides a polynucleotide encoding a CD70-specific CAR, wherein the polynucleotide comprises a nucleic-acid sequence that shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 297 and shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 298; or shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 307 and shares at least 95%, 96%, 97%, 98%, 99%, ot 100% with SEQ ID NO: 308.

[0091] In some embodiments, the disclosure provides CAR comprising an antigen binding molecule that specifically binds to CD70, wherein the antigen binding molecule comprises at least one of: a variable heavy chain CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 49-51, 55-57, 61-63, 67-69, 73-75, 79-81, 85-87, 91-93, 97-99, 103-105, 109-111, 115-117, 121-123, 127-129, 133-135, 139-141, 145-147, 151-

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153, 157-159, 163-165, 169-171, 175-177, 181-183, 187-189, 382-384, 388-390, 394-396, 400-402, 406-408, 412-414, 418-420, 424-426, 430-432, 436-438, 442-444, 448-450, 454-456, 460-462, 466-468, 472-474, 478-480, 484-486, 490-492, 496-498, 502-504, and 508-510; a variable heavy chain CDR2 comprising an amino acid sequence selected from the group consisting of SEQ NOs 52, 53, 58, 59, 64, 65, 70, 71, 76, 77, 82, 83, 88, 89, 94, 95, 100, 101, 106, 107, 112, 113, 118, 119, 124, 125, 130, 131, 136, 137, 142, 143, 148, 149, 154, 155, 160, 161, 166, 167, 172, 173, 178, 179, 184, 185, 190, 191, 385, 386, 391, 392, 397, 398, 403, 404, 409, 410, 415, 416, 421, 422, 427, 428, 433, 434, 439, 440, 445, 446, 451, 452, 457, 458, 463, 464, 469, 470, 475, 476, 481, 482, 487, 488, 493, 494, 499, 500, 505, 506, 511, and 512; a variable heavy chain CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 387, 393, 399, 405, 411, 417, 423, 429, 435, 441, 447, 453, 459, 465, 471, 477, 483, 489, 495, 501, 507, and 513; a variable light chain CDR1 comprising an amino acid sequence selected from the group consisting of SEQ NOs: 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 235, 238, 241, 244, 247, 250, 253, 256, 259, 262, 514, 517, 520, 523, 526, 529, 532, 535, 538, 541, 544, 547, 550, 553, 556, 559, 562, 565, 568, 571, 574, and 577; a variable light chain CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs. 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 233, 236, 239, 242, 245, 248, 251, 254, 257, 260, 263, 515, 518, 521, 524, 527, 530, 533, 536, 539, 542, 545, 548, 551, 554, 557, 560, 563, 566, 569, 572, 575, and 578; and a variable light chain CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs. 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 234, 237, 240, 243, 246, 249, 252, 255, 258, 261, 264, 516, 519, 522, 525, 528, 531, 534, 537, 540, 543, 546, 549, 552, 555, 558, 561, 564, 567, 570, 573, 576, and 579.

[0092] In some embodiments, the antigen binding molecule comprises a variable heavy chain domain comprising amino acid sequences for CDRH1, CDRH2, and CDRH3, respectively, selected from one of SEQ ID NOs: 49-51, 52-53, 54; 55-57, 58-59, 60; 61-63, 64-65, 66; 67-69, 70-71, 72; 73-75, 76-77, 78; 79-81, 82-83, 84; 85-87, 88-89, 90; 91-93, 94-95, 96; 97-99, 100-101, 102; 103-105, 106-107, 108; 109-111, 112-113, 114; 115-117, 118-119, 120; 121-123, 124-125, 126; 127-129, 130-131, 132; 133-135, 136-137, 138; 139-141, 142-143, 144; 145-147, 148-149, 150; 151-153, 154-155, 156; 157-159, 160-161, 162; 163-165, 166-167,

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168; 169-171, 172-173, 174; 175-177, 178-179, 180; 181-183, 184-185, 186; 187-189, 190-191, 192; 382-384, 385-386, 387; 388-390, 391-392, 393; 394-396, 397-398, 399; 400-402, 403-404, 405; 406-408, 409-410, 411; 412-414, 415-416, 417; 418-420, 421-422, 423; 424-426, 427-428, 429; 430-432, 433-434, 435; 436-438, 439-440, 441; 442-444, 445-446, 447; 448-450, 451-452, 453; 454-456, 457-458, 459; 460-462, 463-464, 465; 466-468, 469-470, 471; 472-474, 475-476, 477; 478-480, 481-482, 483; 484-486, 487-488, 489; 490-492, 493-494, 495; 496-498, 499-500, 501; 502-504, 505-506, 507; or 508-510, 511-512, 513; and a variable light chain domain comprising amino acid sequences for CDRL1, CDRL2, and CDRL3, respectively, selected from one of SEQ ID NOs: 193, 194, 195; 196, 197, 198; 199, 200, 201; 202, 203, 204; 205, 206, 207; 208, 209, 210; 211, 212, 213; 214, 215, 216; 217, 218, 219; 220, 221, 222; 223, 224, 225; 226, 227, 228; 229, 230, 231; 232, 233, 234; 235, 236, 237; 238, 239, 240; 241, 242, 243; 244, 245, 246; 247, 248, 249; 250, 251, 252; 253, 254, 255; 256, 257, 258; 259, 260, 261; 262, 263, 264; 514, 515, 516; 517, 518, 519; 520, 521, 522; 523, 524, 525; 526, 527, 528; 529, 530, 531; 532, 533, 534; 535, 536, 537; 538, 539, 540; 541, 542, 543; 544, 545, 546; 547, 548, 549; 550, 551, 552; 553, 554, 555; 556, 557, 558; 559, 560, 561; 562, 563, 564; 565, 566, 567; 568, 569, 570; 571, 572, 573; 574, 575, 576; and 577, 578, 579.

[0093] In some embodiments, the antigen binding molecule comprises amino acid sequences for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and CDRL3, respectively, selected from one of SEQ ID NOs 49-51, 52-53, 54, 193, 194, 195; 55-57, 58-59, 60, 196, 197, 198; 61-63, 64-65, 66, 199, 200, 201; 67-69, 70-71, 72, 202, 203, 204; 73-75, 76-77, 78, 205, 206, 207; 79-81, 82-83, 84, 208, 209, 210; 85-87, 88-89, 90, 211, 212, 213; 91-93, 94-95, 96, 214, 215, 216; 97-99, 100-101, 102, 217, 218, 219; 103-105, 106-107, 108, 220, 221, 222; 109-111, 112-113, 114, 223, 224, 225; 115-117, 118-119, 120, 226, 227, 228; 121-123, 124-125, 126, 229, 230, 231; 127-129, 130-131, 132, 232, 233, 234; 133-135, 136-137, 138, 235, 236, 237; 139-141, 142-143, 144, 238, 239, 240; 145-147, 148-149, 150, 241, 242, 243; 151-153, 154-155, 156, 244, 245, 246; 157-159, 160-161, 162, 247, 248, 249; 163-165, 166-167, 168, 250, 251, 252; 169-171, 172-173, 174, 253, 254, 255; 175-177, 178-179, 180, 256, 257, 258; 181-183, 184-185, 186, 259, 260, 261; 187-189, 190-191, 192, 262, 263, 264; 382-384, 385-386, 387, 514, 515, 516; 388-390, 391-392, 393, 517, 518, 519; 394-396, 397-398, 399, 520, 521, 522; 400-402, 403-404, 405, 523, 524, 525; 406-408, 409-410, 411, 526, 527, 528; 412-414, 415-416, 417, 529, 530, 531; 418-420, 421-422, 423, 532, 533, 534; 424-426, 427-428, 429,

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535, 536, 537; 430-432, 433-434, 435, 538, 539, 540; 436-438, 439-440, 441, 541, 542, 543; 442-444, 445-446, 447, 544, 545, 546; 448-450, 451-452, 453, 547, 548, 549; 454-456, 457-458, 459, 550, 551, 552; 460-462, 463-464, 465, 553, 554, 555; 466-468, 469-470, 471, 556, 557, 558; 472-474, 475-476, 477, 559, 560, 561; 478-480, 481-482, 483, 562, 563, 564; 484-486, 487-488, 489, 565, 566, 567; 490-492, 493-494, 495, 568, 569, 570; 496-498, 499-500, 501, 571, 572, 573; 502-504, 505-506, 507, 574, 575, 576; and 508-510, 511-512, 513, 577, 578, 579.

[0094] In some embodiments, the antigen binding molecule comprises a variable light chain domain comprising an amino acid sequences for CDRH1, CDRH2, and CDRH3, respectively, selected from one of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, and 380; and a variable heavy chain domain comprising amino acid sequences for CDRL1, CDRL2, and CDRH3, respectively, selected from one of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, and 381.

[0095] In some embodiments, the antigen binding molecule comprises amino acid sequences for light chain variable domain and heavy chain variable domain, respectively, selected from one of SEQ ID NOs: 1 and 2; 3 and 4; 5 and 6; 7 and 8; 9 and 10; 11 and 12; 13 and 14; 15 and 16; 17 and 18; 19 and 20; 21 and 22; 23 and 24; 25 and 26; 27 and 28; 29 and 30; 31 and 32; 33 and 34; 35 and 36; 37 and 38; 39 and 40; 41 and 42; 43 and 44; 45 and 46; 47 and 48; 338 and 339; 340 and 341; 342 and 343; 344 and 345; 346 and 347; 348 and 349; 350 and 351; 352 and 353; 354 and 355; 356 and 357; 358 and 359; 360 and 361; 362 and 363; 364 and 365; 366 and 367; 368 and 369; 370 and 371; 372 and 373; 374 and 375; 376 and 377; 378 and 379; and 380 and 381.

[0096] In another aspect, the disclosure provides antibodies, which specifically bind to Cluster of Differentiation 70 (CD70).

[0097] In some embodiments, the antibody comprises a VH region shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 662, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, or 381; and/or a VL region shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19,

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21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 661, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, or 380.

[0098] In some embodiments, the antibody comprises a heavy chain variable (VH) region comprising (i) a VH CDR1 comprising the sequence shown in SEQ ID NO: 49, 50, 51, 55, 56, 57, 61, 62, 63, 67, 68, 69, 73, 74, 75, 79, 80, 81, 85, 86, 87, 91, 92, 93, 97, 98, 99, 103, 104, 105, 109, 110, 111, 115, 116, 117, 121, 122, 123, 127, 128, 129, 133, 134, 135, 139, 140, 141, 145, 146, 147, 151, 152, 153, 157, 158, 159, 163, 164, 165, 169, 170, 171, 175, 176, 177, 181, 182, 183, 187, 188, 189, 382, 383, 384, 388, 389, 390, 394, 395, 396, 400, 401, 402, 406, 407, 408, 412, 413, 414, 418, 419, 420, 424, 425, 426, 430, 431, 432, 663, 664, 665, 436, 437, 438, 442, 443, 444, 448, 449, 450, 454, 455, 456, 460, 461, 462, 466, 467, 468, 472, 473, 474, 478, 479, 480, 484, 485, 486, 490, 491, 492, 496, 497, 498, 502, 503, 504, 508, 509, or 510; (ii) a VH CDR2 comprising the sequence shown in SEQ ID NO: 52, 53, 58, 59, 64, 65, 70, 71, 76, 77, 82, 83, 88, 89, 94, 95, 100, 101, 106, 107, 112, 113, 118, 119, 124, 125, 130, 131, 136, 137, 142, 143, 148, 149, 154, 155, 160, 161, 166, 167, 172, 173, 178, 179, 184, 185, 190, 191, 385, 386, 391, 392, 397, 398, 403, 404, 409, 410, 415, 416, 421, 422, 427, 428, 433, 434, 666, 667, 439, 440, 445, 446, 451, 452, 457, 458, 463, 464, 469, 470, 475, 476, 481, 482, 487, 488, 493, 494, 499, 500, 505, 506, 511, or 512; and iii) a VH CDR3 comprising the sequence shown in SEQ ID NO: 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 387, 393, 399, 405, 411, 417, 423, 429, 435, 668, 441, 447, 453, 459, 465, 471, 477, 483, 489, 495, 501, 507, or 513; and/or a light chain variable (VL) region comprising (i) a VL CDR1 comprising the sequence shown in SEQ ID NO: 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 235, 238, 241, 244, 247, 250, 253, 256, 259, 262, 514, 517, 520, 523, 526, 529, 532, 535, 538, 669, 541, 544, 547, 550, 553, 556, 559, 562, 565, 568, 571, 574, or 577; (ii) a VL CDR2 comprising the sequence shown in SEQ ID NO: 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 233, 236, 239, 242, 245, 248, 251, 254, 257, 260, 263, 515, 518, 521, 524, 527, 530, 533, 536, 539, 670, 542, 545, 548, 551, 554, 557, 560, 563, 566, 569, 572, 575, or 578; and (iii) a VL CDR3 comprising the sequence shown in SEQ ID NO: 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 234, 237, 240, 243, 246, 249, 252, 255, 258, 261, 264, 516, 519, 522, 525, 528, 531, 534, 537, 540, 671, 543, 546, 549, 552, 555, 558, 561, 564, 567, 570, 573, 576, or 579.

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[0099] In some embodiments, the antibody comprises a VH region comprising a VH CDR1, VH CDR2, and VH CDR3 of the VH sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 662, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, or 381; and/or a VL region comprising VL CDR1, VL CDR2, and VL CDR3 of the VL sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 661, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, or 380.

[00100] In yet further aspects, the disclosure provides nucleic acids, vectors, host cells, pharmaceutical compositions, methods of making, and method of treating conditions with the antibodies disclosed.

BRIEF DESCRIPTION OF THE DRAWINGS

[00101] FIG. 1 is a plot showing. 1 tumor volumes of mice treated with different doses of 4F11 CAR T-cells in a subcutaneous xenograft model.

[0100] FIG. 2 is a plot showing body weights of mice treated with different doses of 4F11 CAR T-cells in a subcutaneous xenograft model.

[0101] FIG. 3 is a plot showing tumor volumes of mice treated with 4F11 and P08F08 CAR T with or without CD70 KO in a subcutaneous xenograft model.

[0102] FIG. 4 is a plot showing body weights of mice treated with 4F11 and P08F08 CAR T with or without CD70 KO in a subcutaneous xenograft model.

[0103] FIGs. 5A-5C is a series of plots showing tumor flux values of mice treated with control cells, cells expressing the CAR 4F11 with or without CD70 KO and with or without TCRa KO, and mice treated with cells expressing the CAR P08F08 with or without CD70 KO and with or without TCRa KO, across 3 donors in the ACHN lung metastasis model.

[0104] FIG. 5A shows results obtained with control cells, cells expressing the 4F11 CAR with CD70, TCRa or both CD70 and TCR KOs, and cells expressing the P08F08 CAR with TCR KO; cells were obtained from Donor D419.

[0105] FIG. 5B shows results obtained with control cells, cells expressing the 4F11 CAR with or without a CD70 KO, and cells expressing the P08F08 CAR; cells were obtained from Donor D710.

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[0106] FIG. 5C shows results obtained with control cells, cells expressing the 4F11 CAR with or without a CD70 KO, and cells expressing the P08F08 CAR; cells were obtained from Donor D503.

[0107] FIGs. 6A-6F show five exemplary, non-limiting CAR designs. In each of FIGs. 6A-6F an approximate distance of the antigen-binding fragment of the CD70-specific domain to the cell membrane is indicated by a double arrow, labeled with the number of amino-acid residues (aa) between the scFv and the transmembrane domain.

[0108] FIG. 6A shows a second-generation CAR design including an extracellular domain comprising an scFv specific for CD70, a hinge, a transmembrane domain, a first intracellular domain (a 4-1BB domain), and a second intracellular domain (a CD3ζ signaling domain).

[0109] FIG. 6B shows the SR2 CAR format in which a suicide switch is created by the insertion of two RTX epitopes (*i.e.* CD20 epitopes) between the hinge and the scFv.

[0110] FIG. 6C shows the RSRQR CAR format, which adds a third RTX epitope and the CD34 epitope.

[0111] FIG. 6D shows the RSR format, which two RTX epitopes flanking the scFv.

[0112] FIG. 6E shows a modification of the RSR CAR format in which the hinge domain is shorten (termed RSR-short).

[0113] FIG. 6F shows the R2S CAR format, in which the two RTX epitopes of the R2 CAR format are moved to N-terminal to the scFv.

[0114] FIG. 7 shows viability of target cells after exposure to the CD70-specific CARs in four formats or non-transduced (NTD) control cells.

[0115] FIGs. 8A-8D is a series of plots showing cell killing of 786-0, ACHN, or REH cells using CD70-specific CAR T cells where the CAR extracellular domain comprises the scFvs indicated in the legend in FIG. 8D.

[0116] FIG. 8A shows cell killing of 786-0, where the CAR extracellular domain comprises the scFvs indicated in the legend shown in FIG. 8D.

[0117] FIG. 8B shows cell killing of ACHN, where the CAR extracellular domain comprises the scFvs indicated in the legend shown in FIG. 8D.

[0118] FIG. 8C shows cell killing of REH, where the CAR extracellular domain comprises the scFvs indicated in the legend shown in FIG. 8D.

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[0119] FIGs. 9A-9D are a series of plots showing serial killing of 786-0, ACHN, or REH cells using CD70-specific CAR T cells where the CAR extracellular domain comprises the scFvs indicated in the legend in Figure 9D.

[0120] FIG. 9A is a plot showing the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled 786-O target cells (CAR T cells were transferred to a 96-well plate containing fresh targets every 2-3 days). The E:T ratio was 3:1. The CARs were expressed in cells from donor D503.

[0121] FIG. 9B is a plot showing the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled ACHN target cells (CAR T cells were transferred to a 96-well plate containing fresh targets every 2-3 days). The E:T ratio was 10:1. The CARs were expressed in cells from donor D503.

[0122] FIG. 9C is a plot showing the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled REH target cells ($2x10^6$ cells added at indicated time-points). The E:T ratio was 1:5. The CARs were expressed in cells from donor D503.

[0123] FIG. 10 is a series of plots showing the efficacy of CD70-specific CARs in either R2S, SR2, or RSRQR format upon repeated exposure to luciferase-labeled REH target cells ($2x10^6$ cells added at indicated time-points). The E:T ratio was 1:5. The CARs were expressed in cells from donor D772.

[0124] FIG. 11 is a plot showing tumor flux values of mice treated with control cells or cells expressing various CAR scFvs in the ACHN lung metastasis model.

[0125] FIGs. 12A-12C is a series of plots showing the quantification of CD70 expression in terms of CD70 antibody binding capacity (ABC) on various tested cell lines or cell lines and RCC patient-derived cells. The data from RCC patient-derived cells is also shown.

[0126] FIG. 12A shows the quantification of CD70 expression in terms of CD70 antibody binding capacity (ABC) on various tested cell lines.

[0127] FIG. 12B shows the quantification of CD70 expression in terms of CD70 antibody binding capacity (ABC) on RCC patient-derived cells.

[0128] FIG. 12C shows the data from RCC patient-derived cells.

[0129] FIGs. 13A-13C is a series of plots showing killing of target cells from RCC patient WD-59279, patient-derived cell lines, or ACHN and antibody binding capacity is indicated in each panel.

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[0130] FIG. 13A-B show killing of target cells from RCC patients, and antibody binding capacity.

[0131] FIG. 13C shows killing of target ACHN cells, and antibody binding capacity.

[0132] FIGs. 14A-14B is a series of bar graphs showing quantification of CD70 receptor numbers and heme tumor-cell killing by 4F11 CAR in the QR3 format at 1:1 E:T for further cell lines expressing CD70 at varied levels.

[0133] FIG. 14A is a bar graph showing quantification of CD70 receptor numbers of the 4F11 CAR in the QR3 format at 1:1 E:T for further cell lines expressing CD70 at varied levels.

[0134] FIG. 14B is a bar graph showing heme tumor-cell killing by 4F11 CAR in the QR3 format at 1:1 E:T for further cell lines expressing CD70 at varied levels.

[0135] FIGs. 15A-15B show is a series of plots showing tumor volumes and body weights of mice treated with 4F11 and P08F08 CAR T at $10x10^6$ cell or $5x10^6$ cell dose in a subcutaneous xenograft model.

[0136] FIG. 15A is a plot showing tumor volumes of mice treated with 4F11 and P08F08 CAR T at $10x10^6$ cell or $5x10^6$ cell dose in a subcutaneous xenograft model.

[0137] FIG. 15B is a plot showing body weights of mice treated with 4F11 and P08F08 CAR T at $10x10^6$ cell or $5x10^6$ cell dose in a subcutaneous xenograft model.

DETAILED DESCRIPTION

[0138] The disclosure disclosed herein provides chimeric antigen receptors (CARs) and immune cells comprising CARs (*e.g.* CAR-T cells) that specifically bind to CD70 (*e.g.*, human CD70). The disclosure also provides polynucleotides encoding these CARs, compositions comprising these CAR-T cells, and methods of making and using these CARs and CAR-T cells. The disclosure also provides methods for treating a condition associated with malignant CD70 expression in a subject, such as cancer.

General Techniques

[0139] The compositions and methods of the disclosure will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, Molecular Cloning: A Laboratory Manual, second edition (Sambrook et al., 1989) Cold Spring Harbor Press; Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Methods in Molecular Biology, Humana

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Press; Cell Biology: A Laboratory Notebook (J.E. Cellis, ed., 1998) Academic Press; Animal Cell Culture (R.I. Freshney, ed., 1987); Introduction to Cell and Tissue Culture (J.P. Mather and P.E. Roberts, 1998) Plenum Press; Cell and Tissue Culture: Laboratory Procedures (A. Doyle, J.B. Griffiths, and D.G. Newell, eds., 1993-1998) J. Wiley and Sons; Methods in Enzymology (Academic Press, Inc.); Handbook of Experimental Immunology (D.M. Weir and C.C. Blackwell, eds.); Gene Transfer Vectors for Mammalian Cells (J.M. Miller and M.P. Calos, eds., 1987); Current Protocols in Molecular Biology (F.M. Ausubel et al., eds., 1987); PCR: The Polymerase Chain Reaction, (Mullis et al., eds., 1994); Current Protocols in Immunology (J.E. Coligan et al., eds., 1991); Short Protocols in Molecular Biology (Wiley and Sons, 1999); Immunobiology (C.A. Janeway and P. Travers, 1997); Antibodies (P. Finch, 1997); Antibodies: a practical approach (D. Catty., ed., IRL Press, 1988-1989); Monoclonal antibodies: a practical approach (P. Shepherd and C. Dean, eds., Oxford University Press, 2000); Using antibodies: a laboratory manual (E. Harlow and D. Lane (Cold Spring Harbor Laboratory Press, 1999); The Antibodies (M. Zanetti and J.D. Capra, eds., Harwood Academic Publishers, 1995).

Definitions

[0140] The term "extracellular ligand-binding domain" as used herein refers to an oligo- or polypeptide that is capable of binding a ligand. In some exemplary embodiments, the domain will be capable of interacting with a cell surface molecule. For example, the extracellular ligand-binding domain may be chosen to recognize a ligand that acts as a cell surface marker on target cells associated with a particular disease state.

[0141] The term "stalk domain" or "hinge domain" are used interchangeably herein to refer to any oligo- or polypeptide that functions to link the transmembrane domain to the extracellular ligand-binding domain in a CAR. In particular, stalk domains are used to provide more flexibility and accessibility for the extracellular ligand-binding domain.

[0142] The term "intracellular signaling domain" refers to the portion of a protein which transduces the effector signal function signal and directs the cell to perform a specialized function.

[0143] A "co-stimulatory molecule" as used herein refers to the cognate binding partner on an immune cell, *e.g.*, a T cell, that specifically binds with a co-stimulatory ligand, thereby mediating a co-stimulatory response by the cell, such as, but not limited to proliferation. Co-stimulatory molecules include, but are not limited to an MHC class I molecule, BTLA and

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Toll ligand receptor. Examples of costimulatory molecules include CD27, CD28, CD8, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3 and a ligand that specifically binds with CD83 and the like.

[0144] A "co-stimulatory ligand" refers to a molecule on an antigen presenting cell that specifically binds a cognate co-stimulatory signal molecule on an immune cell, *e.g.*, a T cell, thereby providing a signal which, in addition to the primary signal provided by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, mediates a T cell response, including, but not limited to, proliferation activation, differentiation and the like. A co-stimulatory ligand can include but is not limited to CD7, B7-1 (CD80), B7-2 (CD86), PD-L1, PD-L2, 4-1BBL, OX40L, inducible costimulatory igand (ICOS-L), intercellular adhesion molecule (ICAM, CD30L, CD40, CD70, CD83, HLA-G, MICA, M1CB, HVEM, lymphotoxin β receptor, 3/TR6, ILT3, ILT4, an agonist or antibody that binds Toll ligand receptor and a ligand that specifically binds with B7-H3. A co-stimulatory ligand also encompasses, inter alia, an antibody that specifically binds with a co-stimulatory molecule present on a T cell, such as but not limited to, CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LTGHT, NKG2C, B7-H3, a ligand that specifically binds with CD83.

[0145] An "antibody" is an immunoglobulin molecule capable of specific binding to a target, such as a carbohydrate, polynucleotide, lipid, polypeptide, etc., through at least one antigen recognition site, located in the variable region of the immunoglobulin molecule. As used herein, the term encompasses not only intact polyclonal or monoclonal antibodies, but also fragments thereof (such as Fab, Fab', $F(ab')_2$, Fv), single chain (scFv) and domain antibodies (including, for example, shark and camelid antibodies), and fusion proteins comprising an antibody, and any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site. An antibody includes an antibody of any class, such as IgG, IgA, IgE, IgD, or IgM (or sub-class thereof), and the antibody need not be of any particular class. Depending on the antibody amino acid sequence of the constant region of its heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2. The heavy-chain constant regions that correspond to the different classes of immunoglobulins are

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called alpha, delta, epsilon, gamma, and mu, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

[0146] The term "antigen binding fragment" or "antigen binding portion" of an antibody, as used herein, refers to one or more fragments of an intact antibody that retain the ability to specifically bind to a given antigen (*e.g.*, CD70). Antigen binding functions of an antibody can be performed by fragments of an intact antibody. Examples of binding fragments encompassed within the term "antigen binding fragment" of an antibody include Fab; Fab'; $F(ab')_2$; an Fd fragment consisting of the VH and CH1 domains; an Fv fragment consisting of the VL and VH domains of a single arm of an antibody; a single domain antibody (dAb) fragment (Ward et al., Nature 341:544-546, 1989), and an isolated complementarity determining region (CDR).

[0147] An antibody, an antigen-binding fragment, an antibody conjugate, or a polypeptide that "preferentially binds" or "specifically binds" (used interchangeably herein) to a target (*e.g.*, CD70 protein) is a term well understood in the art, and methods to determine such specific or preferential binding are also well known in the art. A molecule is said to exhibit "specific binding" or "preferential binding" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance than it does with alternative cells or substances. An antibody "specifically binds" or "preferentially binds" to a target if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances. For example, an antibody that specifically or preferentially binds to a CD70 epitope is an antibody that binds this epitope with greater affinity, avidity, more readily, and/or with greater duration than it binds to other CD70 epitopes or non-CD70 epitopes. It is also understood that by reading this definition, for example, an antibody (or moiety or epitope) that specifically or preferentially binds to a first target may or may not specifically or preferentially bind to a second target. As such, "specific binding" or "preferential binding" does not necessarily require (although it can include) exclusive binding. Generally, but not necessarily, reference to binding means preferential binding.

[0148] A "variable region" of an antibody refers to the variable region of the antibody light chain or the variable region of the antibody heavy chain, either alone or in combination. As known in the art, the variable regions of the heavy and light chain each consist of four framework regions (FR) connected by three complementarity determining regions (CDRs)

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also known as hypervariable regions. The CDRs in each chain are held together in close proximity by the FRs and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies. There are at least two techniques for determining CDRs: (1) an approach based on cross-species sequence variability (*i.e.*, Kabat et al. Sequences of Proteins of Immunological Interest, (5th ed., 1991, National Institutes of Health, Bethesda MD); and (2) an approach based on crystallographic studies of antigen-antibody complexes (Al-lazikani et al., 1997, J. Molec. Biol. 273:927-948). As used herein, a CDR may refer to CDRs defined by either approach or by a combination of both approaches.

[0149] A "CDR" of a variable domain are amino acid residues within the variable region that are identified in accordance with the definitions of the Kabat, Chothia, the accumulation of both Kabat and Chothia, AbM, contact, and/or conformational definitions or any method of CDR determination well known in the art. Antibody CDRs may be identified as the hypervariable regions originally defined by Kabat et al. See, *e.g.*, Kabat et al., 1992, Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, NIH, Washington D.C. The positions of the CDRs may also be identified as the structural loop structures originally described by Chothia and others. See, *e.g.*, Chothia et al., Nature 342:877-883, 1989. Other approaches to CDR identification include the "AbM definition," which is a compromise between Kabat and Chothia and is derived using Oxford Molecular's AbM antibody modeling software (now Accelrys®), or the "contact definition" of CDRs based on observed antigen contacts, set forth in MacCallum et al., J. Mol. Biol., 262:732-745, 1996. In another approach, referred to herein as the "conformational definition" of CDRs, the positions of the CDRs may be identified as the residues that make enthalpic contributions to antigen binding. See, *e.g.*, Makabe et al., Journal of Biological Chemistry, 283:1156-1166, 2008. Still other CDR boundary definitions may not strictly follow one of the above approaches, but will nonetheless overlap with at least a portion of the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. As used herein, a CDR may refer to CDRs defined by any approach known in the art, including combinations of approaches. The methods used herein may utilize CDRs defined according to any of these approaches. For any given embodiment containing more than one CDR, the CDRs may be defined in accordance with any of Kabat, Chothia, extended, AbM, contact, and/or conformational definitions.

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[0150] As used herein, "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the disclosure may be made by the hybridoma method first described by Kohler and Milstein, Nature 256:495, 1975, or may be made by recombinant DNA methods such as described in U.S. Pat. No. 4,816,567. The monoclonal antibodies may also be isolated from phage libraries generated using the techniques described in McCafferty et al., Nature 348:552-554, 1990, for example.

[0151] As used herein, "humanized" antibody refers to forms of non-human (*e.g.* murine) antibodies that are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen binding subsequences of antibodies) that contain minimal sequence derived from non-human immunoglobulin. In some exemplary embodiments, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementarity determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, the humanized antibody may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences, but are included to further refine and optimize antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region or domain (Fc), typically that of a

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human immunoglobulin. Exemplary embodiments are antibodies having Fc regions modified as described in WO 99/58572. Other forms of humanized antibodies have one or more CDRs (CDR L1, CDR L2, CDR L3, CDR H1, CDR H2, or CDR H3) which are altered with respect to the original antibody, which are also termed one or more CDRs "derived from" one or more CDRs from the original antibody.

[0152] As used herein, "human antibody" means an antibody having an amino acid sequence corresponding to that of an antibody produced by a human and/or which has been made using any of the techniques for making human antibodies known to those skilled in the art or disclosed herein. This definition of a human antibody includes antibodies comprising at least one human heavy chain polypeptide or at least one human light chain polypeptide. One such example is an antibody comprising murine light chain and human heavy chain polypeptides. Human antibodies can be produced using various techniques known in the art. In some embodiments, the human antibody is selected from a phage library, where that phage library expresses human antibodies (Vaughan et al., Nature Biotechnology, 14:309-314, 1996; Sheets et al., Proc. Natl. Acad. Sci. (USA) 95:6157-6162, 1998; Hoogenboom and Winter, J. Mol. Biol., 227:381, 1991; Marks et al., J. Mol. Biol., 222:581, 1991). Human antibodies can also be made by immunization of animals into which human immunoglobulin loci have been transgenically introduced in place of the endogenous loci, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely disrupted or inactivated. This approach is described in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; and 5,661,016. Alternatively, the human antibody may be prepared by immortalizing human B lymphocytes that produce an antibody directed against a target antigen (such B lymphocytes may be recovered from an individual or from single cell cloning of the cDNA, or may have been immunized *in vitro).* See, *e.g.*, Cole et al. Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77, 1985; Boerner et al., J. Immunol., 147 (1):86-95, 1991; and U.S. Pat. No. 5,750,373.

[0153] The term "chimeric antibody" is intended to refer to antibodies in which the variable region sequences are derived from one species and the constant region sequences are derived from another species, such as an antibody in which the variable region sequences are derived from a mouse antibody and the constant region sequences are derived from a human antibody.

[0154] The terms "polypeptide", "oligopeptide", "peptide," and "protein" are used interchangeably herein to refer to chains of amino acids of any length—in some

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embodiments, relatively short (*e.g.*, 10-100 amino acids). The chain may be linear or branched, it may comprise modified amino acids, and/or may be interrupted by non-amino acids. The terms also encompass an amino acid chain that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), as well as other modifications known in the art. It is understood that the polypeptides can occur as single chains or associated chains.

[0155] A "monovalent antibody" comprises one antigen binding site per molecule (*e.g.*, IgG or Fab). In some instances, a monovalent antibody can have more than one antigen binding sites, but the binding sites are from different antigens.

[0156] A "bivalent antibody" comprises two antigen binding sites per molecule (*e.g.*, IgG). In some instances, the two binding sites have the same antigen specificities. However, bivalent antibodies may be bispecific.

[0157] Antibodies of the disclosure can be produced using techniques well known in the art, *e.g.*, recombinant technologies, phage display technologies, synthetic technologies or combinations of such technologies or other technologies readily known in the art (see, for example, Jayasena, S.D., Clin. Chem., 45: 1628-50, 1999 and Fellouse, F.A., et al, J. MoI. Biol., 373(4):924-40, 2007).

[0158] As known in the art, "polynucleotide" or "nucleic acid," as used interchangeably herein, refer to chains of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a chain by DNA or RNA polymerase. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the chain. 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. Other types of modifications include, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.) and with charged

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linkages (*e.g.*, phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (*e.g.*, nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (*e.g.*, acridine, psoralen, etc.), those containing chelators (*e.g.*, metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (*e.g.*, alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s). Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carbocyclic sugar analogs, alpha- or beta-anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside. One or more phosphodiester linkages may be replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S("thioate"), P(S)S ("dithioate"), (O)NR_2 ("amidate"), P(O)R, P(O)OR', CO or CH_2 ("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl (1-20 C) optionally containing an ether (-O-) linkage, aryl, alkenyl, cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical. The preceding description applies to all polynucleotides referred to herein, including RNA and DNA.

[0159] As known in the art a "constant region" of an antibody refers to the constant region of the antibody light chain or the constant region of the antibody heavy chain, either alone or in combination.

[0160] As used herein, "substantially pure" refers to material which is at least 50% pure (*i.e.*, free from contaminants), at least 90% pure, at least 95% pure, at least 98% pure, or at least 99% pure.

[0161] A "host cell" includes an individual cell or cell culture that can be or has been a recipient for vector(s) for incorporation of polynucleotide inserts. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology

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or in genomic DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in vivo with a polynucleotide(s) of this disclosure.

[0162] As used herein, "immune cell" refers to a cell of hematopoietic origin functionally involved in the initiation and/or execution of innate and/or adaptative immune response.

[0163] As known in the art, the term "Fc region" is used to define a C-terminal region of an immunoglobulin heavy chain. The "Fc region" may be a native sequence Fc region or a variant Fc region. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc region is usually defined to stretch from an amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof. The numbering of the residues in the Fc region is that of the EU index as in Kabat. Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991. The Fc region of an immunoglobulin generally comprises two constant regions, CH2 and CH3.

[0164] As used in the art, "Fc receptor" and "FcR" describe a receptor that binds to the Fc region of an antibody. In some embodiments, the FcR is a native sequence human FcR. Moreover, in some embodiments, the FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. FcRs are reviewed in Ravetch and Kinet, Ann. Rev. Immunol., 9:457-92, 1991; Capel et al., Immunomethods, 4:25-34, 1994; and de Haas et al., J. Lab. Clin. Med., 126:330-41, 1995. "FcR" also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol., 117:587, 1976; and Kim et al., J. Immunol., 24:249, 1994).

[0165] The term "compete", as used herein with regard to an antibody, means that a first antibody, or an antigen binding fragment (or portion) thereof, binds to an epitope in a manner sufficiently similar to the binding of a second antibody, or an antigen binding portion thereof, such that the result of binding of the first antibody with its cognate epitope is detectably decreased in the presence of the second antibody compared to the binding of the first antibody in the absence of the second antibody. The alternative, where the binding of the second

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antibody to its epitope is also detectably decreased in the presence of the first antibody, can, but need not be the case. That is, a first antibody can inhibit the binding of a second antibody to its epitope without that second antibody inhibiting the binding of the first antibody to its respective epitope. However, where each antibody detectably inhibits the binding of the other antibody with its cognate epitope or ligand, whether to the same, greater, or lesser extent, the antibodies are said to "cross-compete" with each other for binding of their respective epitope(s). Both competing and cross-competing antibodies are encompassed by the disclosure. Regardless of the mechanism by which such competition or cross-competition occurs (*e.g.*, steric hindrance, conformational change, or binding to a common epitope, or portion thereof), the skilled artisan would appreciate, based upon the teachings provided herein, that such competing and/or cross-competing antibodies are encompassed and can be useful for the methods disclosed herein.

[0166] As used herein "autologous" means that cells, a cell line, or population of cells used for treating patients are originating from said patient.

[0167] As used herein "allogeneic" means that cells or population of cells used for treating patients are not originating from said patient but from a donor.

[0168] As used herein, "treatment" is an approach for obtaining beneficial or desired clinical results. For purposes of this disclosure, beneficial or desired clinical results include, but are not limited to, one or more of the following: reducing the proliferation of (or destroying) neoplastic or cancerous cells, inhibiting metastasis of neoplastic cells, shrinking or decreasing the size of CD70 expressing tumor such as a renal cell carcinoma (RCC) lymphoma, leukemia, or glioma, remission of a CD70 associated disease (*e.g.*, cancer), decreasing symptoms resulting from a CD70 associated disease (*e.g.*, cancer), increasing the quality of life of those suffering from a CD70 associated disease (*e.g.*, cancer), decreasing the dose of other medications required to treat a CD70 associated disease (*e.g.*, cancer), delaying the progression of a CD70 associated disease (*e.g.*, cancer), curing a CD70 associated disease (e..g, cancer), and/or prolong survival of patients having a CD70 associated disease (*e.g.*, cancer).

[0169] "Ameliorating" means a lessening or improvement of one or more symptoms as compared to not administering a CD70-specific CAR or a CD70-specific CAR-T-cell. "Ameliorating" also includes shortening or reduction in duration of a symptom.

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[0170] As used herein, an "effective dosage" or "effective amount" of drug, compound, or pharmaceutical composition is an amount sufficient to effect any one or more beneficial or desired results. For prophylactic use, beneficial or desired results include eliminating or reducing the risk, lessening the severity, or delaying the onset of the disease, including biochemical, histological and/or behavioral symptoms of the disease, its complications and intermediate pathological phenotypes presenting during development of the disease. For therapeutic use, beneficial or desired results include clinical results such as reducing incidence or amelioration of one or more symptoms of various CD70 associated diseases or conditions (such as for example multiple myeloma), decreasing the dose of other medications required to treat the disease, enhancing the effect of another medication, and/or delaying the progression of the CD70 associated disease of patients. An effective dosage can be administered in one or more administrations. For purposes of this disclosure, an effective dosage of drug, compound, or pharmaceutical composition is an amount sufficient to accomplish prophylactic or therapeutic treatment either directly or indirectly. As is understood in the clinical context, an effective dosage of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition. Thus, an "effective dosage" may be considered in the context of administering one or more therapeutic agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved.

[0171] An "individual," "patient," or a "subject" is a mammal—in some embodiments, a human. Mammals include, but are not limited to, humans, monkeys, pigs, and other farm animals, sport animals, pets, primates, horses, dogs, cats, rodents including mice, rats, guinea pigs, etc. A subject is a mammal and the terms are used interchangeably herein. In some embodiments, the subject is a human. In some embodiments, the subject is a non-human primate. In some embodiments, the subject is a human or a monkey, *e.g.*, a cynomolgus monkey.

[0172] As used herein, "vector" means a construct, which is capable of delivering, and, in some embodiments, expressing, one or more gene(s) or sequence(s) of interest in a host cell. Examples of vectors include, but are not limited to, viral vectors, naked DNA or RNA expression vectors, plasmid, cosmid or phage vectors, DNA or RNA expression vectors associated with cationic condensing agents, DNA or RNA expression vectors encapsulated in liposomes, and certain eukaryotic cells, such as producer cells.

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[0173] As used herein, "expression control sequence" means a nucleic acid sequence that directs transcription of a nucleic acid. An expression control sequence can be a promoter, such as a constitutive or an inducible promoter, or an enhancer. The expression control sequence is operably linked to the nucleic acid sequence to be transcribed.

[0174] As used herein, "pharmaceutically acceptable carrier" or "pharmaceutical acceptable excipient" includes any material which, when combined with an active ingredient, allows the ingredient to retain biological activity and is non-reactive with the subject's immune system. Examples include, but are not limited to, any of the standard pharmaceutical carriers such as a phosphate buffered saline solution, water, emulsions such as oil/water emulsion, and various types of wetting agents. Exemplary diluents for aerosol or parenteral administration are phosphate buffered saline (PBS) or normal (0.9%) saline. Compositions comprising such carriers are formulated by well known conventional methods (see, for example, Remington's Pharmaceutical Sciences, 18th edition, A. Gennaro, ed., Mack Publishing Co., Easton, PA, 1990; and Remington, The Science and Practice of Pharmacy 21st Ed. Mack Publishing, 2005).

[0175] The term "k_{on}", as used herein, refers to the rate constant for association of an antibody or scFv or CAR to an antigen.

[0176] The term "k_{off}", as used herein, refers to the rate constant for dissociation of an antibody or scFv or CAR from the antibody/antigen complex.

[0177] The term "K_D", as used herein, refers to the equilibrium dissociation constant of an antibody-antigen or scFv-antigen or CAR-antigen interaction.

[0178] Reference to "about" a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter per se. For example, description referring to "about X" includes description of "X." Numeric ranges are inclusive of the numbers defining the range.

[0179] It is understood that wherever embodiments are described herein with the language "comprising," otherwise analogous embodiments described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0180] Where aspects or embodiments of the invention are described in terms of a Markush group or other grouping of alternatives, the invention encompasses not only the entire group listed as a whole, but each member of the group individually and all possible subgroups of the main group, but also the main group absent one or more of the group members. The

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invention also envisages the explicit exclusion of one or more of any of the group members in the claimed invention.

[0181] Unless otherwise defined, 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. In case of conflict, the present specification, including definitions, will control. Throughout this specification and claims, the word "comprise," or variations such as "comprises" or "comprising" will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[0182] Exemplary methods and materials are described herein, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the invention. The materials, methods, and examples are illustrative only and not intended to be limiting.

CD70-SPECIFIC CARS AND METHODS OF MAKING THEREOF

[0183] The instant disclosure provides CARs that bind to CD70 (*e.g.*, human CD70 (*e.g.*, SEQ ID NO: 335), such as those deposited under the provisions of the Budapest Treaty and assigned accession number: P32970-1. CD70-specific CARs provided herein include single chain CARS and multichain CARs. In some embodiments, the CARs have the ability to redirect T cell specificity and reactivity toward CD70 in a non-MHC-restricted manner, exploiting the antigen-binding properties of monoclonal antibodies. The non-MHC-restricted antigen recognition gives T cells expressing CARs the ability to recognize an antigen independent of antigen processing, thus bypassing a major mechanism of tumor escape.

[0184] In some embodiments, CARs provided herein comprise an extracellular ligand-binding domain (*e.g.*, a single chain variable fragment (scFv)), a transmembrane domain, and an intracellular signaling domain. In some embodiments, the CARs provided herein further comprises a "hinge" or "stalk" domain, which can be situated between the extraceullar ligand-binding domain and the transmembrane domain. In some embodiments, the extracellular ligand-binding domain, transmembrane domain, and intracellular signaling domain are in one polypeptide, *i.e.*, in a single chain. Multichain CARs and polypeptides are also provided herein. In some embodiments, the multichain CARs comprise: a first polypeptide comprising a transmembrane domain and at least one extracellular ligand-binding

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domain, and a second polypeptide comprising a transmembrane domain and at least one intracellular signaling domain, wherein the polypeptides assemble together to form a multichain CAR. In some embodiments, the CARs are inducible, such as by small molecule (*e.g.*, AP1903) or protein (*e.g.*, Epo, Tpo, or PD-1). In some embodiments, a CD70-specific multichain CAR is based on the high affinity receptor for IgE (FcεRI). The FcεRI expressed on mast cells and basophiles triggers allergic reactions. FcεRI is a tetrameric complex composed of a single α subunit, a single β subunit, and two disulfide-linked γ subunits. The α subunit contains the IgE-binding domain. The β and γ subunits contain ITAMs that mediate signal transduction. In some embodiments, the extracellular domain of the FcRα chain is deleted and replaced by a CD70-specific extracellular ligand-binding domain. In some embodiments, the multichain CD70-specific CAR comprises an scFv that binds specifically to CD70, the CD8α hinge, and the ITAM of the FcRβ chain. In some embodiments, the CAR may or may not comprise the FcRγ chain.

[0185] In some embodiments, the extracellular ligand-binding domain comprises an scFv comprising the light chain variable (VL) region and the heavy chain variable (VH) region of a target antigen (i.e., CD70) specific monoclonal antibody joined by a flexible linker. Single chain variable region fragments are made by linking light and/or heavy chain variable regions by using a short linking peptide (Bird et al., Science 242:423-426, 1988). An example of a linking peptide is the GS linker having the amino acid sequence $(GGGGS)_3$ (SEQ ID NO: 296), which bridges approximately 3.5 nm between the carboxy terminus of one variable region and the amino terminus of the other variable region. Linkers of other sequences have been designed and used (Bird et al., 1988, supra). Other exemplary linkers can generally include other GS linkers can generally include (GGGGS)x, where x is 1, 2, 3, 4, 5 (SEQ ID NO: 613). In some embodiments, x is 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or any integer less than about 20. In some embodiments, the linker is $(GGGGS)_4$ (SEQ ID NO: 602). In some embodiments the linker is GSTSGSGKPGSGEGSTKG (SEQ ID NO: 612), as described in Whitlow et al, *Protein Eng.* (1993) 6(8): 989-895. In general, linkers can be short, flexible polypeptides, which in some embodiments are comprised of about 20 or fewer amino acid residues. Linkers can in turn be modified for additional functions, such as attachment of drugs or attachment to solid supports. The single chain variants can be produced either recombinantly or synthetically. For synthetic production of scFv, an automated synthesizer can be used. For recombinant production of scFv, a suitable plasmid containing

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polynucleotide that encodes the scFv can be introduced into a suitable host cell, either eukaryotic, such as yeast, plant, insect or mammalian cells, or prokaryotic, such as E. coli. Polynucleotides encoding the scFv of interest can be made by routine manipulations such as ligation of polynucleotides. The resultant scFv can be isolated using standard protein purification techniques known in the art.

[0186] In another aspect, provided is a CAR, which specifically binds to CD70, wherein the CAR comprises an extracellular ligand-binding domain comprising: a VH region comprising a VH CDR1, VH CDR2, and VH CDR3 of the VH sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46 or 48; and/or a VL region comprising VL CDR1, VL CDR2, and VL CDR3 of the VL sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45 or 47. In some embodiments, the VH and VL are linked together by a flexible linker. In some embodiments a flexible linker comprises the amino acid sequence shown in SEQ ID NO: 296.

[0187] In some embodiments, a CAR of the disclosure comprises an extracellular ligand-binding domain having any one of partial light chain sequence as listed in Table 1 and/or any one of partial heavy chain sequence as listed in Table 1. In Table 1, the underlined sequences are CDR sequences according to Kabat and in bold according to Chothia.

Table 1

mAb	Light Chain	Heavy Chain
31H1	DIVMTQNPLSSPVTLGQPASISC**RSS QSLVHSDGNTYLS**WLQQRPGQSPR LLIY**KISNRFS**GVPDRFSGSGAGTDF TLKISRVEAEDVGVYYC**MQATQFP LT**IGGGSKVEIK (SEQ ID NO: 1)	QVQLVQSGAEVKKPGSSVKVSCKAS **GGTFSSY**GFSWVRQAPGQGLEWMG GI**IPIFGS**ANYAQKFQGRVTITADKS TSTVYMELISLRSEDTAVYYCAR**GG SSSPFAY**WGQGTLVTVSS (SEQ ID NO: 2)
63B2	DIVMTQTPLSSPVTLGQPASISC**RSS QSLVHSDGNTYLS**WLQQRPGQSPR LLIY**KISNRFS**GVPDRFSGSGAGTDF TLKISRVEAEDVGVYYC**MQATQFP LT**IGGGSKVEIK (SEQ ID NO: 3)	QVQLVQSGAEVKKPGSSVKVSCKAS **GGTFSSY**GFSWVRQAPGQGLEWMG GI**IPIFGT**ANYAQKFQGRVTITADKS TSTVFMELISLRSEYTAVYYCAR**GGS SSPFAY**WGQGTLVTVSS (SEQ ID NO: 4)

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mAb	Light Chain	Heavy Chain
40E3	DIQMTQSPSSLSASVGDRVTITC**RASQGISNYLA**WFQQKPGKAPKSLIY**AASSLQS**GVPSKFSGSGSGTDFTLTISSLQPEDFATYYC**QQYNSYPLT**FGGGTKVEIK (SEQ ID NO: 5)	QVQLQESGPGLVKPSETLSLTCTVS**GGSISSY**YWNWIRQPPGKGLEWIG**YIYYSGS**TNYNPSLKSRVTISVDTSKNQFSLKLRSVTAADTAVYYCAR**DIRTW**GQGTLVTVSS (SEQ ID NO: 6)
42C3	DVVMTQSPLSLPVTLGQPASISC**RSSQSLVYSDENTYLN**WFQQRPGQSLRRLIY**QVSNRDS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC**MQGTYWPPT**FGGGTKVEIK (SEQ ID NO: 7)	EVQLVESGGGLVQPGGSLRLSCAAS**GFTFRNS**WMSWVRQAPGKGLEWVANI**KRDGSE**KYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DQTGSFDY**WGQGTLVTVSS (SEQ ID NO: 8)
45F11	EIVMTQSPATLSMSLGERATLSC**RASQSVSSSLA**WYQQKPGQAPRLLIY**GASTRAT**GIPARFGGSGSGTEFTLTISSLQSEDFAVYYC**QQYINWPH**FGGGTKVEIK (SEQ ID NO: 9)	QVQLRGSGPGLVKPSETLSLTCTVS**DDSISVY**YWSWIRQPAGKGLEWIGRV**YSSGN**INYNPSLESRVTMSVDTSKSRFSLNLSSVTAADTAVYYCAR**GLDAFDI**WGQGTMVTVSS (SEQ ID NO: 10)
64F9	DIQMTQSPSSLSASVGDRVTITC**QASQDISNYLN**WYQQKPGKAPKILIY**GASNLET**GVPSRFSGSGSGTDFTFAISSLQPEDVATYYC**QQYDNFPIT**FGQGTRLEIK (SEQ ID NO: 11)	EVQLLESGGGLVQPGESLRLSCEVS**GFTFTSY**AMSWVRQVPGKGLEWVS**IISGVAFT**TYYADSVKGRFTISRDHSKNTLYLQMNGLRAEDTAVYYCVK**VDGEVY**WGQGTLVTVSS (SEQ ID NO: 12)
72C2	EIVMTQSPDTLSVSPGERAILSC**RASQSVSSNLA**WYQQKPGQAPRLLIY**SASTRAS**GIPARFSGSGSGTEFTLSISSLQSEDFAVYYC**QQYDNWPPLT**FGGGTKVEIK (SEQ ID NO: 13)	QVQLVQSGAEVKKPGSSVKVSCEAS**GGTFITY**AISWVRQAPGQGLEWMGGI**IPFFGT**ANYAQKFQGRVTITADKSTSTASMELRSLRSEDTAMYYCAQ**WELFFFDF**WGQGTPVTVSS (SEQ ID NO: 14)

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mAb	Light Chain	Heavy Chain
2F10	EIVLTQSPGTLSLSPGERATLSC**RAS QSVSSSYLA**WYQQQPGQAPRLLIY **GASSRAT**GIPDRFSGSGSGTDFTLTI SRLEPEDFAIYYC**QQYGSSPLT**FGG GTKVEIK (SEQ ID NO: 15)	AVQLVESGGGLVQPGGSLRLSCAAS **GFTFTYY**SMNWVRQAPGKGLEWVS HI**SIRSST**IYFADSAKGRFTISRDNAK NSLYLQMNSLRDEDTAVYYCAR**GS GWYGDYFDYWGQGTLVTVSS** (SEQ ID NO: 16)
4F11	DIQMTQSPSAMSASVGDRVTITC**RA SQDISNYLA**WFQQKPGKVPKRLIY**A ASSLQS**GVPSRFSGSGSGTEFTLTISS LLPEDFATYYC**LQLNSFPFT**FGGGT KVEIN (SEQ ID NO: 17)	QVTLKESGPVLVKPTETLTLTCTVS**G FSLSNARM**GVTWIRQPPGKALEWL AHI**FSNDE**KSYSTSLKSRLTISKDTSK TQVVLTMTNMDPVDTATYYCAR**IR DYYDISSYYDY**WGQGTLVSVSS (SEQ ID NO: 18)
10H10	DIQMTQSPSSVSASVGDRVTITC**RAS QGISSWLA**WYQQKPGKAPKVLIY**A ASSLQS**GVPSRFSGSGSGTDFTLTIS SLQPEDFATYYC**QQAFSFPFT**FGPG TKVDIK (SEQ ID NO: 19)	EVQLVESGGGLVQPGGSLRLSCAVS **GFTFSNH**NIHWVRQAPGKGLEWISY I**SRSSST**IYYADSVKGRFTISRDNAKN SLYLQMNSLRDEDTAVYYCAR**DHA QWYGMDV**WGQGTTVTVSS (SEQ ID NO: 20)
17G6	DIVMTQSPDSLAVSLGERATINC**KSS QSVLYSYNNKNYVA**WYQQKPGQP PNLLIF**WASTRES**GVPDRFSGSGSG TDFTLTISSLQAEDVAVYYC**QQYYS TLT**FGGGTKVEIK (SEQ ID NO: 21)	EVQLVESGGGLVQPGGSLRLSCVAS **GFTFSSY**WMSWVRQAPGKGLEWV ASI**KQDGSE**KYYVDSVKGRFTISRD NAKNSVYLQMNSLRAEDTGVYYCA R**EGVNWGWRLYWHFDL**WGRGTL VTVSS (SEQ ID NO: 22)
65E11	EIVLTQSPGTLSLSPGERVTLSC**RAS QSVSSSYLA**WYQQKPGQAPRLLIY **DASSRAT**GIPDRFSGSGSGTDFTLTI SRLEPEDFAVYYC**QQYGSSPLT**FGG GTKVEIK (SEQ ID NO: 23)	EVQVVESGGGLVQPGGSLRLSCAAS **GFTFSSY**SMNWVRQAPGKGLEWVS HS**SISRGN**IYFADSVKGRFTISRDNA KNSLYLQMNSLRDEDTAVYYCAR**G SGWYGDYFDY**WGQGTLVTVSS (SEQ ID NO: 24)

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mAb	Light Chain	Heavy Chain
P02B10	ELQSVLTQPPSASGTPGQRVTISC**SG SSSNIGSNYVY**WYQQLPGTAPKLLI Y**RNNQRPS**GVPDRFSGSKSGTSASL AISGLRSEDEADYYC**AAWDDSLSG VV**FGGGTKLTVL (SEQ ID NO: 25)	EVQLLESGGGLVQPGGSLRLSCAAS **GFAFSNY**AMSWVRQAPGKGLEWVS AI**RGGGGS**TYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR **DFISGTWYPDY**WGQGTLVTVSS (SEQ ID NO: 26)
P07D03	ELQSVLTQPPSASGTPGQRVTISC**SG SRSNIGSNYVY**WYQQLPGTAPKLLI Y**RNNQRPS**GVPDRFSGSKSGTSASL AISGLRSEDEADYYC**ASWDGSLSA VV**FGTGTKLTVL (SEQ ID NO: 27)	EVQLVQSGAEVKKPGESLKISCKGS **GYRFTSY**WIGWVRQMPGKGLEWM GSI**YPDDSD**TRYSPSFQGQVTISADK SISTAYLQWSSLKASDTAMYYCAS**S TVDYPGYSYFDY**WGQGTLVTVSS ((SEQ ID NO: 28)
P08A02	ELQSVLTQPPSASGTPGQRVTISC**SG SSSNIGSNYVY**WYQQLPGTAPKLLI Y**RNNQRPS**GVPDRFSGSKSGTSASL AISGLRSEDEADYYC**ATWDDSLGS PV**FGTGTKLTVL (SEQ ID NO: 29)	EVQLVQSGAEVKKPGESLKISCKGS **GYTFTNY**WIAWVRQMPGKGLEWM GII**YPDGSD**TRYSPSFQGQVTISADKS ISTAYLQWSSLKASDTAMYYCAR**DI TSWYYGEPAFDI**WGQGTLVTVSS ((SEQ ID NO: 30)
P08E02	ELDIQMTQSPSSLSASVGDRVTITC**R ASQSISRYLN**WYQQKPGKAPKLLIY **AASILQT**GVPSRFSGSGSGTDFTLTI SSLQPEDFATYYC**QQSYSTTMWT**F GQGTKVEIK (SEQ ID NO: 31)	EVQLVQSGAEVKKPGESLKISCKGS **GYSFTSS**WIGWVRQMPGKGLEWMG II**YPGDSD**TRYSPSFQGQVTISADKSI STAYLQWSSLKASDTAMYYCAK**GL SQAMTGFGFDY**WGQGTLVTVSS (SEQ ID NO: 32)
P08F08	ELQSVLTQPPSASGTPGQRVTISC**SG SSSNIGSNYVN**WYQQLPGTAPKLLI Y**GDYQRPS**GVPDRFSGSKSGTSASL AISGLRSEDEADYYC**ATRDDSLSGS VV**FGTGTKLTVL (SEQ ID NO: 33)	EVQLVQSGAEVKKPGESLKISCKGS **GYGFTSY**WIGWVRQMPGKGLEWM GII**HPDDSD**TKYSPSFQGQVTISADKS ISTAYLQWSSLKASDTAMYYCAS**SY LRGLWGGYFDY**WGQGTLVTVSS ((SEQ ID NO: 34)

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mAb	Light Chain	Heavy Chain
P08G02	ELDIQMTQSPSSLSASVGDRVTITC**RASQSIYDYLH**WYQQKPGKAPKLLIY**DASNLQS**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYTTPLFT**FGQGTKVEIK (SEQ ID NO: 35)	EVQLVQSGAEVKKPGESLKISCKGS**GYTFPSS**WIGWVRQMPGKGLEWMGII**YPDTSH**TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR**ASYFDRGTGYSSWWMDV**WGQGTLVTVSS ((SEQ ID NO: 36)
P12B09	ELDIQMTQSPSSLSASVGDRVTITC**RASQYIGRYLN**WYQQKRGKAPKLLIH**GATSLAS**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYSTTSPT**FGQGTKVEIK (SEQ ID NO: 37)	EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSQY**SMSWVRQAPGKGLEWVSAI**SGGGVS**TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAS**DISDSGGSHWYFDY**WGQGTLVTVSS (SEQ ID NO: 38)
P12F02	ELQSVLTQPPSASGTPGQRVTISC**SGSTSNIGRNYVY**WYQQLPGTAPKLLIY**RTNQRPS**GVPDRFSGSKSGTSASLAISGLRSEDEADYYC**AAWDDSLSGRV**FGTGTKLTVL (SEQ ID NO: 39)	EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSSY**AMSWVRQAPGKGLEWVSTI**SGTGGT**TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK**VRAGIDPTASDV**WGQGTLVTVSS (SEQ ID NO: 40)
P12G07	ELQSVLTQPPSASGTPGQRVTISC**SGSSSNIGSNYVY**WYQQLPGTAPKPLIY**MNNQRPS**GVPDRFSGSKSGTSASLAISGLRSEDEADYYC**AAWDDSLSAVV**FGTGTKLTVL ((SEQ ID NO: 41)	EVQLLESGGGLVQPGGSLRLSCAAS**GFTFNNF**AMSWVRQAPGKGLEWVSGI**SGSGDN**TYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK**DRDIGLGWYSYYLDV**WGQGTLVTVSS (SEQ ID NO: 42)

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mAb	Light Chain	Heavy Chain
P13F04	ELQSVLTQPPSASGTPGQRVTISC**SG SNSNIGTNYVS**WYQQLPGTAPKLLI Y**RSSRRPS**GVPDRFSGSKSGTSASL AISGLRSEDEADYYC**AAWDGSLSG HWV**FGTGTKLTVL (SEQ ID NO: 43)	QVQLVQSGAEVKKPGSSVKVSCKAS **GGTFSSY**AISWVRQAPGQGLEWMG EI**IPIFGT**ASYAQKFQGRVTITADEST STAYMELSSLRSEDTAVYYCAR**AG WDDSWFDY**WGQGTLVTVSS (SEQ ID NO: 44)
P15D02	ELDIQMTQSPSSLSASVGDRVTITC**R ASQSIDTYLN**WYQQKPGKAPKLLI Y**SASSLHS**GVPSRFSGSGSGTDFTLT ISSLQPEDFATYYC**QQSYSTTAWT**F GQGTKVEIK (SEQ ID NO: 45)	EVQLVQSGAEVKKPGESLKISCKGS **GYSFASY**WIGWVRQMPGKGLEWM GVI**YPGTSE**TRYSPSFQGQVTISADK SISTAYLQWSSLKASDTAMYYCAK**G LSASASGYSFQY**WGQGTLVTVSS ((SEQ ID NO: 46)
P16C05	ELDIQMTQSPSSLSASVGDRVTITC**R ASQSIGQSLN**WYQQKPGKAPKLLI Y**GASSLQS**GVPSRFSGSGSGTDFTL TISSLQPEDFATYYC**QQSYSTPIT**FG QGTKVEIK (SEQ ID NO: 47)	EVQLVQSGAEVKKPGESLKISCKGS **GYSFTDY**WIGWVRQMPGKGLEWM GMI**SPGGST**TIYRPSFQGQVTISADK SISTAYLQWSSLKASDTAMYYCAR**E MYTGGYGGSWYFDY**WGQGTLVTV SS(SEQ ID NO: 48)
10A1	DIQMTQSPSTLSASVGDRVTITC**RAS QSISTWLA**WYQQKPGKAPKVLIY**K ASSLES**GVPSRFSGSGSGTEFILTINS LQPDDFASYYC**QQYKSYSHT**FGQG TKLEIK (SEQ ID NO: 338)	QVQLQESGPGLVKPSETLSLTCTVS**G GSISYY**YWTWIRQPPGKGLEWIGHI **YYSGS**TNYNPSLKSRVTISIDTSKNLF SLKLSSVTAADTAVYYCAR**AEGSID AFDF**WGQGTMVTVSS (SEQ ID NO: 339)
10E2	DIQMTQSPSTLSASVGDRVTITC**RAS QSISSWLA**WYQQKPGKAPKVLIY**K ASSLES**GVPSRFSGSGSGTEFTLTINS LQPDDFATYYC**QQYKSFSLT**FGQG TKLEIK (SEQ ID NO: 340)	EVQLVESGGGLIQPGGSLRLSCAAS**G FTVSSN**YMTWVRQAPGKGLEWVSV I**YSGGS**TYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAR**NWG DYW**GQGTLVTVSS (SEQ ID NO: 341)

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mAb	Light Chain	Heavy Chain
11A1	DIQMTQSPSTLSASVGDRVTITC**RAS QSISSWLA**WYQQKPGKAPKVLIY**K ASTLES**GVPSRFSGSGSGTEFTLTISS LQPDDFATYYC**QQYNSYSYT**FGHG TKLEIK (SEQ ID NO: 342)	QVQLQESGPGLVKPSGTLSLTCTVS**G GSIDYY**FWNWFRQSPVKGLEWIGH V**YDIGN**TKYNPSLKSRVTISIDTSEN QFSLKLNSVTAADTAVYYCAR**GEG AlDAFDI**WGQGTMVTVSS (SEQ ID NO: 343)
11C1	DIQMTQSPSILSASVGDRVTITC**RAS QSVSSWLA**WYQQKPGKAPKVLIY**K ASSLES**GVPSRFSGTGSGTEFTLTISS LQSDDFATYYC**QQYNTYSHT**FGQG TKLEIK (SEQ ID NO: 344)	QVQLQESGPGLVKPSETLSLNCTVS**G GSISYY**YWTWIRQPPGKGLEWIGHV **IYSGT**TNYNPSLKSRVTISVDTSKNQ FSLKLNSVTAADTAVYYCVR**AEGSl DAFDL**WGQGTMVTVSS (SEQ ID NO: 345)
11D1	AIQMTQSPSSLSASVGDRVTITC**RAS QGIRNDLG**WYQQKPGKAPKLLIY**A ASSLQS**GVPSRFSGSGSGTDFTLTIS SLQPEDFATYYC**LQDYNYPFT**FGPG TKVDIK (SEQ ID NO: 346)	QVQLVESGGGVVQPGRSLRLSCVAS **GFTFSDY**GIHWVRQAPGMGQEWVA VI**WYDGSi**KKYSDSVKGRFIISRDNS ENTVYLQMNSLRGEDTAIYYCAR**DE VGtfGAFDF**WGQGTKVTVSS (SEQ ID NO: 347)
11E1	DIQMTQSPSSLSASVGDSITITC**RAS QDIDNYLA**WYQQKTGKVPKVLIY**A ASALQS**GVPSRFSGSGSGTDFTLTIS SLQPEDVATYYC**QNYNSGPRT**FGQ GTKVEIK (SEQ ID NO: 348)	QVQLQESGPGLVKPLQTLSLTCTVS **GGSISSdgY**YWSWIRQNPGKGLEWI GYM**YYSGS**TYYNPSLKSRVTISVDT SKNQFSLKLRSVTAADTAVYYCTR**D FGWYFDL**WGRGTLVTVSS (SEQ ID NO: 349)
12A2	DIQMTQSPSSLSASVGDRVTITC**RAS QDISNYLT**WYQQKPGRVPEVLIY**A ASALQS**GVPSRFSGSGSGTDFTLTIS SLQPEDVATYYC**QNYNSAPRT**FGQ GTKVEIK (SEQ ID NO: 350)	QVQLQESGPGLVKPSQSLSLTCSVS**G GSVSSdgY**YWSWIRQHPGKGLEWIG YI**YYRRI**TDYNPSLKSRVNISLDTSK NQFSLKLSSVTAADTAVYYCAR**DFG WYFDL**WGRGTLVAVSS (SEQ ID NO: 351)

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mAb	Light Chain	Heavy Chain
12C4	DIVMTQSPLSLPVTPGEPASISC**RSSQSLLHSNGYNYLD**WYLQKPGQSPQVLIL**LGSNRAS**GVPDRVSASGSGTDFTLKISRMQAEDVGIYYC**MQTLQTPFT**FGQGTKLEIK (SEQ ID NO: 352)	QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTGY**YLHWVRQAPGQGLEWMGWI**NpNSGG**TNYAQKFQGRVTMTRDTSITTAYMELSRLRIDDTAVYYCAR**DRGVtmivDGMDD**WGQGTTVTVSS (SEQ ID NO: 353)
12C5	DIQLTQSPSFLSASVGDRVIITC**RASQGINSHLA**WYQQKPGKAPKLLIY**YASTLPS**GVPSRFSGSGSGTEFTLTVTSLQPEDFATYYC**QQLNHYPIT**FGQGTRLDIN (SEQ ID NO: 354)	EVELVESGGGMVQPGRSLRLSCAAS**GFTFSDY**GMHWVRQAPGMGLEWVTVI**WYDGSn**KYYADSVKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCAR**DEVGfvGAFDI**WGQGTMVTVSS (SEQ ID NO: 355)
12C6	DIQLTQSPSFLSASVGDRVIITC**RASQGINSHLA**WYQQKPGKAPKLLIY**YASTLPS**GVPSRFSGSGSGTEFTLTVTSLQPEDFATYYC**QQLNHYPIT**FGQGTRLEIK (SEQ ID NO: 661)	EVELVESGGGMVQPGRSLRLSCAAS**GFTFSDY**GMHWVRQAPGMGLEWVTVI**WYDGSn**KYYADSVKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCAR**DEVGfvGAFDI**WGQGTMVTVSS (SEQ ID NO: 662)
12D3	DIQMTQSPSSLSASVGDRVTITC**RASQGISNYLA**WYQQKPGKVPKLLIY**AASTLHS**GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC**QKYNSAPRT**FGQGTKVEIK (SEQ ID NO: 356)	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISSdgY**YWSWIRQHPGKGLEWIGY**MYYSGI**TYHNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR**DFGWYFDL**WGRGTLVTVSS (SEQ ID NO: 357)
12D6	DIQMTQSPSSLSASVGDRVTITC**RASQDISNYLA**WYQQKPGKVPKLLIY**AASTLHS**GVPSRFSGSGSGTDFTLTISSLQPDDFAAYYC**QKYNSAPRT**FGQGTKVEIK (SEQ ID NO: 358)	QVQLQESGPGLVKPSQTLSLTCTVS**GGSISSdaY**YWSWIRQHPGKGLEWIGY**MYYSGI**TYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR**DFGWYFDL**WGRGTLVTVSS (SEQ ID NO: 359)

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mAb	Light Chain	Heavy Chain
12D7	DIQLTQSPSFLSASVGDRVSITC**RAS QDISSFLA**WYQQKPGKAPVLLIY**VA STLQS**GVPSRFSGSGSGTEFTLTVSS LQPEDFATYYC**QQLHVYPIT**FGQG TRLEIR (SEQ ID NO: 360)	QVQLVESGGGVVQPGRSLRLSCVAS **GFTFSDY**GIHWVRQAPGMGQEWVA VI**WYDGSi**KKYSDSVKGRFIISRDNS ENTVYLQMNSLRGEDTAIYYCAR**DE VGtfGAFDF**WGQGTKVTVSS (SEQ ID NO: 361)
12F5	DIVMTQTPLSLPVTPGEPASISC**RSS QSLLDSDDGNtYLD**WYLQKPGQSP QLLIY**TLSYRAS**GVPDRFSGSGSGT DFTLKISRVEAEDVGVYYC**MQRIEF PFT**FGPGTKVDIK (SEQ ID NO: 362)	EVQLVESGGGLVKPGGSLRLSCAAS **GFTFSNA**WMSWVRQAPGKGLEWV GRI**KsktGGGT**TDYAAPVKGRFTISR DDSKNTLYLQMNSLKTEDTAVYYC TS**LIVGaiSLFDY**WGQGTLVTVSS (SEQ ID NO: 363)
12H4	DIQMTQSPSALSASVGDRVAITC**RA SQTISTWLA**WYQQKPGKAPKVLIY **KASNLES**GVPSRFSGSGSGTEFTLTI NSLQPDDFATYYC**QQYQTFSHT**FG QGTKLEIK (SEQ ID NO: 364)	QVQLRESGPGLVKPSETLSLTCTIS**G GSISYY**FWTWIRQPPGRGLEWIG**QIY YSGN**TNSNPSLKSRVTISIDTSKNQFS LKLTSVTVADTAVYYCVR**AEGSlDA FDI**WGQGTMVAVSS (SEQ ID NO: 365)
8C8	DMQMTQSPSSLSASVGDRVTLTC**R ASQGISNYLA**WFQLKPGKVPKLLIY **AASTLQS**GVPSRFSGSGSGTDFALTI SSLQPEDVATYYC**QKYNSAPLT**FG GGTKVEIK (SEQ ID NO: 366)	EVQLVESGGGLVKPGGSLRLSCVAS **GFTFSSY**SMNWVRQFPGKGLEWVS **SlStSSNY**IHYADSLQGRFTISRDNAK NSLYLQMSSLRVEDTAVYYCVR**DK GTtltnWYFDL**WGRGTLVTVSS (SEQ ID NO: 367)
8F7	DIVMTQSPLSLPVTPGEPASISC**RSS QTLVHSNGYNYLN**WYLQKPGQSP QLLIY**LGSNRAS**GVPDRFSGSGSGS DFTLKISRMEAEDVGVYYC**MQAIQ TPYT**FGQGTNVEIK (SEQ ID NO: 368)	QVQLVESGGGVVQPGRSLRLSCGAS **GFTFSSY**GMHWVRQAPGKGLEWV AVI**WYDGSn**KYYADSLKGRFTISRD NSKNTLYLQMNSLRAEDTAVYYCA R**DGYSgssDAFDI**WGQGTMVTVSS (SEQ ID NO: 369)

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mAb	Light Chain	Heavy Chain
8F8	DIQMTQSPSTLSASVGDRVTITC**RAS QSISSWLA**WYQQKPGKAPKVLIY**K ASNLES**GVPSRFSGSGSGTEFTLTISS LQPDDFATYYC**QQYNSYSCT**FGQG TKLEIK (SEQ ID NO: 370)	QVQLQESGPGLVQPSETLSLTCTVS**G GSISYYYWS**WIRQPPGKGLEWIG**NIN YMGNT**IYNPSLKSRVTISVDTSKDQF SLKLTSVSAADTAVYYCVR**AEGSID AFDF**WGQGTLVAVSL (SEQ ID NO: 371)
9D8	DIQMTQSPSSLSASVGDRIIFTC**QAS QDINNYLH**WYQQKPGKAPKLLIY**D ASDWET**GVPSRFSGSGSGTDFTFTIS SLQPEDIATYYC**QQYDHLPIT**FGQG TRVEIK (SEQ ID NO: 372)	QVQLVQSGAEVTKPGASVKVSCKAS **GYIFTGY**YIYWVRQAPGQGLEWMG WI**NpSSGG**TNYAQKFQGRVTMARD TSISTAYMELSSLRSDDTAVYYCAR**D RKReyyynFGMDV**WGQGTTVTVST (SEQ ID NO: 373)
9E10	DIQMTQSPSSLSASVGDRVILTC**QAS QDISNYLH**WYQQKPGKAPKLLIY**D ASDLET**GVPSRFSGSGSGADFTFTIS NLQPEDFATYYC**QQYDHLPIT**FGQ GTRLEIK (SEQ ID NO: 374)	QVQLVQSGAEVTKPGASVKVSCKAS **GYTFTSH**YIYWVRQAPGQGLEWMG WI**NpNSGG**TNYAQKFQDRVTMARD TSISTAYMELSRLRSDDTAVYYCAK **DRKReyyynFGMDV**WGQGTTVTVSA (SEQ ID NO: 375)
9E5	DIQMTQSPSSLSASVGDRVILTC**QAS QDISNYLH**WYQQKPGKAPKLLIY**D ASDLET**GVPSRFSGSGSGADFTFTIS NLQPEDFATYYC**QQYDHLPIT**FGQ GTRLEIK (SEQ ID NO: 376)	QVQLVQFGVEVRKPGASVKVSCKVS **GFTFTSH**YIYWVRQAPGQGLEWMG WI**NpNSGG**TKYAQKFQDRVTMARD TSISTAYMELSRLRSDDTSVYYCVK**D RKReyyynFGMDV**WGQGTTVTVSS (SEQ ID NO: 377)
9F4	DIQMTQSPSSLSASVGDRVTITC**QAS QDISNYLN**WYQQKPGKAPKLLIY**D ASNLET**GVPSRFSGSGSGTDFTFTIS SLQPEDIATYYC**QQYDNLPYT**FGQ GTKLEIK (SEQ ID NO: 378)	EVQMLESGGGLIQPGGSLRLSCKTS**G FTLSIY**AIHWVRQAPGRGLEWVS**SF GgRGSS**TYFADSVKGRFTISRDASEN SLYLHMNSLRAEDTAVYYCAK**EKD WgRGFDY**WGQGTLVTVSS (SEQ ID NO: 379)

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mAb	Light Chain	Heavy Chain
9F8	DIVMTQSPLSLPVTPGEPASISC**RSS QSLLYSNGYNYLD**WYLQKPGQSPQ LLIF**LNSNRAS**GVPDRFSGSGSGTDF TLKISRVEAEDVGVYFC**MQALQTP LT**FGGGTKVEIK (SEQ ID NO: 380)	EVQLVESGGGLVKPGGSLRLSCAAS **GFTFSNY**SMNWVRQAPGKGLEWVS S**ISsSTIY**IYYADSVKGRFTISRDNAK KSLYLQMNSLRAEDTAVYYCAR**DIG WevftLGFDY**WGQGTQVTVSS (SEQ ID NO: 381)

[0188] Also provided herein are CDR portions of extracellular ligand-binding domains of CARs to CD70 (including Chothia, Kabat CDRs, and CDR contact regions). Determination of CDR regions is well within the skill of the art. It is understood that in some embodiments, CDRs can be a combination of the Kabat and Chothia CDR (also termed "combined CRs" or "extended CDRs"). In some embodiments, the CDRs are the Kabat CDRs. In other embodiments, the CDRs are the Chothia CDRs. In other words, in embodiments with more than one CDR, the CDRs may be any of Kabat, Chothia, combination CDRs, or combinations thereof. Tables 2A-2B provide examples of CDR sequences provided herein.

Table 2A

Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
31H1	SYGFS (SEQ ID NO: 49) (Kabat); GGTFSSY (SEQ ID NO: 50) (Chothia); GGTFSSYGFS (SEQ ID NO: 51) (Extended)	GIIPIFGSANYAQK FQG (SEQ ID NO: 52) (Kabat); IPIFGS (SEQ ID NO: 53) (Chothia)	GGSSSPFAY (SEQ ID NO: 54)
63B2	SYGFS (SEQ ID NO: 55) (Kabat); GGTFSSY (SEQ ID NO: 56) (Chothia) GGTFSSYGFS (Extended) (SEQ ID NO: 57)	GIIPIFGTANYAQK FQG (SEQ ID NO: 58) (Kabat); IPIFGT (SEQ ID NO: 59) (Chothia)	GGSSSPFAY (SEQ ID NO: 60)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
40E3	SYYWN (SEQ ID NO: 61) (Kabat); GGSISSY (SEQ ID NO: 62) (Chothia); GGSISSYYWN (SEQ ID NO: 63) (Extended)	YIYYSGSTNYNPSLKS (SEQ ID NO: 64) (Kabat); YYSGS (SEQ ID NO: 65) (Chothia)	DIRTW (SEQ ID NO: 66)
42C3	NSWMS (SEQ ID NO: 67) (Kabat); GFTFRNS (SEQ ID NO: 68) (Chothia); GFTFRNSWMS (SEQ ID NO: 69) (Extended)	NIKRDGSEKYYVDSVKG (SEQ ID NO: 70) (Kabat); KRDGSE (SEQ ID NO: 71) (Chothia)	DQTGSFDY (SEQ ID NO: 72)
45F11	VYYWS (SEQ ID NO: 73) (Kabat); DDSISVY (SEQ ID NO: 74) (Chothia); DDSISVYYWS (SEQ ID NO: 75) (Extended)	VYSSGNINYNPSLES (SEQ ID NO: 76) (Kabat); YSSGN (SEQ ID NO: 77) (Chothia)	GLDAFDI (SEQ ID NO: 78)
64F9	SYAMS (SEQ ID NO: 79) (Kabat); GFTFTSY (SEQ ID NO: 80) (Chothia); GFTFTSYAMS (SEQ ID NO: 81) (Extended)	RVYSSGNINYNPSLES (SEQ ID NO: 82) (Kabat); YSSGN (SEQ ID NO: 83) (Chothia)	GLDAFDI (SEQ ID NO: 84)
72C2	TYAIS (SEQ ID NO: 85) (Kabat); GGTFITY (SEQ ID NO: 86) (Chothia); GGTFITYAIS (SEQ ID NO: 87) (Extended)	GIIPFFGTANYAQKFQG (SEQ ID NO: 88) (Kabat); IPFFGT (SEQ ID NO: 89) (Chothia)	WELFFFDF (SEQ ID NO: 90)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
2F10	YYSMN (SEQ ID NO: 91) (Kabat); GFTFTYY (SEQ ID NO: 92) (Chothia); GFTFTYYSMN (SEQ ID NO: 93) (Extended)	HISIRSSTIYFADS AKG (SEQ ID NO: 94) (Kabat); SIRSST (SEQ ID NO: 95) (Chothia)	GSGWYGDYFDY (SEQ ID NO: 96)
4F11	NARMGVT (SEQ ID NO: 97) (Kabat); GFSLSNARM (SEQ ID NO: 98) (Chothia); GFSLSNARMGVT (SEQ ID NO: 99) (Extended)	HIFSNDEKSYSTS LKS (SEQ ID NO: 100) (Kabat); FSNDE (SEQ ID NO: 101) (Chothia)	IRDYYDISSYYDY (SEQ ID NO: 102)
10H10	NHNIH (SEQ ID NO: 103) (Kabat); GFTFSNH (SEQ ID NO: 104) (Chothia); GFTFSNHNIH (SEQ ID NO: 105) (Extended)	YISRSSSTIYYADS VKG (SEQ ID NO: 106) (Kabat); SRSSST (SEQ ID NO: 107) (Chothia)	DHAQWYGMDV (SEQ ID NO: 108)
17G6	SYWMS (SEQ ID NO: 109) (Kabat); GFTFSSY (SEQ ID NO: 110) (Chothia); GFTFSSYWMS (SEQ ID NO: 111) (Extended)	SIKQDGSEKYYV DSVKG (SEQ ID NO: 112) (Kabat); KQDGSE (SEQ ID NO: 113) (Chothia)	EGVNWGWRLYW HFDL (SEQ ID NO: 114)
65E11	SYSMN (SEQ ID NO: 115) (Kabat); GFTFSSY (SEQ ID NO: 116) (Chothia); GFTFSSYSMN (SEQ ID NO: 117) (Extended)	HSSISRGNIYFADS VKG (SEQ ID NO: 118) (Kabat); SISRGN (SEQ ID NO: 119) (Chothia)	GSGWYGDYFDY (SEQ ID NO: 120)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
P02B10	NYAMS (SEQ ID NO: 121) (Kabat); GFAFSNY (SEQ ID NO: 122) (Chothia); GFAFSNYAMS (SEQ ID NO: 123) (Extended)	AIRGGGGSTYYA DSVKG (SEQ ID NO: 124) (Kabat); RGGGGS (SEQ ID NO: 125) (Chothia)	DFISGTWYPDY (SEQ ID NO: 126)
P07D03	SYWIG (SEQ ID NO: 127) (Kabat); GYRFTSY (SEQ ID NO: 128) (Chothia); GYRFTSYWIG (SEQ ID NO: 129) (Extended)	SIYPDDSDTRYSP SFQG (SEQ ID NO: 130) (Kabat); YPDDSD (SEQ ID NO: 131) (Chothia)	STVDYPGYSYFD Y (SEQ ID NO: 132)
P08A02	NYWIA (SEQ ID NO: 133) (Kabat); GYTFTNY (SEQ ID NO: 134) (Chothia); GYTFTNYWIA (SEQ ID NO: 135) (Extended)	IIYPDGSDTRYSPS FQG (SEQ ID NO: 136) (Kabat); YPDGSD (SEQ ID NO: 137) (Chothia)	DITSWYYGEPAF DI (SEQ ID NO: 138)
P08E02	SSWIG (SEQ ID NO: 139) (Kabat); GYSFTSS (SEQ ID NO: 140) (Chothia); GYSFTSSWIG (SEQ ID NO: 141) (Extended)	IIYPGDSDTRYSPS FQG (SEQ ID NO: 142) (Kabat); YPGDSD (SEQ ID NO: 143) (Chothia)	GLSQAMTGFGFD Y (SEQ ID NO: 144)
P08F08	SYWIG (SEQ ID NO: 145) (Kabat); GYGFTSY (SEQ ID NO: 146) (Chothia); GYGFTSYWIG (SEQ ID NO: 147) (Extended)	IIHPDDSDTKYSPS FQG (SEQ ID NO: 148) (Kabat); HPDDSD (SEQ ID NO: 149) (Chothia)	SYLRGLWGGYFD Y (SEQ ID NO: 150)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
P08G02	SSWIG (SEQ ID NO: 151) (Kabat); GYTFPSS (SEQ ID NO: 152) (Chothia); GYTFPSSWIG (SEQ ID NO: 153) (Extended)	IIYPDTSHTRYSPSFQ (SEQ ID NO: 154) (Kabat); YPDTSH (SEQ ID NO: 155) (Chothia)	ASYFDRGTGYSSWWMDV (SEQ ID NO: 156)
P12B09	QYSMS (SEQ ID NO: 157) (Kabat); GFTFSQY (SEQ ID NO: 158) (Chothia); GFTFSQYSMS (SEQ ID NO: 159) (Extended)	AISGGGVSTYYADSVKG (SEQ ID NO: 160) (Kabat); SGGGVS (SEQ ID NO: 161) (Chothia)	DISDSGGSHWYFDY (SEQ ID NO: 162)
P12F02	SYAMS (SEQ ID NO: 163) (Kabat); GFTFSSY (SEQ ID NO: 164) (Chothia); GFTFSSYAMS (SEQ ID NO: 165) (Extended)	TISGTGGTTYYADSVKG (SEQ ID NO: 166) (Kabat); SGTGGT (SEQ ID NO: 167) (Chothia)	VRAGIDPTASDV (SEQ ID NO: 168)
P12G07	NFAMS (SEQ ID NO: 169) (Kabat); GFTFNNF (SEQ ID NO: 170) (Chothia); GFTFNNFAMS (SEQ ID NO: 171) (Extended)	GISGSGDNTYYADSVKG (SEQ ID NO: 172) (Kabat); SGSGDN (SEQ ID NO: 173) (Chothia)	DRDIGLGWYSYYLDV (SEQ ID NO: 174)
P13F04	SYAIS (SEQ ID NO: 175) (Kabat); GGTFSSY (SEQ ID NO: 176) (Chothia); GGTFSSYAIS (SEQ ID NO: 177) (Extended)	EIIPIFGTASYAQKFQG (SEQ ID NO: 178) (Kabat); IPIFGT (SEQ ID NO: 179) (Chothia)	AGWDDSWFDY (SEQ ID NO: 180)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
P15D02	SYWIG (SEQ ID NO: 181) (Kabat); GYSFASY (SEQ ID NO: 182) (Chothia); GYSFASYWIG (SEQ ID NO: 183) (Extended)	VIYPGTSETRYSPS FQG (SEQ ID NO: 184) (Kabat); YPGTSE (SEQ ID NO: 185) (Chothia)	GLSASASGYSFQ Y (SEQ ID NO: 186)
P16C05	DYWIG (SEQ ID NO: 187) (Kabat); GYSFTDY (SEQ ID NO: 188) (Chothia); GYSFTDYWIG (SEQ ID NO: 189) (Extended)	MISPGGSTTIYRPS FQG (SEQ ID NO: 190) (Kabat); SPGGST (SEQ ID NO: 191) (Chothia)	MYTGGYGGSWY FDY (SEQ ID NO: 192)
10A1	YYYWT (SEQ ID NO: 382) (Kabat); GGSISYY (SEQ ID NO: 383) (Chothia); GGSISYYYWT (SEQ ID NO: 384) (Extended)	HIYYSGSTNYNPS LKS (SEQ ID NO: 385) (Kabat); YYSGS (SEQ ID NO: 386) (Chothia)	AEGSlDAFDF (SEQ ID NO: 387)
10E2	SNYMT (SEQ ID NO: 388) (Kabat); GFTVSSN (SEQ ID NO: 389) (Chothia); GFTVSSNYMT (SEQ ID NO: 390) (Extended)	VIYSGGSTYYADS VKG (SEQ ID NO: 391) (Kabat); YSGGS (SEQ ID NO: 392) (Chothia)	NWGDYW (SEQ ID NO: 393)
11A1	YYFWN (SEQ ID NO: 394) (Kabat); GGSIDYY (SEQ ID NO: 395) (Chothia); GGSIDYYFWN (SEQ ID NO: 396) (Extended)	HVYDIGNTKYNP SLKS (SEQ ID NO: 397) (Kabat); YDIGN (SEQ ID NO: 398) (Chothia)	GEGAlDAFDI (SEQ ID NO: 399)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
11C1	YYYWT (SEQ ID NO: 400) (Kabat); GGSISYY (SEQ ID NO: 401) (Chothia); GGSISYYYWT (SEQ ID NO: 402) (Extended)	HVIYSGTTNYNPSLKS (SEQ ID NO: 403) (Kabat); IYSGT (SEQ ID NO: 404) (Chothia)	AEGSlDAFDL (SEQ ID NO: 405)
11D1	DYGIH (SEQ ID NO: 406) (Kabat); GFTFSDY (SEQ ID NO: 407) (Chothia); GFTFSDYGIH (SEQ ID NO: 408) (Extended)	VIWYDGSiKKYSDSVKG (SEQ ID NO: 409) (Kabat); WYDGSi (SEQ ID NO: 410) (Chothia)	DEVGtfGAFDF (SEQ ID NO: 411)
11E1	SdgYYWS (SEQ ID NO: 412) (Kabat); GGSISSdgY (SEQ ID NO: 413) (Chothia); GGSISSdgYYWS (SEQ ID NO: 414) (Extended)	YMYYSGSTYYNPSLKS (SEQ ID NO: 415) (Kabat); YYSGS (SEQ ID NO: 416) (Chothia)	DFGWYFDL (SEQ ID NO: 417)
12A2	SdgYYWS (SEQ ID NO: 418) (Kabat); GGSVSSdgY (SEQ ID NO: 419) (Chothia); GGSVSSdgYYWS (SEQ ID NO: 420) (Extended)	YIYYRRITDYNPSLKS (SEQ ID NO: 421) (Kabat); YYRRI (SEQ ID NO: 422) (Chothia)	DFGWYFDL (SEQ ID NO: 423)
12C4	GYYLH (SEQ ID NO: 424) (Kabat); GYTFTGY (SEQ ID NO: 425) (Chothia); GYTFTGYYLH (SEQ ID NO: 426) (Extended)	WINpNSGGTNYAQKFQG (SEQ ID NO: 427) (Kabat); NpNSGG (SEQ ID NO: 428) (Chothia)	DRGVtmivDGMDD (SEQ ID NO: 429)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
12C5	DYGMH (SEQ ID NO: 430) (Kabat); GFTFSDY (SEQ ID NO: 431) (Chothia); GFTFSDYGMH (SEQ ID NO: 432) (Extended)	VIWYDGSnKYYA DSVKG (SEQ ID NO: 433) (Kabat); WYDGSn (SEQ ID NO: 434) (Chothia)	DEVGfvGAFDI (SEQ ID NO: 435)
12C6	DYGMH (SEQ ID NO: 663) (Kabat); GFTFSDY (SEQ ID NO: 664) (Chothia); GFTFSDYGMH (SEQ ID NO: 665) (Extended)	VIWYDGSnKYYA DSVKG (SEQ ID NO: 666) (Kabat); WYDGSn (SEQ ID NO: 667) (Chothia)	DEVGfvGAFDI (SEQ ID NO: 668)
12D3	SdgYYWS (SEQ ID NO: 436) (Kabat); GGSISSdgY (SEQ ID NO: 437) (Chothia); GGSISSdgYYWS (SEQ ID NO: 438) (Extended)	YMYYSGITYHNP SLKS (SEQ ID NO: 439) (Kabat); YYSGI (SEQ ID NO: 440) (Chothia)	DFGWYFDL (SEQ ID NO: 441)
12D6	SdaYYWS (SEQ ID NO: 442) (Kabat); GGSISSdaY (SEQ ID NO: 443) (Chothia); GGSISSdaYYWS (SEQ ID NO: 444) (Extended)	YMYYSGITYYNP SLKS (SEQ ID NO: 445) (Kabat); YYSGI (SEQ ID NO: 446) (Chothia)	DFGWYFDL (SEQ ID NO: 447)
12D7	DYGIH (SEQ ID NO: 448) (Kabat); GFTFSDY (SEQ ID NO: 449) (Chothia); GFTFSDYGIH (SEQ ID NO: 450) (Extended)	VIWYDGSiKKYSD SVKG (SEQ ID NO: 451) (Kabat); WYDGSi (SEQ ID NO: 452) (Chothia)	DEVGtfGAFDF (SEQ ID NO: 453)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
12F5	NAWMS (SEQ ID NO: 454) (Kabat); GFTFSNA (SEQ ID NO: 455) (Chothia); GFTFSNAWMS (SEQ ID NO: 456) (Extended)	RIKsktGGGTTDYA APVKG (SEQ ID NO: 457) (Kabat); KsktGGGT (SEQ ID NO: 458) (Chothia)	LIVGaiSLFDY (SEQ ID NO: 459)
12H4	YYFWT (SEQ ID NO: 460) (Kabat); GGSISYY (SEQ ID NO: 461) (Chothia); GGSISYYFWT (SEQ ID NO: 462) (Extended)	QIYYSGNTNSNPS LKS (SEQ ID NO: 463) (Kabat); YYSGN (SEQ ID NO: 464) (Chothia)	AEGSlDAFDI (SEQ ID NO: 465)
8C8	SYSMN (SEQ ID NO: 466) (Kabat); GFTFSSY (SEQ ID NO: 467) (Chothia); GFTFSSYSMN (SEQ ID NO: 468) (Extended)	SIStSSNYIHYADS LQG (SEQ ID NO: 469) (Kabat); StSSNY (SEQ ID NO: 470) (Chothia)	DKGTtltnWYFDL (SEQ ID NO: 471)
8F7	SYGMH (SEQ ID NO: 472) (Kabat); GFTFSSY (SEQ ID NO: 473) (Chothia); GFTFSSYGMH (SEQ ID NO: 474) (Extended)	VIWYDGSnKYYA DSLKG (SEQ ID NO: 475) (Kabat); WYDGSn (SEQ ID NO: 476) (Chothia)	DGYSgssDAFDI (SEQ ID NO: 477)
8F8	YYYWS (SEQ ID NO: 478) (Kabat); GGSISYY (SEQ ID NO: 479) (Chothia); GGSISYYYWS (SEQ ID NO: 480) (Extended)	NINYMGNTIYNPS LKS (SEQ ID NO: 481) (Kabat); NYMGN (SEQ ID NO: 482) (Chothia)	AEGSlDAFDF (SEQ ID NO: 483)

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Heavy Chain			
mAb	**CDRH1**	**CDRH2**	**CDRH3**
9D8	GYYIY (SEQ ID NO: 484) (Kabat); GYIFTGY (SEQ ID NO: 485) (Chothia); GYIFTGYYIY (SEQ ID NO: 486) (Extended)	WINpSSGGTNYA QKFQG (SEQ ID NO: 487) (Kabat); NpSSGG (SEQ ID NO: 488) (Chothia)	DRKReyyynFGMD V (SEQ ID NO: 489)
9E10	SHYIY (SEQ ID NO: 490) (Kabat); GYTFTSH (SEQ ID NO: 491) (Chothia); GYTFTSHYIY (SEQ ID NO: 492) (Extended)	WINpNSGGTNYA QKFQD (SEQ ID NO: 493) (Kabat); NpNSGG (SEQ ID NO: 494) (Chothia)	DRKReyyynFGMD V (SEQ ID NO: 495)
9E5	SHYIY (SEQ ID NO: 496) (Kabat); GFTFTSH (SEQ ID NO: 497) (Chothia); GFTFTSHYIY (SEQ ID NO: 498) (Extended)	WINpNSGGTKYA QKFQD (SEQ ID NO: 499) (Kabat); NpNSGG (SEQ ID NO: 500) (Chothia)	DRKReyyynFGMD V (SEQ ID NO: 501)
9F4	IYAIH (SEQ ID NO: 502) (Kabat); GFTLSIY (SEQ ID NO: 503) (Chothia); GFTLSIYAIH (SEQ ID NO: 504) (Extended)	SFGgRGSSTYFAD SVKG (SEQ ID NO: 505) (Kabat); GgRGSS (SEQ ID NO: 506) (Chothia)	EKDWgRGFDY (SEQ ID NO: 507)
9F8	NYSMN (SEQ ID NO: 508) (Kabat); GFTFSNY (SEQ ID NO: 509) (Chothia); GFTFSNYSMN (SEQ ID NO: 510) (Extended)	SISsSTIYIYYADS VKG (SEQ ID NO: 511) (Kabat); SsSTIY (SEQ ID NO: 512) (Chothia)	DIGWevftLGFDY (SEQ ID NO: 513)

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Table 2B

Light Chain			
mAb	**CDRL1**	**CDRL2**	**CDRL3**
31H1	RSSQSLVHSDGNTYLS (SEQ ID NO: 193);	KISNRFS (SEQ ID NO: 194)	MQATQFPLT (SEQ ID NO: 195)
63B2	RSSQSLVHSDGNTYLS (SEQ ID NO: 196);	KISNRFS (SEQ ID NO: 197)	MQATQFPLT (SEQ ID NO: 198)
40E3	RASQGISNYLA (SEQ ID NO: 199);	AASSLQS (SEQ ID NO: 200)	QQYNSYPLT (SEQ ID NO: 201)
42C3	RSSQSLVYSDENTYLN (SEQ ID NO: 202);	QVSNRDS (SEQ ID NO: 203)	MQGTYWPPT (SEQ ID NO: 204)
45F11	RASQSVSSSLA (SEQ ID NO: 205);	GASTRAT (SEQ ID NO: 206)	QQYINWPH (SEQ ID NO: 207)
64F9	QASQDISNYLN (SEQ ID NO: 208);	GASNLET (SEQ ID NO: 209)	QQYDNFPIT (SEQ ID NO: 210)
72C2	RASQSVSSNLA (SEQ ID NO: 211);	SASTRAS (SEQ ID NO: 212)	QQYDNWPPLT (SEQ ID NO: 213)
2F10	RASQSVSSSYLA (SEQ ID NO: 214);	GASSRAT (SEQ ID NO: 215)	QQYGSSPLT (SEQ ID NO: 216)
4F11	RASQDISNYLA (SEQ ID NO: 217);	AASSLQS (SEQ ID NO: 218)	LQLNSFPFT (SEQ ID NO: 219)
10H10	RASQGISSWLA (SEQ ID NO: 220);	AASSLQS (SEQ ID NO: 221)	QQAFSFPFT (SEQ ID NO: 222)
17G6	KSSQSVLYSYNNKNYVA (SEQ ID NO: 223);	WASTRES (SEQ ID NO: 224)	QQYYSTLT (SEQ ID NO: 225)
65E11	RASQSVSSSYLA (SEQ ID NO: 226);	DASSRAT (SEQ ID NO: 227)	QQYGSSPLT (SEQ ID NO: 228)
P02B10	SGSSSNIGSNYVY (SEQ ID NO: 229);	RNNQRPS (SEQ ID NO: 230)	AAWDDSLSGVV (SEQ ID NO: 231)
P07D03	SGSRSNIGSNYVY (SEQ ID NO: 232);	RNNQRPS (SEQ ID NO: 233)	ASWDGSLSAVV (SEQ ID NO: 234)

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Light Chain			
mAb	**CDRL1**	**CDRL2**	**CDRL3**
P08A02	SGSSSNIGSNYVY (SEQ ID NO: 235);	RNNQRPS (SEQ ID NO: 236)	ATWDDSLGSPV (SEQ ID NO: 237)
P08E02	RASQSISRYLN (SEQ ID NO: 238);	AASILQT (SEQ ID NO: 239)	QQSYSTTMWT (SEQ ID NO: 240)
P08F08	SGSSSNIGSNYVN (SEQ ID NO: 241);	GDYQRPS (SEQ ID NO: 242)	ATRDDSLSGSVV (SEQ ID NO: 243)
P08G02	RASQSIYDYLH (SEQ ID NO: 244);	DASNLQS (SEQ ID NO: 245)	QQSYTTPLFT (SEQ ID NO: 246)
P12B09	RASQYIGRYLN (SEQ ID NO: 247);	GATSLAS (SEQ ID NO: 248)	QQSYSTTSPT (SEQ ID NO: 249)
P12F02	SGSTSNIGRNYVY (SEQ ID NO: 250);	RTNQRPS (SEQ ID NO: 251)	AAWDDSLSGRV (SEQ ID NO: 252)
P12G07	SGSSSNIGSNYVY (SEQ ID NO: 253);	MNNQRPS (SEQ ID NO: 254)	AAWDDSLSAVV (SEQ ID NO: 255)
P13F04	SGSNSNIGTNYVS (SEQ ID NO: 256);	RSSRRPS (SEQ ID NO: 257)	AAWDGSLSGHW V (SEQ ID NO: 258)
P15D02	RASQSIDTYLN (SEQ ID NO: 259);	SASSLHS (SEQ ID NO: 260)	QQSYSTTAWT (SEQ ID NO: 261)
P16C05	RASQSIGQSLN (SEQ ID NO: 262);	GASSLQS (SEQ ID NO: 263)	QQSYSTPIT (SEQ ID NO: 264)
10A1	RASQSISTWLA (SEQ ID NO: 514);	KASSLES (SEQ ID NO: 515)	QQYKSYSHT (SEQ ID NO: 516)
10E2	RASQSISSWLA (SEQ ID NO: 517);	KASSLES (SEQ ID NO: 518)	QQYKSFSLT (SEQ ID NO: 519)
11A1	RASQSISSWLA (SEQ ID NO: 520);	KASTLES (SEQ ID NO: 521)	QQYNSYSYT (SEQ ID NO: 522)
11C1	RASQSVSSWLA (SEQ ID NO: 523);	KASSLES (SEQ ID NO: 524)	QQYNTYSHT (SEQ ID NO: 525)

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Light Chain			
mAb	**CDRL1**	**CDRL2**	**CDRL3**
11D1	RASQGIRNDLG (SEQ ID NO: 526);	AASSLQS (SEQ ID NO: 527)	LQDYNYPFT (SEQ ID NO: 528)
11E1	RASQDIDNYLA (SEQ ID NO: 529);	AASALQS (SEQ ID NO: 530)	QNYNSGPRT (SEQ ID NO: 531)
12A2	RASQDISNYLT (SEQ ID NO: 532);	AASALQS (SEQ ID NO: 533)	QNYNSAPRT (SEQ ID NO: 534)
12C4	RSSQSLLHSNGYNYLD (SEQ ID NO: 535);	LGSNRAS (SEQ ID NO: 536)	MQTLQTPFT (SEQ ID NO: 537)
12C5	RASQGINSHLA (SEQ ID NO: 538);	YASTLPS (SEQ ID NO: 539)	QQLNHYPIT (SEQ ID NO: 540)
12C6	RASQGINSHLA (SEQ ID NO: 669);	YASTLPS (SEQ ID NO: 670)	QQLNHYPIT (SEQ ID NO: 671)
12D3	RASQGISNYLA (SEQ ID NO: 541);	AASTLHS (SEQ ID NO: 542)	QKYNSAPRT (SEQ ID NO: 543)
12D6	RASQDISNYLA (SEQ ID NO: 544);	AASTLHS (SEQ ID NO: 545)	QKYNSAPRT (SEQ ID NO: 546)
12D7	RASQDISSFLA (SEQ ID NO: 547);	VASTLQS (SEQ ID NO: 548)	QQLHVYPIT (SEQ ID NO: 549)
12F5	RSSQSLLDSDDGNtYLD (SEQ ID NO: 550);	TLSYRAS (SEQ ID NO: 551)	MQRIEFPFT (SEQ ID NO: 552)
12H4	RASQTISTWLA (SEQ ID NO: 553);	KASNLES (SEQ ID NO: 554)	QQYQTFSHT (SEQ ID NO: 555)
8C8	RASQGISNYLA (SEQ ID NO: 556);	AASTLQS (SEQ ID NO: 557)	QKYNSAPLT (SEQ ID NO: 558)
8F7	RSSQTLVHSNGYNYLN (SEQ ID NO: 559);	LGSNRAS (SEQ ID NO: 560)	MQAIQTPYT (SEQ ID NO: 561)
8F8	RASQSISSWLA (SEQ ID NO: 562);	KASNLES (SEQ ID NO: 563)	QQYNSYSCT (SEQ ID NO: 564)

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Light Chain			
mAb	**CDRL1**	**CDRL2**	**CDRL3**
9D8	QASQDINNYLH (SEQ ID NO: 565);	DASDWET (SEQ ID NO: 566)	QQYDHLPIT (SEQ ID NO: 567)
9E10	QASQDISNYLH (SEQ ID NO: 568);	DASDLET (SEQ ID NO: 569)	QQYDHLPIT (SEQ ID NO: 570)
9E5	QASQDISNYLH (SEQ ID NO: 571);	DASDLET (SEQ ID NO: 572)	QQYDHLPIT (SEQ ID NO: 573)
9F4	QASQDISNYLN (SEQ ID NO: 574);	DASNLET (SEQ ID NO: 575)	QQYDNLPYT (SEQ ID NO: 576)
9F8	RSSQSLLYSNGYNYLD (SEQ ID NO: 577);	LNSNRAS (SEQ ID NO: 578)	MQALQTPLT (SEQ ID NO: 579)

[0189] The disclosure encompasses modifications to the CARs and polypeptides comprising the sequences shown in Tables 1 or 2A-2B, including functionally equivalent CARs having modifications which do not significantly affect their properties and variants which have enhanced or decreased activity and/or affinity. For example, the amino acid sequence may be mutated to obtain an antibody with the desired binding affinity to CD70. Modification of polypeptides is routine practice in the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or which mature (enhance) the affinity of the polypeptide for its ligand, or use of chemical analogs.

[0190] Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue or the antibody fused to an epitope tag. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody of an enzyme or a polypeptide which increases the half-life of the antibody in the blood circulation.

[0191] Substitution variants have at least one amino acid residue in the antibody molecule removed and a different residue inserted in its place. The sites of greatest interest for

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substitutional mutagenesis include the hypervariable regions, but FR alterations are also contemplated. Conservative substitutions are shown in Table 3 under the heading of "conservative substitutions." If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 3, or as further described below in reference to amino acid classes, may be introduced and the products screened.

Table 3: Amino Acid Substitutions

Original Residue (naturally occurring amino acid)	Conservative Substitutions	Exemplary Substitutions
Ala (A)	Val	Val; Leu; Ile
Arg (R)	Lys	Lys; Gln; Asn
Asn (N)	Gln	Gln; His; Asp, Lys; Arg
Asp (D)	Glu	Glu; Asn
Cys (C)	Ser	Ser; Ala
Gln (Q)	Asn	Asn; Glu
Glu (E)	Asp	Asp; Gln
Gly (G)	Ala	Ala
His (H)	Arg	Asn; Gln; Lys; Arg
Ile (I)	Leu	Leu; Val; Met; Ala; Phe; Norleucine
Leu (L)	Ile	Norleucine; Ile; Val; Met; Ala; Phe
Lys (K)	Arg	Arg; Gln; Asn
Met (M)	Leu	Leu; Phe; Ile
Phe (F)	Tyr	Leu; Val; Ile; Ala; Tyr
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr	Tyr; Phe
Tyr (Y)	Phe	Trp; Phe; Thr; Ser
Val (V)	Leu	Ile; Leu; Met; Phe; Ala; Norleucine

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[0192] In some embodiments, the disclosure provides a CAR comprising an extracellular ligand-binding domain that binds to CD70 and competes for binding to CD70 with a CAR described herein, including CAR comprising an extracellular domain comprising an ScFv comprising the sequences of 31H1, 63B2, 40E3, 42C3, 45F11, 64F9, 72C2, 2F10, 4F11, 10H10, 17G6, 65E11, P02B10, P07D03, P08A02, P08E02, P08F08, P08G02, P12B09, P12F02, P12G07, P13F04, P15D02, P16C05, 10A1, 10E2, 11A1, 11C1, 11D1, 11E1, 12A2, 12C4, 12C5, 12D3, 12D6, 12D7, 12F5, 12H4, 8C8, 8F7, 8F8, 9D8, 9E10, 9E5, 9F4 or 9F8.

[0193] In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 20; and/or a VL region comprising a sequence shown in SEQ ID NO: 19. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 22; and/or a VL region comprising a sequence shown in SEQ ID NO: 21. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 28; and/or a VL region comprising a sequence shown in SEQ ID NO: 27. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 36; and/or a VL region comprising a sequence shown in SEQ ID NO: 35. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 46; and/or a VL region comprising a sequence shown in SEQ ID NO: 45. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 18; and/or a VL region comprising a sequence shown in SEQ ID NO: 17. In some embodiments, the disclosure provides a CAR, which specifically binds to CD70, wherein the CAR comprises a VH region comprising a sequence shown in SEQ ID NO: 34; and/or a VL region comprising a sequence shown in SEQ ID NO: 33. In some embodiments, the disclosure also provides CARs comprising CDR portions of antibodies to CD70 antibodies based on CDR contact regions. CDR contact regions are regions of an antibody that imbue specificity to the antibody for an antigen. In general, CDR contact regions include the residue positions in the CDRs and Vernier zones which are constrained in order to maintain proper loop structure for the

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antibody to bind a specific antigen. See, *e.g.*, Makabe et al., J. Biol. Chem., 283:1156-1166, 2007. Determination of CDR contact regions is well within the skill of the art.

[0194] The binding affinity (KD) of the ligand binding domain of the CD70 specific CAR as described herein to CD70 (such as human CD70) can be for example about 0.1 to about 1000 nM, for example between about 0.5nM to about 500nM, or for example between about 1nM to about 250nM. In some embodiments, the binding affinity is about any of 1000 nm, 750 nm, 500 nm, 400 nm, 300 nm, 250 nm, 200 nM, 100 nM, 90 nM, 80 nM, 70 nM, 60 nM, 50 nM, 45 nM, 40 nM, 35 nM, 30 nM, 25 nM, 20 nM, 19 nm, 18 nm, 17 nm, 16 nm, 15 nM, 10 nM, 8 nM, 7.5 nM, 7 nM, 6.5 nM, 6 nM, 5.5 nM, 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.5 nM, 0.3 nM or 0.1 nM.

[0195] In some embodiments, the binding affinity (KD) of the scFv of the ligand binding domain of the CD70-specific CAR as described herein to CD70 is about 10nM to about 100 nM, about 10nM to about 90nM, about 10nM to about 80nM, about 20nM to about 70nM, about 25nM to about 75nM, or about 40nM to about 110nM. In some embodiments, the binding affinities of the scFv described in this paragraph are for human CD70.

[0196] In some embodiments, the binding affinity is less than about any of 1000 nm, 900 nm, 800 nm, 250 nM, 200 nM, 100 nM, 50 nM, 30 nM, 20 nM, 10 nM, 7.5 nM, 7 nM, 6.5 nM, 6 nM, 5 nM.

[0197] The intracellular signaling domain of a CAR according to the disclosure is responsible for intracellular signaling following the binding of extracellular ligand-binding domain to the target resulting in the activation of the immune cell and immune response. The intracellular signaling domain has the ability to activate of at least one of the normal effector functions of the immune cell in which the CAR is expressed. For example, the effector function of a T cell can be a cytolytic activity or helper activity including the secretion of cytokines.

[0198] In some embodiments, an intracellular signaling domain for use in a CAR can be the cytoplasmic sequences of, for example without limitation, the T cell receptor and co-receptors that act in concert to initiate signal transduction following antigen receptor engagement, as well as any derivative or variant of these sequences and any synthetic sequence that has the same functional capability. Intracellular signaling domains comprise two distinct classes of cytoplasmic signaling sequences: those that initiate antigen-dependent primary activation, and those that act in an antigen- independent manner to provide a secondary or co-stimulatory signal. Primary cytoplasmic signaling sequences can comprise signaling motifs which are

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known as immunoreceptor tyrosine-based activation motifs of ITAMs. ITAMs are well defined signaling motifs found in the intracytoplasmic tail of a variety of receptors that serve as binding sites for syk/zap70 class tyrosine kinases. Examples of ITAM used in the disclosure can include as non limiting examples those derived from TCRζ, FcRγ, FcRβ, FcRε, CD3γ, CD3δ, CD3ε, CD5, CD22, CD79a, CD79b and CD66d. In some embodiments, the intracellular signaling domain of the CAR can comprise the CD3ζ signaling domain which has amino acid sequence with at least about 70%, at least 80%, at least 90%, 95%, 97%, or 99% sequence identity with an amino acid sequence shown in SEQ ID NO: 272 or 683. In some embodiments the intracellular signaling domain of the CAR of the disclosure comprises a domain of a co-stimulatory molecule.

[0199] In some embodiments, the intracellular signaling domain of a CAR of the disclosure comprises a part of co-stimulatory molecule selected from the group consisting of fragment of 41BB (GenBank: AAA53133.) and CD28 (NP_006130.1). In some embodiments, the intracellular signaling domain of the CAR of the disclosure comprises amino acid sequence which comprises at least 70%, at least 80%, at least 90%, 95%, 97%, or 99% sequence identity with an amino acid sequence shown in SEQ ID NO: 271 or 682 and SEQ ID NO: 275. In some embodiments, the intracellular signaling domain of the CAR of the disclosure comprises amino acid sequence which comprises at least 70%, at least 80%, at least 90%, 95%, 97%, or 99% sequence identity with an amino acid sequence shown in SEQ ID NO: 271 or 682 and/or at least 70%, at least 80%, at least 90%, 95%, 97%, or 99% sequence identity with an amino acid sequence shown in SEQ ID NO: 276.

[0200] CARs are expressed on the surface membrane of the cell. Thus, the CAR can comprise a transmembrane domain. Suitable transmembrane domains for a CAR disclosed herein have the ability to (a) be expressed at the surface of a cell, which is in some embodiments an immune cell such as, for example without limitation, a lymphocyte cell, such as a T helper (T_h) cell, cytotoxic T (T_c) cell, T regulatory (T_{reg}) cell, or Natural killer (NK) cells, and/or (b) interact with the ligand-binding domain and intracellular signaling domain for directing cellular response of an immune cell against a predefined target cell. The transmembrane domain can be derived either from a natural or from a synthetic source. The transmembrane domain can be derived from any membrane-bound or transmembrane protein. As non-limiting examples, the transmembrane polypeptide can be a subsequence or subunit of the T cell receptor such as α, β, γ or δ, polypeptide constituting CD3 complex, IL-2 receptor p55 (a

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chain), p75 (β chain) or γ chain, subunit chain of Fc receptors, in particular Fcγ receptor III or CD proteins. Alternatively, the transmembrane domain can be synthetic and can comprise predominantly hydrophobic residues such as leucine and valine. In some embodiments said transmembrane domain is derived from the human CD8α chain (*e.g.*, NP_001139345.1). The transmembrane domain can further comprise a stalk domain between the extracellular ligand-binding domain and said transmembrane domain. A stalk domain may comprise up to 300 amino acids—in some embodiments 10 to 100 amino acids or in some embodiments 25 to 50 amino acids. Stalk region may be derived from all or part of naturally occurring molecules, such as from all or part of the extracellular region of CD8, CD4, CD28, 4-1BB, or IgG (in particular, the hinge region of an IgG), or from all or part of an antibody heavy-chain constant region. Alternatively the stalk domain may be a synthetic sequence that corresponds to a naturally occurring stalk sequence, or may be an entirely synthetic stalk sequence. In some embodiments said stalk domain is a part of human CD8α chain (*e.g.*, NP_001139345.1). In another particular embodiment, said hinge and transmembrane domains comprise a part of human CD8α chain, which in some embodiments comprises at least 70%, at least 80%, at least 90%, 95% 97%, or 99% sequence identity with amino acid sequence selected from the group consisting of SEQ ID NO: 268 and 270. In some embodiments, the stalk domain of CARs described herein comprises a subsequence of CD8α, an IgG1, or an FcγRIIIα, in particular the hinge region of any of an CD8α, an IgG1, or an FcγRIIIα. In some embodiments, the stalk domain comprises a human CD8α hinge, a human IgG1 hinge, or a human FcγRIIIα hinge In some embodiments, CARs disclosed herein can comprise an extracellular ligand-binding domain that specifically binds CD70. In some embodiments the CARs disclosed herein comprise an scFv, CD8α human hinge and transmembrane domains, the CD3ζ signaling domain, and 4-1BB signaling domain.

[0201] Table 4 provides exemplary sequences of domains which can be used in the CARs disclosed herein.

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Table 4: Exemplary sequences of CAR Components

Domain	Amino Acid Sequence	SEQ ID NO:
CD8α signal peptide	MALPVTALLLPLALLLHAARP	266
FcγRIIIα hinge	GLAVSTISSFFPPGYQ	267
CD8α hinge	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD	268
IgG1 hinge	EPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	269
CD8α transmembrane (TM) domain	IYIWAPLAGTCGVLLLSLVITLYC	270
41BB intracellular signaling domain (ISD)	KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL	271
41BB intracellular signaling domain (ISD)	GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL	682
CD3ζ intracellular signaling domain (ISD)	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	272
CD3ζ intracellular signaling domain (ISD)	RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	683

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Domain	Amino Acid Sequence	SEQ ID NO:
FcεRI α-TM-IC (FcεRI α chain transmembrane and intracellular domain)	FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLL NPHPKPNPKNN	273
FcεRIβ-ΔITAM (FcεRI β chain without ITAM)	MDTESNRRANLALPQEPSSVPAFEVLEISPQEVSSGRLLK SASSPPLHTWLTVLKKEQEFLGVTQILTAMICLCFGTVV CSVLDISHIEGDIFSSFKAGYPFWGAIFFSISGMLSIISERR NATYLVRGSLGANTASSIAGGTGITILIINLKKSLAYIHIH SCQKFFETKCFMASFSTEIVVMMLFLTILGLGSAVSLTIC GAGEELKGNKVPE	274
CD28-IC (CD28 co-stimulatory domain)	RSKRSRGGHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRS	276
FcεRIγ-SP (signal peptide)	MIPAVVLLLLLLVEQAAA	277
FcεRI γ-ΔITAM (FcεRI γ chain without ITAM)	LGEPQLCYILDAILFLYGIVLTLLYCRLKIQVRKAAITSYE KS	278
GSG-P2A (GSG-P2A ribosomal skip polypeptide)	GSGATNFSLLKQAGDVEENPGP	279
GSG-T2A (GSG-T2A ribosomal skip polypeptide)	GSGEGRGSLLTCGDVEENPGP	280

[0202] Downregulation or mutation of target antigens is commonly observed in cancer cells, creating antigen-loss escape variants. Thus, to offset tumor escape and render immune cell more specific to target, the CD70-specific CAR can comprise one or more additional

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extracellular ligand-binding domains, to simultaneously bind different elements in target thereby augmenting immune cell activation and function. In some embodiments, the extracellular ligand-binding domains can be placed in tandem on the same transmembrane polypeptide, and optionally can be separated by a linker. In some embodiments, said different extracellular ligand- binding domains can be placed on different transmembrane polypeptides composing the CAR. In some embodiments, the disclosure relates to a population of CARs, each CAR comprising a different extracellular ligand-binding domain. In a particular, the disclosure relates to a method of engineering immune cells comprising providing an immune cell and expressing at the surface of the cell a population of CARs, each CAR comprising different extracellular ligand-binding domains. In another particular embodiment, the disclosure relates to a method of engineering an immune cell comprising providing an immune cell and introducing into the cell polynucleotides encoding polypeptides composing a population of CAR each one comprising different extracellular ligand-binding domains. By population of CARs, it is meant at least two, three, four, five, six or more CARs each one comprising different extracellular ligand-binding domains. The different extracellular ligand-binding domains according to the disclosure can, in some embodiments, simultaneously bind different elements in target thereby augmenting immune cell activation and function. The disclosure also relates to an isolated immune cell which comprises a population of CARs each one comprising different extracellular ligand-binding domains.

[0203] In another aspect, the disclosure provides polynucleotides encoding any of the CARs and polypeptides described herein. Polynucleotides can be made and expressed by procedures known in the art.

[0204] In another aspect, the disclosure provides compositions (such as a pharmaceutical compositions) comprising any of the cells of the disclosure. In some embodiments, the composition comprises a cell comprising a polynucleotide encoding any of the CARs described herein. In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 297 and SEQ ID NO:298, SEQ ID NO: 299 and SEQ ID NO:300, SEQ ID NO: 301 and SEQ ID NO:302, SEQ ID NO: 303 and SEQ ID NO:304, SEQ ID NO: 305 and SEQ ID NO:306, SEQ ID NO: 307 and SEQ ID NO:308 or SEQ ID NO: 309 and SEQ ID NO:310, below:

4F11 heavy chain variable region

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CAGGTCACCTTGAAGGAGTCTGGTCCTGTGCTGGTGAAACCCACAGAGACCCTCAC
GCTGACCTGCACCGTCTCTGGGTTCTCACTCAGTAATGCTAGAATGGGTGTGACCTG
GATCCGTCAGCCCCCAGGGAAGGCCCTGGAGTGGCTTGCACACATTTTTTCGAATGA
CGAAAAATCCTACAGTACATCTCTGAAGAGCAGGCTCACCATCTCCAAGGACACTT
CCAAAACCCAGGTGGTCCTTACCATGACCAACATGGACCCTGTGGACACAGCCACA
TATTACTGTGCACGGATACGAGATTACTATGACATTAGTAGTTATTATGACTACTGG
GGCCAGGGAACCCTGGTCAGCGTCTCCTCA (SEQ ID NO: 297)

4F11 light chain variable region

GACATCCAGATGACCCAGTCTCCATCTGCCATGTCTGCATCTGTAGGAGACAGAGTC
ACCATCACTTGTCGGGCGAGTCAGGACATTAGCAATTATTTAGCCTGGTTTCAGCAG
AAACCAGGGAAAGTCCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGCAAAGTGG
GGTCCCATCAAGGTTCAGCGGCAGTGGATCGGGGACAGAATTCACTCTCACAATCA
GCAGCCTGCTGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCTTAATAGTTTCCC
GTTCACTTTTGGCGGAGGGACCAAGGTGGAGATCAAC (SEQ ID NO: 298)

[0205] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 299 and SEQ ID NO:300 below:

17G6 heavy chain variable region

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAG
ACTCTCCTGTGTAGCCTCTGGATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAGCATAAAGCAAGATGGAAGT
GAGAAATACTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGC
CAAGAACTCAGTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGGTGTGT
ATTACTGTGCGAGAGAAGGAGTCAACTGGGGATGGAGACTCTACTGGCACTTCGAT
CTCTGGGGCCGTGGAACCCTGGTCACTGTCTCCTCA (SEQ ID NO: 299)

17G6 light chain variable region

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCC
ACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTACAACAATAAGAACTA
CGTAGCTTGGTACCAGCAGAAACCAGGACAACCTCCTAACCTACTCATTTTCTGGGC
ATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAG

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ATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTACTACTGTC
AGCAATATTATAGTACGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
(SEQ ID NO: 300).

[0206] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 301 and SEQ ID NO:302 below:

10H10 heavy chain variable region

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAG
ACTCTCCTGTGCAGTCTCTGGATTCACCTTCAGTAACCATAACATACACTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATTTCATACATTAGTCGAAGTAGTAGTA
CCATATATTACGCAGACTCTGTGAAGGGCCGATTCACAATCTCCAGAGACAATGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGACGAAGACACGGCTGTGTA
TTACTGTGCGAGAGATCACGCTCAGTGGTACGGTATGGACGTTTGGGGCCAAGGGA
CCACGGTCACCGTCTCCTCA (SEQ ID NO: 301).

10H10 light chain variable region

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCGGTAGGAGACAGAGTC
ACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCA
GAAACCAGGGAAAGCCCCTAAGGTCCTGATCTATGCTGCATCCAGTTTGCAAAGTG
GGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCA
GCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTTTCAGTTTCC
CATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA (SEQ ID NO: 302).

[0207] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 303 and SEQ ID NO:304 below:

P07D03 heavy chain variable region

GAAGTGCAGCTTGTCCAGAGCGGAGCCGAAGTGAAGAAGCCTGGCGAGAGCCTGA
AGATCAGCTGCAAGGGCTCCGGATATCGCTTCACAAGTTACTGGATAGGGTGGGTG
CGCCAGATGCCTGGTAAGGGACTGGAATGGATGGGCTCTATATATCCTGATGATTCC
GACACACGTTATAGCCCAAGCTTTCAGGGCCAGGTCACAATCAGCGCTGACAAGAG
CATCAGCACCGCCTACCTTCAGTGGTCGTCTCTGAAGGCCAGCGACACCGCAATGTA

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CTACTGCGCCTCTAGCACAGTTGACTACCCGGGATACAGTTACTTCGACTACTGGGG
CCAAGGTACACTGGTCACCGTCAGCAGC (SEQ ID NO: 303)

P07D03 light chain variable region

GAGCTCCAGAGCGTGCTGACCCAGCCTCCTAGCGCAAGCGGCACCCCTGGACAGCG
TGTGACAATTAGCTGTAGCGGAAGTCGTAGCAATATCGGATCAAACTATGTGTATTG
GTATCAGCAATTGCCCGGTACAGCACCCAAATTGCTCATATATAGAAATAATCAGA
GACCTAGCGGAGTGCCTGATCGTTTTAGCGGTAGCAAAAGCGGCACCAGCGCATCA
CTGGCAATTTCAGGCCTGCGTAGCGAAGATGAGGCGGATTATTACTGTGCGAGTTG
GGATGGTTCGCTGAGTGCTGTTGTGTTCGGCACCGGTACAAAACTGACCGTTCTG
(SEQ ID NO: 304)

[0208] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 305 and SEQ ID NO:306 below:

P08G02 heavy chain variable region

GAAGTGCAGCTTGTCCAGAGCGGAGCCGAAGTGAAGAAGCCTGGCGAGAGCCTGA
AGATCAGCTGCAAGGGCTCCGGATACACCTTTCCTTCATCATGGATAGGTTGGGTGC
GCCAGATGCCTGGTAAGGGACTGGAATGGATGGGCATCATATACCCTGATACTAGC
CATACCCGTTACAGCCCAAGCTTTCAGGGCCAGGTCACAATCAGCGCTGACAAGAG
CATCAGCACCGCCTACCTTCAGTGGTCGTCTCTGAAGGCCAGCGACACCGCAATGTA
CTACTGTGCCCGTGCGAGCTATTTCGATCGTGGAACAGGGTATAGTTCTTGGTGGAT
GGATGTGTGGGGCCAAGGTACACTGGTCACCGTCAGCAGC (SEQ ID NO: 305)

P08G02 light chain variable region

GAGCTCGATATTCAGATGACCCAGAGCCCTAGCAGCCTGAGCGCAAGCGTGGGCGA
TAGAGTGACCATTACCTGTAGGGCCTCACAATCCATATACGACTATTTGCACTGGTA
TCAGCAGAAACCCGGGAAAGCACCCAAACTGCTGATTTACGATGCTTCCAACCTAC
AGAGTGGCGTTCCTTCACGTTTTAGCGGTAGCGGTTCAGGCACCGATTTCACCCTGA
CCATTAGCAGCCTTCAGCCCGAAGATTTCGCTACGTATTATTGCCAGCAATCATACA
CCACGCCGTTGTTTACATTCGGCCAGGGTACCAAAGTGGAAATCAAA (SEQ ID NO: 306)

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[0209] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 307 and SEQ ID NO: 308 below:

P08F08 heavy chain variable region

GAAGTGCAGCTTGTCCAGAGCGGAGCCGAAGTGAAGAAGCCTGGCGAGAGCCTGA
AGATCAGCTGCAAGGGCTCCGGATACGGATTCACAAGTTATTGGATAGGTTGGGTG
CGCCAGATGCCTGGTAAGGGACTGGAATGGATGGGTATCATTCATCCCGATGATAG
CGACACCAAATACAGCCCAAGCTTTCAGGGCCAGGTCACAATCAGCGCTGACAAGA
GCATCAGCACCGCCTACCTTCAGTGGTCGTCTCTGAAGGCCAGCGACACCGCAATGT
ACTACTGTGCCTCTAGCTATTTGCGTGGCTTGTGGGGAGGCTATTTTGACTATTGGG
GCCAAGGTACACTGGTCACCGTCAGCAGC (SEQ ID NO: 307)

P08F08 light chain variable region

GAGCTCCAGAGCGTGCTGACCCAGCCTCCTAGCGCAAGCGGCACCCCTGGACAGCG
TGTGACAATTAGCTGTAGCGGATCAAGCTCAAACATTGGCTCAAATTATGTGAATTG
GTATCAGCAATTGCCCGGTACAGCACCCAAACTGCTCATTTATGGAGATTATCAACG
ACCTAGCGGAGTGCCTGATCGTTTTAGCGGTAGCAAAAGCGGCACCAGCGCATCAC
TGGCAATTTCAGGCCTGCGTAGCGAAGATGAGGCGGATTATTACTGTGCTACCCGC
GACGATTCGTTATCTGGGTCTGTCGTTTTTGGCACCGGTACAAAACTGACCGTGCTG
(SEQ ID NO: 308)

[0210] In still other embodiments, the composition comprises either or both of the polynucleotides shown in SEQ ID NO: 309 and SEQ ID NO:310 below:

P15D02 heavy chain variable region

GAAGTGCAGCTTGTCCAGAGCGGAGCCGAAGTGAAGAAGCCTGGCGAGAGCCTGA
AGATCAGCTGCAAGGGCTCCGGATACAGTTTTGCCTCATACTGGATCGGTTGGGTGC
GCCAGATGCCTGGTAAGGGACTGGAATGGATGGGCGTAATTTACCCCGGAACTAGC
GAGACACGTTACAGCCCAAGCTTTCAGGGCCAGGTCACAATCAGCGCTGACAAGAG
CATCAGCACCGCCTACCTTCAGTGGTCGTCTCTGAAGGCCAGCGACACCGCAATGTA
CTACTGCGCTAAAGGGTTGAGTGCGAGTGCAAGTGGATATTCTTTCCAATATTGGGG
CCAAGGTACACTGGTCACCGTCAGCAGC (SEQ ID NO: 309)

P15D032 light chain variable region

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GAGCTCGATATTCAGATGACCCAGAGCCCTAGCAGCCTGAGCGCAAGCGTGGGCGA
TAGAGTGACCATTACCTGTAGGGCCTCACAAAGCATCGACACATATTTAAACTGGT
ATCAGCAGAAACCCGGGAAAGCACCCAAACTGCTGATTTATTCAGCTAGTAGCCTA
CACAGTGGCGTTCCTTCACGTTTTAGCGGTAGCGGTTCAGGCACCGATTTCACCCTG
ACCATTAGCAGCCTTCAGCCCGAAGATTTCGCTACGTATTATTGCCAACAATCATAC
AGCACAACTGCTTGGACATTCGGCCAGGGTACCAAAGTGGAAATCAAA (SEQ ID NO: 310)

[0211] Expression vectors, and administration of polynucleotide compositions are further described herein.

[0212] In another aspect, the disclosure provides a method of making any of the polynucleotides described herein.

[0213] Polynucleotides complementary to any such sequences are also encompassed by the disclosure. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the disclosure, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

[0214] Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes an antibody or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants contain one or more substitutions, additions, deletions and/or insertions such that the immunoreactivity of the encoded polypeptide is not diminished, relative to a native immunoreactive molecule. The effect on the immunoreactivity of the encoded polypeptide may generally be assessed as described herein. Variants embodiments exhibit at least about 70% identity, at least about 80% identity, at least about 90% identity, or at least about 95% identity to a polynucleotide sequence that encodes a native antibody or a portion thereof.

[0215] Two polynucleotide or polypeptide sequences are said to be “identical” if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare

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local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, or 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

[0216] Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O., 1978, A model of evolutionary change in proteins - Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J., 1990, Unified Approach to Alignment and Phylogenes pp. 626-645 Methods in Enzymology vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M., 1989, CABIOS 5:151-153; Myers, E.W. and Muller W., 1988, CABIOS 4:11-17; Robinson, E.D., 1971, Comb. Theor. 11:105; Santou, N., Nes, M., 1987, Mol. Biol. Evol. 4:406-425; Sneath, P.H.A. and Sokal, R.R., 1973, Numerical Taxonomy the Principles and Practice of Numerical Taxonomy, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J., 1983, Proc. Natl. Acad. Sci. USA 80:726-730.

[0217] The "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.* the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

[0218] Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native antibody (or a complementary sequence).

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[0219] Suitable "moderately stringent conditions" include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1 % SDS.

[0220] As used herein, "highly stringent conditions" or "high stringency conditions" are those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0221] It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the disclosure. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the disclosure. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

[0222] The polynucleotides of this disclosure can be obtained using chemical synthesis, recombinant methods, or PCR. Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the

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sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

[0223] For preparing polynucleotides using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification, as further discussed herein. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct uptake, endocytosis, transfection, F-mating or electroporation. Once introduced, the exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide so amplified can be isolated from the host cell by methods well known within the art. See, *e.g.*, Sambrook et al., 1989.

[0224] Alternatively, PCR allows reproduction of DNA sequences. PCR technology is well known in the art and is described in U.S. Patent Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as PCR: The Polymerase Chain Reaction, Mullis et al. eds., Birkauswer Press, Boston, 1994.

[0225] RNA can be obtained by using the isolated DNA in an appropriate vector and inserting it into a suitable host cell. When the cell replicates and the DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook et al., 1989, supra, for example.

[0226] Suitable cloning vectors may be constructed according to standard techniques, or may be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate, may possess a single target for a particular restriction endonuclease, and/or may carry genes for a marker that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, *e.g.*, pUC18, pUC19, Bluescript (*e.g.*, pBS SK+) and its derivatives, mp18, mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Strategene, and Invitrogen.

[0227] Expression vectors generally are replicable polynucleotide constructs that contain a polynucleotide according to the disclosure. It is implied that an expression vector must be replicable in the host cells either as episomes or as an integral part of the chromosomal DNA.

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Suitable expression vectors include but are not limited to plasmids, viral vectors, including adenoviruses, adeno-associated viruses, retroviruses, cosmids, and expression vector(s) disclosed in PCT Publication No. WO87/04462, or the lentiviral pLVX vector available from Clonetech. Vector components may generally include, but are not limited to, one or more of the following: a signal sequence; an origin of replication; one or more marker genes; suitable transcriptional controlling elements (such as promoters, enhancers and terminator). For expression (*i.e.*, translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons.

[0228] The vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (*e.g.*, where the vector is an infectious agent such as vaccinia virus). The choice of introducing vectors or polynucleotides will often depend on features of the host cell.

[0229] A polynucleotide encoding a CD70-specific CAR disclosed herein may exist in an expression cassette or expression vector (*e.g.*, a plasmid for introduction into a bacterial host cell, or a viral vector such as a baculovirus vector for transfection of an insect host cell, or a plasmid or viral vector such as a lentivirus for transfection of a mammalian host cell). In some embodiments, a polynucleotide or vector can include a nucleic acid sequence encoding ribosomal skip sequences such as, for example without limitation, a sequence encoding a 2A peptide. 2A peptides, which were identified in the Aphthovirus subgroup of picornaviruses, causes a ribosomal "skip" from one codon to the next without the formation of a peptide bond between the two amino acids encoded by the codons (see (Donnelly and Elliott 2001; Atkins, Wills et al. 2007; Doronina, Wu et al. 2008)). By "codon" is meant three nucleotides on an mRNA (or on the sense strand of a DNA molecule) that are translated by a ribosome into one amino acid residue. Thus, two polypeptides can be synthesized from a single, contiguous open reading frame within an mRNA when the polypeptides are separated by a 2A oligopeptide sequence that is in frame. Such ribosomal skip mechanisms are well known in the art and are known to be used by several vectors for the expression of several proteins encoded by a single messenger RNA.

[0230] To direct transmembrane polypeptides into the secretory pathway of a host cell, in some embodiments, a secretory signal sequence (also known as a leader sequence, prepro sequence

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or pre sequence) is provided in a polynucleotide sequence or vector sequence. The secretory signal sequence is operably linked to the transmembrane nucleic acid sequence, *i.e.*, the two sequences are joined in the correct reading frame and positioned to direct the newly synthesized polypeptide into the secretory pathway of the host cell. Secretory signal sequences are commonly positioned 5' to the nucleic acid sequence encoding the polypeptide of interest, although certain secretory signal sequences may be positioned elsewhere in the nucleic acid sequence of interest (see, *e.g.*, Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830). In some embodiments the signal peptide comprises the amino acid sequence shown in SEQ ID NO: 266 or 277. Those skilled in the art will recognize that, in view of the degeneracy of the genetic code, considerable sequence variation is possible among these polynucleotide molecules. In some embodiments, nucleic acid sequences of the disclosure are codon-optimized for expression in mammalian cells, or in some embodiments for expression in human cells. Codon-optimization refers to the exchange in a sequence of interest of codons that are generally rare in highly expressed genes of a given species by codons that are generally frequent in highly expressed genes of such species, such codons encoding the amino acids as the codons that are being exchanged.

CD70-SPECIFIC ANTIBODIES AND METHODS OF MAKING THEREOF

[0231] Provided herein are CD70 antibodies.

[0232] In some embodiments, a CD70 antibody of the disclosure comprises any one of the partial light chain sequence as listed in Table 1 and/or any one of the partial heavy chain sequence as listed in Table 1. In Table 1, the underlined sequences are CDR sequences according to Kabat and in bold according to Chothia.

[0233] Tables 2A-2B provide examples of CDR sequences of the CD70 antibodies provided herein.

[0234] In some embodiments, the disclosure provides an antibody (*e.g.* including antibody fragments, such as single chain variable fragments (scFvs) which specifically binds to Cluster of Differentiation 70 (CD70), wherein the antibody comprises (a) a heavy chain variable (VH) region comprising (i) a VH complementarity determining region one (CDR1) comprising the sequence shown in SEQ ID NO: 49, 50, 51, 55, 56, 57, 61, 62, 63, 67, 68, 69, 73, 74, 75, 79, 80, 81, 85, 86, 87, 91, 92, 93, 97, 98, 99, 103, 104, 105, 109, 110, 111, 115, 116, 117, 121, 122, 123, 127, 128, 129, 133, 134, 135, 139, 140, 141, 145, 146, 147, 151, 152, 153, 157, 158, 159, 163, 164, 165, 169, 170, 171, 175, 176, 177, 181, 182, 183, 187,

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188, 189, 382, 383, 384, 388, 389, 390, 394, 395, 396, 400, 401, 402, 406, 407, 408, 412, 413, 414, 418, 419, 420, 424, 425, 426, 430, 431, 432, 663, 664, 665, 436, 437, 438, 442, 443, 444, 448, 449, 450, 454, 455, 456, 460, 461, 462, 466, 467, 468, 472, 473, 474, 478, 479, 480, 484, 485, 486, 490, 491, 492, 496, 497, 498, 502, 503, 504, 508, 509, or 510; (ii) a VH CDR2 comprising the sequence shown in SEQ ID NO: 52, 53, 58, 59, 64, 65, 70, 71, 76, 77, 82, 83, 88, 89, 94, 95, 100, 101, 106, 107, 112, 113, 118, 119, 124, 125, 130, 131, 136, 137, 142, 143, 148, 149, 154, 155, 160, 161, 166, 167, 172, 173, 178, 179, 184, 185, 190, 191, 385, 386, 391, 392, 397, 398, 403, 404, 409, 410, 415, 416, 421, 422, 427, 428, 433, 434, 666, 667, 439, 440, 445, 446, 451, 452, 457, 458, 463, 464, 469, 470, 475, 476, 481, 482, 487, 488, 493, 494, 499, 500, 505, 506, 511, or 512; and iii) a VH CDR3 comprising the sequence shown in SEQ ID NO: 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 387, 393, 399, 405, 411, 417, 423, 429, 435, 668, 441, 447, 453, 459, 465, 471, 477, 483, 489, 495, 501, 507, or 513; and/or a light chain variable (VL) region comprising (i) a VL CDR1 comprising the sequence shown in SEQ ID NO: 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 235, 238, 241, 244, 247, 250, 253, 256, 259, 262, 514, 517, 520, 523, 526, 529, 532, 535, 538, 669, 541, 544, 547, 550, 553, 556, 559, 562, 565, 568, 571, 574, or 577; (ii) a VL CDR2 comprising the sequence shown in SEQ ID NO: 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 233, 236, 239, 242, 245, 248, 251, 254, 257, 260, 263, 515, 518, 521, 524, 527, 530, 533, 536, 539, 670, 542, 545, 548, 551, 554, 557, 560, 563, 566, 569, 572, 575, or 578; and (iii) a VL CDR3 comprising the sequence shown in SEQ ID NO: 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 234, 237, 240, 243, 246, 249, 252, 255, 258, 261, 264, 516, 519, 522, 525, 528, 531, 534, 537, 540, 671, 543, 546, 549, 552, 555, 558, 561, 564, 567, 570, 573, 576, or 579.

[0235] In some embodiments, the disclosure provides an antibody (e.g. a scFv), which specifically binds to Cluster of Differentiation 70 (CD70), wherein the antibody comprises a heavy chain variable (VH) region comprising a VH CDR1, VH CDR2, and VH CDR3 of the VH sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 662, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, or 381; and/or a light chain variable (VL) region comprising VL CDR1, VL CDR2, and VL CDR3 of the VL sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47,

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338, 340, 342, 344, 346, 348, 350, 352, 354, 661, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, or 380.

[0236] In some embodiments, the disclosure provides an isolated antibody which specifically binds to CD70 and competes with any of the foregoing antibodies.

[0237] In some embodiments, the present invention provides an antibody that binds to CD70 and competes with an antibody as described herein, including 31H1, 63B2, 40E3, 42C3, 45F11, 64F9, 72C2, 2F10, 4F11, 10H10, 17G6, 65E11, P02B10, P07D03, P08A02, P08E02, P08F08, P08G02, P12B09, P12F02, P12G07, P13F04, P15D02, P16C05, 10A1, 10E2, 11A1, 11C1, 11D1, 11E1, 12A2, 12C4, 12C5, 12D3, 12D6, 12D7, 12F5, 12H4, 8C8, 8F7, 8F8, 9D8, 9E10, 9E5, 9F4 or 9F8.

[0238] In some embodiments, the invention also provides CDR portions of antibodies to CD70 antibodies based on CDR contact regions. CDR contact regions are regions of an antibody that imbue specificity to the antibody for an antigen. In general, CDR contact regions include the residue positions in the CDRs and Vernier zones which are constrained in order to maintain proper loop structure for the antibody to bind a specific antigen. See, *e.g.*, Makabe et al., *J. Biol. Chem.*, 283:1156-1166, 2007. Determination of CDR contact regions is well within the skill of the art.

[0239] The binding affinity (K_D) of the CD70 antibody as described herein to CD70 (such as human CD70 (e.g., (SEQ ID NO: 335)) can be about 0.001 to about 5000 nM. In some embodiments, the binding affinity is about any of 5000 nM, 4500 nM, 4000 nM, 3500 nM, 3000 nM, 2500 nM, 2000 nM, 1789 nM, 1583 nM, 1540 nM, 1500 nM, 1490 nM, 1064 nM, 1000 nM, 933 nM, 894 nM, 750 nM, 705 nM, 678 nM, 532 nM, 500 nM, 494 nM, 400 nM, 349 nM, 340 nM, 353 nM, 300 nM, 250 nM, 244 nM, 231 nM, 225 nM, 207 nM, 200 nM, 186 nM, 172 nM, 136 nM, 113 nM, 104 nM, 101 nM, 100 nM, 90 nM, 83 nM, 79 nM, 74 nM, 54 nM, 50 nM, 45 nM, 42 nM, 40 nM, 35 nM, 32 nM, 30 nM, 25 nM, 24 nM, 22 nM, 20 nM, 19 nM, 18 nM, 17 nM, 16 nM, 15 nM, 12 nM, 10 nM, 9 nM, 8 nM, 7.5 nM, 7 nM, 6.5 nM, 6 nM, 5.5 nM, 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.5 nM, 0.3 nM, 0.1 nM, 0.01 nM, or 0.001 nM. In some embodiments, the binding affinity is less than about any of 5000 nM, 4000 nM, 3000 nM, 2000 nM, 1000 nM, 900 nM, 800 nM, 250 nM, 200 nM, 100 nM, 50 nM, 30 nM, 20 nM, 10 nM, 7.5 nM, 7 nM, 6.5 nM, 6 nM, 5 nM, 4.5 nM, 4 nM, 3.5 nM, 3 nM, 2.5 nM, 2 nM, 1.5 nM, 1 nM, or 0.5 nM.

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[0240] In some embdoiments, the disclosure provides a nucleic acid encoding any of the foregoing isolated antibodies. In some embodiments, the disclosure provides a vector comprising such a nucleic acid. In some embodiments, the disclosure provides a host cell comprising such a nucleic acid.

[0241] The disclosure further provides any of the antibodies of the foregoing antibodies for use as a medicament. In some embodiments, the medicament is for us in treatment of a CD70-related cancer selected from the group consisting of Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom’s macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

[0242] In some embodiments, the disclosure provides a method of treating a subject in need thereof, comprising providing any of the foregoing antibodies, and administering said antibody to said subject.

[0243] In some embodiments, the disclosure provides a pharmaceutical composition comprising any of the foregoing antibodies.

[0244] In some embodiments, the disclosure provides a method of treating a condition associated with malignant cells expressing CD70 in a subject comprising administering to a subject in need thereof an effective amount of any one of the foregoing antibodies or a pharmaceutical composition comprising any one of the foregoing antibodies. In some embodiments, the condition is cancer. In some embodiments, the cancer is an CD70 related cancer selected from the group consisting of Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom’s macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

[0245] In some embodiments, the disclosure provides, a method of inhibiting tumor growth or progression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of a pharmaceutical composition of the disclosure to the subject.

[0246] In some embodiments, the disclosure provides, a method of inhibiting metastasis of malignant cells expressing CD70 in a subject, comprising administering to the subject in need thereof an effective amount of a pharmaceutical composition of the disclosure to the subject.

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[0247] In some embodiments, the disclosure provides, a method of inducing tumor regression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of a pharmaceutical composition of the disclosure to the subject.

[0248] In some embodiments, the antibody, comprising culturing the host cell of the disclosure under conditions that result in production of the antibody, and isolating the antibody from the host cell or culture.

[0249] The antibodies useful in the present invention can encompass monoclonal antibodies, polyclonal antibodies, antibody fragments (*e.g.*, Fab, Fab', F(ab')2, Fv, Fc, etc.), chimeric antibodies, bispecific antibodies, heteroconjugate antibodies, single chain (ScFv), mutants thereof, fusion proteins comprising an antibody portion (e.g., a domain antibody), humanized antibodies, and any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site of the required specificity, including glycosylation variants of antibodies, amino acid sequence variants of antibodies, and covalently modified antibodies. The antibodies may be murine, rat, human, or any other origin (including chimeric or humanized antibodies).

[0250] In some embodiments, the CD70 monospecific antibody as described herein is a monoclonal antibody. For example, the CD70 monospecific antibody is a human monoclonal antibody.

[0251] The disclosure further provides the following illustrative embodiments:

1. An isolated antibody, which specifically binds to Cluster of Differentiation 70 (CD70), wherein the antibody comprises

(a) a heavy chain variable (VH) region comprising (i) a VH complementarity determining region one (CDR1) comprising the sequence shown in SEQ ID NO: 49, 50, 51, 55, 56, 57, 61, 62, 63, 67, 68, 69, 73, 74, 75, 79, 80, 81, 85, 86, 87, 91, 92, 93, 97, 98, 99, 103, 104, 105, 109, 110, 111, 115, 116, 117, 121, 122, 123, 127, 128, 129, 133, 134, 135, 139, 140, 141, 145, 146, 147, 151, 152, 153, 157, 158, 159, 163, 164, 165, 169, 170, 171, 175, 176, 177, 181, 182, 183, 187, 188, 189, 382, 383, 384, 388, 389, 390, 394, 395, 396, 400, 401, 402, 406, 407, 408, 412, 413, 414, 418, 419, 420, 424, 425, 426, 430, 431, 432, 663, 664, 665, 436, 437, 438, 442, 443, 444, 448, 449, 450, 454, 455, 456, 460, 461, 462, 466, 467, 468, 472, 473, 474, 478, 479, 480, 484, 485, 486, 490, 491, 492, 496, 497, 498, 502, 503, 504, 508, 509, or 510; (ii) a VH CDR2 comprising the sequence shown in

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SEQ ID NO: 52, 53, 58, 59, 64, 65, 70, 71, 76, 77, 82, 83, 88, 89, 94, 95, 100, 101, 106, 107, 112, 113, 118, 119, 124, 125, 130, 131, 136, 137, 142, 143, 148, 149, 154, 155, 160, 161, 166, 167, 172, 173, 178, 179, 184, 185, 190, 191, 385, 386, 391, 392, 397, 398, 403, 404, 409, 410, 415, 416, 421, 422, 427, 428, 433, 434, 666, 667, 439, 440, 445, 446, 451, 452, 457, 458, 463, 464, 469, 470, 475, 476, 481, 482, 487, 488, 493, 494, 499, 500, 505, 506, 511, or 512; and iii) a VH CDR3 comprising the sequence shown in SEQ ID NO: 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, 120, 126, 132, 138, 144, 150, 156, 162, 168, 174, 180, 186, 192, 387, 393, 399, 405, 411, 417, 423, 429, 435, 668, 441, 447, 453, 459, 465, 471, 477, 483, 489, 495, 501, 507, or 513; and/or

(b) a light chain variable (VL) region comprising (i) a VL CDR1 comprising the sequence shown in SEQ ID NO: 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 235, 238, 241, 244, 247, 250, 253, 256, 259, 262, 514, 517, 520, 523, 526, 529, 532, 535, 538, 669, 541, 544, 547, 550, 553, 556, 559, 562, 565, 568, 571, 574, or 577; (ii) a VL CDR2 comprising the sequence shown in SEQ ID NO: 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 233, 236, 239, 242, 245, 248, 251, 254, 257, 260, 263, 515, 518, 521, 524, 527, 530, 533, 536, 539, 670, 542, 545, 548, 551, 554, 557, 560, 563, 566, 569, 572, 575, or 578; and (iii) a VL CDR3 comprising the sequence shown in SEQ ID NO: 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 234, 237, 240, 243, 246, 249, 252, 255, 258, 261, 264, 516, 519, 522, 525, 528, 531, 534, 537, 540, 671, 543, 546, 549, 552, 555, 558, 561, 564, 567, 570, 573, 576, or 579.

2. An isolated antibody which specifically binds to Cluster of Differentiation 70 (CD70), wherein the antibody comprises:

(a) a VH region comprising a VH CDR1, VH CDR2, and VH CDR3 of the VH sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 339, 341, 343, 345, 347, 349, 351, 353, 355, 662, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, or 381; and/or

(b) a VL region comprising VL CDR1, VL CDR2, and VL CDR3 of the VL sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 338, 340, 342, 344, 346, 348, 350, 352, 354, 661, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, or 380.

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3. An isolated antibody which specifically binds to CD70 and competes with the antibody of embodiment 1.

4. A nucleic acid encoding the antibody of any one of embodiments 1-3.

5. A vector comprising the nucleic acid of embodiment 4.

6. A host cell comprising the nucleic acid of embodiment 4.

7. The antibody of any one of embodiments 1-3 for use as a medicament.

8. The antibody of embodiment 7, wherein the medicament is for use in treatment of an CD70 related cancer selecting from the group consisting of Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom's macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

9. A method of treating a subject in need thereof comprising:

a. providing the antibody according to any one of embodiments 1-3; and

b. administering said antibody to said subject.

10. A pharmaceutical composition comprising the antibody of any one of embodiments 1-3.

11. A method of treating a condition associated with malignant cells expressing CD70 in a subject comprising administering to a subject in need thereof an effective amount of the antibody of any one of embodiments 1-3 or the pharmaceutical composition of embodiment 10.

12. The method of embodiment 11, wherein the condition is a cancer.

13. The method of embodiment 12, wherein the cancer is an CD70 related cancer selected from the group consisting of Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom's macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

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14. A method of inhibiting tumor growth or progression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition of embodiment 10 to the subject.

15. A method of inhibiting metastasis of malignant cells expressing CD70 in a subject, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition of embodiment 10 to the subject.

16. A method of inducing tumor regression in a subject who has malignant cells expressing CD70, comprising administering to the subject in need thereof an effective amount of the pharmaceutical composition of embodiment 10 to the subject.

17. A method of producing an antibody, comprising culturing the host cell of embodiment 6 under conditions that result in production of the antibody, and isolating the antibody from the host cell or culture.

METHODS OF ENGINEERING AN IMMUNE CELL

[0252] Methods of preparing immune cells for use in immunotherapy are provided herein. In some embodiments, the methods comprise introducing a CAR according to the disclosure into immune cells, and expanding the cells. In some embodiments, the disclosure relates to a method of engineering an immune cell comprising: providing a cell and expressing at the surface of the cell at least one CAR as described above. Methods for engineering immune cells are described in, for example, PCT Patent Application Publication Nos. WO/2014/039523, WO/2014/184741, WO/2014/191128, WO/2014/184744, and WO/2014/184143, each of which is incorporated herein by reference in its entirety. In some embodiments, the method comprises: transfecting the cell with at least one polynucleotide encoding CAR as described above, and expressing the polynucleotides in the cell.

[0253] In some embodiments, the polynucleotides are present in lentiviral vectors for stable expression in the cells.

[0254] In some embodiments, the method can further comprise a step of genetically modifying a cell by disrupting or inactivating at least one gene expressing, for example without limitation, a component of the TCR, a target for an immunosuppressive agent, an HLA gene, CD70 and/or an immune checkpoint protein such as, for example, PDCD1 or CTLA-4. By disrupting or inactivating a gene it is intended that the gene of interest is not expressed in a functional protein form. In some embodiments, the gene to be disrupted or inactivated is

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selected from the group consisting of, for example without limitation, TCRα, TCRβ, CD52, GR, PD-1, CD70 and CTLA-4. In some embodiments the method comprises disrupting or inactivating one or more genes by introducing into the cells a rare-cutting endonuclease able to selectively inactivate a gene by selective DNA cleavage. In some embodiments the rare-cutting endonuclease can be, for example, a zinc finger nuclease (ZFN), megaTAL nuclease, meganuclease, transcription activator-like effector nuclease (TALE-nuclease), or CRISPR-associated endonuclease.

[0255] In some embodiments, an additional catalytic domain is used with a rare-cutting endonuclease to enhance its capacity to inactivate targeted genes. For example, an additional catalytic domain can be a DNA end-processing enzyme. Non-limiting examples of DNA end-processing enzymes include 5-3′ exonucleases, 3-5′ exonucleases, 5-3′ alkaline exonucleases, 5′ flap endonucleases, helicases, hosphatase, hydrolases and template-independent DNA polymerases. Non-limiting examples of such catalytic domain comprise of a protein domain or catalytically active derivate of the protein domain selected from the group consisting of hExoI (EXO1_HUMAN), Yeast ExoI (EXO1_YEAST), *E. coli* ExoI, Human TREX2, Mouse TREX1, Human TREX1, Bovine TREX1, Rat TREX1, TdT (terminal deoxynucleotidyl transferase) Human DNA2, Yeast DNA2 (DNA2_YEAST). In some embodiments, an additional catalytic domain can have a 3′-5′-exonuclease activity, and In some embodiments, said additional catalytic domain is TREX, such as a TREX2 catalytic domain (WO2012/058458). In some embodiments, said catalytic domain is encoded by a single chain TREX polypeptide. The additional catalytic domain may be fused to a nuclease fusion protein or chimeric protein. In some embodiments, the additional catalytic domain is fused using, for example, a peptide linker.

[0256] In some embodiments, the method further comprises a step of introducing into cells an exogeneous nucleic acid comprising at least a sequence homologous to a portion of the target nucleic acid sequence, such that homologous recombination occurs between the target nucleic acid sequence and the exogeneous nucleic acid. In some embodimentss, said exogenous nucleic acid comprises first and second portions which are homologous to region 5′ and 3′ of the target nucleic acid sequence, respectively. The exogenous nucleic acid may also comprise a third portion positioned between the first and the second portion which comprises no homology with the regions 5′ and 3′ of the target nucleic acid sequence. Following cleavage of the target nucleic acid sequence, a homologous recombination event is stimulated between

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the target nucleic acid sequence and the exogenous nucleic acid. In some embodiments, homologous sequences of at least about 50 bp, greater than about 100 bp, or greater than about 200 bp can be used within the donor matrix. The exogenous nucleic acid can be, for example without limitation, from about 200 bp to about 6000 bp, or from about 1000 bp to about 2000 bp. Shared nucleic acid homologies are located in regions flanking upstream and downstream the site of the break, and the nucleic acid sequence to be introduced is located between the two arms.

[0257] In some embodiments, a nucleic acid successively comprises a first region of homology to sequences upstream of said cleavage; a sequence to inactivate a targeted gene selected from the group consisting of TCRα, TCRβ, CD52, CD70, glucocorticoid receptor (GR), deoxycytidine kinase (DCK), and an immune checkpoint protein such as for example programmed death-1 (PD-1); and a second region of homology to sequences downstream of the cleavage. The polynucleotide introduction step can be simultaneous, before or after the introduction or expression of the rare-cutting endonuclease. Depending on the location of the target nucleic acid sequence wherein break event has occurred, such exogenous nucleic acid can be used to knock-out a gene, *e.g.* when exogenous nucleic acid is located within the open reading frame of the gene, or to introduce new sequences or genes of interest. Sequence insertions by using such exogenous nucleic acid can be used to modify a targeted existing gene, by correction or replacement of the gene (allele swap as a non-limiting example), or to up- or down-regulate the expression of the targeted gene (promoter swap as non-limiting example), the targeted gene correction or replacement. In some embodiments, inactivation of a gene selected from the group consisting of TCRα, TCRβ, CD52, CD70, GR, DCK, and immune checkpoint proteins, can be done at a precise genomic location targeted by a specific TALE-nuclease, wherein said specific TALE-nuclease catalyzes a cleavage and wherein the exogenous nucleic acid successively comprising at least a region of homology and a sequence to inactivate one targeted gene selected from the group consisting of TCRα, TCRβ, CD52, CD70, GR, DCK, immune checkpoint proteins which is integrated by homologous recombination. In some embodiments, several genes can be, successively or at the same time, disrupted or inactivated by using several TALE-nucleases respectively and specifically targeting one defined gene and several specific polynucleotides for specific gene inactivation.

[0258] In some embodiments, the method comprises inactivation of one or more additional genes selected from the group consisting of TCRα, TCRβ, CD52, CD70, GR, DCK, and

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immune checkpoint proteins. In some embodiments, inactivation of a gene can be accomplished by introducing into the cells at least one rare-cutting endonuclease such that the rare-cutting endonuclease specifically catalyzes cleavage in a targeted sequence of the cell genome; and optionally, introducing into the cells an exogenous nucleic acid successively comprising a first region of homology to sequences upstream of the cleavage, a sequence to be inserted in the genome of the cell, and a second region of homology to sequences downstream of the cleavage; wherein the introduced exogenous nucleic acid inactivates a gene and integrates at least one exogenous polynucleotide sequence encoding at least one recombinant protein of interest. In some embodiments, the exogenous polynucleotide sequence is integrated within a gene encoding a protein selected from the group consisting of TCRα, TCRβ, CD52, CD70, GR, DCK, and immune checkpoint protein.

[0259] In another aspect, a step of genetically modifying cells can comprise: modifying T cells by disrupting or inactivating at least one gene expressing a target for an immunosuppressive agent, and; expanding the cells, optionally in presence of the immunosuppressive agent. An immunosuppressive agent is an agent that suppresses immune function by one of several mechanisms of action. An immunosuppressive agent can diminish the extent and/or voracity of an immune response. Non-limiting examples of immunosuppressive agents iinclude calcineurin inhibitors, targets of rapamycin, interleukin-2 α-chain blockers, inhibitors of inosine monophosphate dehydrogenase, inhibitors of dihydrofolic acid reductase, corticosteroids, and immunosuppressive antimetabolites. Some cytotoxic immunosuppressants act by inhibiting DNA synthesis. Others may act through activation of T cells or by inhibiting the activation of helper cells. The methods according to the disclosure allow conferring immunosuppressive resistance to T cells for immunotherapy by disrupting or inactivating the target of the immunosuppressive agent in T cells. As non-limiting examples, targets for immunosuppressive agent can be a receptor for an immunosuppressive agent such as for example without limtiation CD52, glucocorticoid receptor (GR), FKBP family gene members, and cyclophilin family gene members.

[0260] In some embodiments, the genetic modification of the method involves expression, in provided cells to engineer, of one rare-cutting endonuclease such that the rare-cutting endonuclease specifically catalyzes cleavage in one targeted gene, thereby disrupting or inactivating the targeted gene. In some embodiments, a method of engineering cells comprises at least one of the following steps: providing a T cell, such as from a cell culture or

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from a blood sample; selecting a gene in the T cell expressing a target for an immunosuppressive agent; introducing into the T cell a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) the gene encoding a target for the immunosuppressive agent, and expanding the cells, optionally in presence of the immunosuppressive agent.

[0261] In some embodiments, the method comprises: providing a T cell, such as from a cell culture or from a blood sample; selecting a gene in the T cell wherein the gene expresses a target for an immunosuppressive agent; transfecting the T cell with nucleic acid encoding a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) the gene encoding a target for the immunosuppressive agent, and expressing the rare-cutting endonucleases into the T cells; and expanding the cells, optionally in presence of the immunosuppressive agent.

[0262] In some embodiments, the rare-cutting endonuclease specifically targets CD52 or GR. In some embodiments, the gene selected for inactivation encodes CD52, and the immunosuppressive treatment comprises a humanized antibody targeting CD52 antigen. In some embodiments, the gene selected for inactivation encodes GR, and the immunosuppressive treatment comprises a corticosteroid such as dexamethasone. In some embodiments, the gene selected for inactivation is a FKBP family gene member or a variant thereof and the immunosuppressive treatment comprises FK506, also known as Tacrolimus or fujimycin. In some embodiments, the FKBP family gene member is FKBP12 or a variant thereof. In some embodiments, gene selected for inactivation is a cyclophilin family gene member or a variant thereof and the immunosuppressive treatment comprises cyclosporine.

[0263] In some embodiments, the rare-cutting endonuclease can be, for example, zinc finger nuclease (ZFN), megaTAL nuclease, meganuclease, transcription activator-like effector nuclease (TALE-nuclease), or CRISPR-associated endonuclease. In some embodiments, the rare-cutting endonuclease is a TALE-nuclease. In some embodiments, the rare-cutting nuclease is a CRISPR nuclease, with a guide RNA at least partially complementary or fully complementary to a target site.

[0264] Generally, a CRISPR-associated nuclease is supplied with a guide RNA (gRNA) or the functional equivalent. The gRNA is comprised of two parts; a crispr-RNA (crRNA) that is specific for a target genomic DNA sequence, and a trans-activating RNA (tracrRNA) that facilitates Cas binding to the DNA. In some embodiments, the crRNA and tracrRNA may be

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present in the same RNA oligonucleotide, referred to as a single guide-RNA (sgRNA). In some embodiments, the crRNA and tracrRNA may be present as separate RNA oligonucleotides. As used herein, the term "guide RNA" or "gRNA" refers to the combination of a tracrRNA and a crRNA, present as either an sgRNA or a crRNA:tracrRNA duplex. In some embodiments, the CRISPR-associated nuclease is a Cas9 nuclease. In some embodiments, the Cas9 protein can be derived from *Streptococcus pyogenes* (SpCas9). In some embodiments, the Cas9 protein can be derived from other bacteria strains including *Staphylococcus aureus* (SaCas9). In some embodiments, the Cas endonuclease is selected from the group comprising SpCas9, SpCas9-HF1, SpCas9-HF2, SpCas9-HF3, SpCas9-HF4, SaCas9, FnCpf, FnCas9, eSpCas9, C2C1, C2C3, Cpf1, Casl, CaslB, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csnl and Csx12), Cas10, Csyl, Csy2, Csy3, Csel, Cse2, Cscl, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmrl, Cmr3, Cmr4, Cmr5, Cmr6, Csbl, Csb2, Csb3, Csxl7, Csxl4, Csx10, Csx16, CsaX, Csx3, Csxl, Csxl5, Csfl, Csf2, Csf3, or Csf4.

[0265] Studies suggest that adoptive transfer of T cells derived from less-differentiated (*i.e.*, T_{SCM} or T_{CM}) subset leads to prolonged persistence *in vivo* (see, *e.g.*, Berger, C. et al., The Journal of Clinical Investigation, 118(1): 294-305 (2008)). Thus, genetic knockdown of CD70 in the CAR T product is an important consideration to prevent T cell differentiation.

[0266] In some embodiments, the genetic modification of the method involves expression, in provided cells to engineer, of one rare-cutting endonuclease such that the rare-cutting endonuclease specifically catalyzes cleavage in th CD70 gene, thereby disrupting or inactivating the the CD70 gene. In some embodiments, a method of engineering cells comprises at least one of the following steps: providing a T cell, such as from a cell culture or from a blood sample; introducing into the T cell a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) the gene encoding CD70, and expanding the cells.

[0267] In some embodiments, the method comprises: providing a T cell, such as from a cell culture or from a blood sample; transfecting the T cell with nucleic acid encoding a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) the gene encoding CD70, and expressing the rare-cutting endonucleases into the T cells; and expanding the cells.

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[0268] In some embodiments, the rare-cutting endonuclease can be, for example, a meganuclease, a zinc finger nuclease, or a TALE-nuclease (TALEN). In some embodiments, the rare-cutting endonuclease is a TALE-nuclease. In some embodiments, the rare-cutting nuclease is a CRISPR-associated nuclease, with a guide RNA at least partially complementary or fully complementary to a target site.

[0269] Also provided herein are methods of engineering T cells, suitable for immunotherapy, wherein the methods comprise: genetically modifying T cells by disrupting or inactivating at least immune checkpoint protein. In some embodiments the immune checkpoint protein is, for example, PD-1 and/or CTLA-4. In some embodiments, methods of genetically modifying a cell comprise: modifying T cells by disrupting or inactivating at least one immune checkpoint protein; and expanding the cells. Immune checkpoint proteins include, but are not limited to Programmed Death 1 (PD-1, also known as PDCD1 or CD279, accession number: NM_005018), Cytotoxic T-Lymphocyte Antigen 4 (CTLA-4, also known as CD152, GenBank accession number AF414120.1), LAG3 (also known as CD223, accession number: NM_002286.5), Tim3 (also known as HAVCR2, GenBank accession number: JX049979.1), BTLA (also known as CD272, accession number: NM_181780.3), BY55 (also known as CD160, GenBank accession number: CR541888.1), TIGIT (also known as VSTM3, accession number: NM_173799), B7H5 (also known as C10orf54, homolog of mouse vista gene, accession number: NM_022153.1), LAIR1 (also known as CD305, GenBank accession number: CR542051.1), SIGLEC10 (GeneBank accession number: AY358337.1), 2B4 (also known as CD244, accession number: NM_001166664.1), which directly inhibit immune cells. For example, CTLA-4 is a cell-surface protein expressed on certain CD4 and CD8 T cells; when engaged by its ligands (B7-1 and B7-2) on antigen presenting cells, T cell activation and effector function are inhibited.

[0270] In some embodiments, said method to engineer cells comprises at least one of the following steps: providing a T cell, such as from a cell culture or from a blood sample; introducing into the T cell a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) one gene encoding a immune checkpoint protein; and expanding the cells. In some embodiments, the method comprises: providing a T cell, such as from a cell culture or from a blood sample; transfecting said T cell with nucleic acid encoding a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) a gene encoding a immune

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checkpoint protein; expressing the rare-cutting endonucleases into the T cells; expanding the cells. In some embodiments, the rare-cutting endonuclease specifically targets a gene selected from the group consisting of: PD-1, CTLA-4, LAG3, Tim3, BTLA, BY55, TIGIT, B7H5, LAIR1, SIGLEC10, 2B4, TCRα, and TCRβ. In some embodiments, the rare-cutting endonuclease can be a meganuclease, a zinc finger nuclease or a TALE-nuclease. In some embodiments, the rare-cutting endonuclease is a TALE-nuclease. In some embodiments, the rare-cutting nuclease is a Cas9 nuclease, with a guide RNA at least partially complementary or fully complementary to a target site.

[0271] In some embodiments, the present disclosure can be particularly suitable for allogeneic immunotherapy. In such embodiments, cells may be modified by a method comprising: disrupting or inactivating at least one gene encoding a component of the T cell receptor (TCR) in T cells; and expanding the T cells. In some embodiments, the genetic modification of the method relies on the expression, in provided cells to engineer, of one rare-cutting endonuclease such that the rare-cutting endonuclease specifically catalyzes cleavage in one targeted gene thereby disrupting or inactivating the targeted gene. In some embodiments, said method to engineer cells comprises at least one of the following steps: providing a T cell, such as from a cell culture or from a blood sample; introducing into the T cell a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) at least one gene encoding a component of the T cell receptor (TCR), and expanding the cells.

[0272] In some embodiments, the method comprises: providing a T cell, such as from a cell culture or from a blood sample; transfecting said T cell with nucleic acid encoding a rare-cutting endonuclease able to selectively inactivate by DNA cleavage (in some embodiments by double-strand break) at least one gene encoding a component of the T cell receptor (TCR); expressing the rare-cutting endonucleases into the T cells; sorting the transformed T cells, which do not express TCR on their cell surface;and expanding the cells.

[0273] In some embodiments, the rare-cutting endonuclease can be a meganuclease, a zinc finger nucleasec or a TALE-nuclease. In some embodiments, the rare-cutting endonuclease is a TALE-nuclease. In some embodiments the TALE-nucleases recognize and cleave a sequence encoding TCRα or TCRβ. In some embodiments a TALE-nuclease comprises a polypeptide sequence selected from the amino acid sequence shown in SEQ ID NO: 281, 282, 283, 284, 285, 286, 287, 288, 289 or 290.

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TALE-nuclease polypeptide sequences:

Repeat TRAC_T01-L

LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVL
CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQAL
ETVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQ
RLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNG
GGRPALE (SEQ ID NO: 281).

Repeat TRAC_T01-R

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGG
KQALETVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVL
CQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQA
LETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGG
GRPALE (SEQ ID NO: 282).

Repeat TRBC_T01-L

LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGG
GKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQ
QVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNNGGKQA

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LETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAI
ASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAH
GLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQ
RLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGG
GRPALE (SEQ ID NO: 283).

Repeat TRBC_T01-R

NPQRSTVWYLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGG
KQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQ
VVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVL
CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQAL
ETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAI
ASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQA
HGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETV
QRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN
GGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLT
PQQVVAIASNGGGRPALE (SEQ ID NO: 284).

Repeat TRBC_T02-L

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGG
KQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVL
CQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQAL
ETVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAI
ASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETV
QRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN
GGGRPALE (SEQ ID NO: 285).

Repeat TRBC_T02-R

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LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGG
KQALETVQALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPEQ
VVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVL
CQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQAL
ETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAI
ASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETV
QRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN
GGGRPALE (SEQ ID NO: 286).

Repeat CD52_T02-L

LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQA
LETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVA
IASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAH
GLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQ
RLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGG
GRPALE (SEQ ID NO: 287).

Repeat CD52_T02-R

LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGG
GKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQ
QVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASHDGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVA
IASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQA
HGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETV

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QALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASN
GGGRPALE (SEQ ID NO: 288).

Repeat CD70-L

LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDG
GKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQ
QVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQA
LETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVA
IASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQA
HGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQ
ALLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNG
GGRPALE (SEQ ID NO: 289)

Repeat CD70-R

LTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGKQALETVQR
LLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGG
GKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPE
QVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQA
LETVQRLLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPQQVVAI
ASNNGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAH
GLTPQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNNGGKQALETVQ
RLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNG
GGRPALE (SEQ ID NO: 290)

[0274] In another aspect, one another step of genetically modifying cell can be a method of expanding TCRα deficient T cells comprising introducing into the T cell pTα (also known as preTCRα) or a functional variant thereof and expanding the cells, optionally through stimulation of the CD3 complex. In some embodiments, the method comprises: a) transfecting the cells with nucleic acid encoding at least a fragment of pTα to support CD3

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surface expression; b) expressing said pTα into the cells; and c) expanding the cells, optionally through stimulation of the CD3 complex.

[0275] Also provided are methods of preparing T cells for immunotherapy comprising steps of the method for expansion for T cell. In some embodiments, the pTα polynucleotide sequence can be introduced randomly or by homologous recombination. In some embodiments, the insertion can be associated with the inactivation of the TCRα gene.

[0276] Different functional variants of pTα can be used. A "functional variant" of the peptide refers to a molecule substantially similar to either the entire peptide or a fragment thereof. A "fragment" of the pTα or functional variant thereof refers to any subset of the molecule, that is, a shorter peptide than the full-length pTα. In some embodiments, pTα or functional variants can be, for example, full-length pTα or a C-terminal truncated pTα version. C-terminal truncated pTα lacks in C-terminal end one or more residues. As non limiting examples, C-terminal truncated pTα version lacks 18, 48, 62, 78, 92, 110 or 114 residues from the C-terminus of the protein. Amino acid sequence variants of the peptide can be prepared by mutations in the DNA which encodes the peptide. Such functional variants include, for example, deletions from, or insertions or substitutions of, residues within the amino acid sequence. Any combination of deletion, insertion, and substitution may also be made to arrive at the final construct, provided that the final construct possesses the desired activity, in particular the restoration of a functional CD3 complex. In some embodiments, at least one mutation is introduced in the different pTα versions as described above to affect dimerization. As non limiting example, mutated residue can be at least W46R, D22A, K24A, R102A or R117A of the human pTα protein or aligned positions using CLUSTALW method on pTα family or homologue member. In some embodiments, pTα or variant thereof as described above comprise the mutated residue W46R or the mutated residues D22A, K24A, R102A and R117A. In some embodiments, said pTα or variants are also fused to a signal-transducing domain such as CD28, OX40, ICOS, CD27, CD137 (4-1BB) and CD8 as non limiting examples. The extracellular domain of pTα or variants as described above can be fused to a fragment of the TCRα protein, particularly the transmembrane and intracellular domain of TCRα. pTα variants can also be fused to the intracellular domain of TCRα.

[0277] In some embodiments, pTα versions can be fused to an extracellular ligand-binding domain. In some embodiments, pTα or functional variant thereof is fused to a single chain

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antibody fragment (scFv) comprising the light and the heavy variable fragment of a target antigen specific monoclonal antibody joined by a flexible linker.

[0278] The term "TCRα deficient T cell" refers to an isolated T cell that lacks expression of a functional TCRα chain. This may be accomplished by different means, as non limiting examples, by engineering a T cell such that it does not express any functional TCRα on its cell surface or by engineering a T cell such that it produces very little functional TCRα chain on its surface or by engineering a T cell to express mutated or truncated form of TCRα chain. TCRα deficient cells can no longer be expanded through CD3 complex. Thus, to overcome this problem and to allow proliferation of TCRα deficient cells, pTα or functional variant thereof is introduced into the cells, thus restoring a functional CD3 complex. In some embodiments, the method further comprises introducing into said T cells rare-cutting endonucleases able to selectively inactivate by DNA cleavage one gene encoding one component of the T cell receptor (TCR). In some embodiments, the rare-cutting endonuclease is a TALE-nuclease.

[0279] In another aspect, engineered T cells obtained by the methods described herein can be contacted with bispecific antibodies. For example, the T cells can be contacted with bispecific antibodies ex vivo prior to administration to a patient, or in vivo following administration to a patient. Bispecific antibodies comprise two variable regions with distinct antigen properties that facilitate bringing the engineered cells into proximity to a target antigen. As a non-limiting example, a bispecific antibody can be directed against a tumor marker and lymphocyte antigen, such as for example without limitation CD3, and has the potential to redirect and activate any circulating T cells against tumors.

[0280] In some embodiments, polynucleotides encoding polypeptides according to the present disclosure can be mRNA which is introduced directly into the cells, for example by electroporation. In some embodiments, cytoPulse technology can be used to transiently permeabilize living cells for delivery of material into the cells. Parameters can be modified in order to determine conditions for high transfection efficiency with minimal mortality.

[0281] Also provided herein are methods of transfecting T cell. In some embodiments, the method comprises: contacting a T cell with RNA and applying to T cell an agile pulse sequence consisting of: (a) an electrical pulse with a voltage range from about 2250 to 3000 V per centimeter; (b) a pulse width of 0.1 ms; (c) a pulse interval of about 0.2 to 10 ms between the electrical pulses of step (a) and (b); (d) an electrical pulse with a voltage range

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from about 2250 to 3000 V with a pulse width of about 100 ms and a pulse interval of about 100 ms between the electrical pulse of step (b) and the first electrical pulse of step (c); and (e) four electrical pulses with a voltage of about 325 V with a pulse width of about 0.2 ms and a pulse interval of 2 ms between each of 4 electrical pulses. In some embodiments, a method of transfecting T cell comprising contacting said T cell with RNA and applying to T cell an agile pulse sequence comprising: (a) an electrical pulse with a voltage of about 2250, 2300, 2350, 2400, 2450, 2500, 2550, 2400, 2450, 2500, 2600, 2700, 2800, 2900 or 3000V per centimeter; (b) a pulse width of 0.1 ms; (c) and a pulse interval of about 0.2, 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 ms between the electrical pulses of step (a) and (b); (d) one electrical pulse with a voltage range from about 2250, of 2250, 2300, 2350, 2400, 2450, 2500, 2550, 2400, 2450, 2500, 2600, 2700, 2800, 2900 or 3000V with a pulse width of 100 ms and a pulse interval of 100 ms between the electrical pulse of step (b) and the first electrical pulse of step (c); and (e) 4 electrical pulses with a voltage of about 325 V with a pulse width of about 0.2 ms and a pulse interval of about 2 ms between each of 4 electrical pulses. Any values included in the value range described above are disclosed in the present application. Electroporation medium can be any suitable medium known in the art, such as BTXpress Cytoporation® Media T4, available from BTX. In some embodiments, the electroporation medium has conductivity in a range spanning about 0.01 to about 1.0 milliSiemens.

[0282] In some embodiments, as non limiting examples, an RNA encodes a rare-cutting endonuclase, one monomer of the rare-cutting endonuclease such as half-TALE-nuclease, a CAR, at least one component of the multi-chain chimeric antigen receptor, a pTα or functional variant thereof, an exogenous nucleic acid, and/or one additional catalytic domain.

ENGINEERED IMMUNE CELLS

[0283] The disclosure also provides engineered immune cells comprising any of the CAR polynucleotides described herein. In some embodiments, a CAR can be introduced into an immune cell as a transgene via a plasmid vector. In some embodiments, the plasmid vector can also contain, for example, a selection marker which provides for identification and/or selection of cells which received the vector.

[0284] CAR polypeptides may be synthesized in situ in the cell after introduction of polynucleotides encoding the CAR polypeptides into the cell. Alternatively, CAR polypeptides may be be produced outside of cells, and then introduced into cells. Methods for introducing a polynucleotide construct into cells are known in the art. In some embodiments,

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stable transformation methods can be used to integrate the polynucleotide construct into the genome of the cell. In other embodiments, transient transformation methods can be used to transiently express the polynucleotide construct, and the polynucleotide construct not integrated into the genome of the cell. In other embodiments, virus-mediated methods can be used. The polynucleotides may be introduced into a cell by any suitable means such as for example, recombinant viral vectors (*e.g.* retroviruses, adenoviruses), liposomes, and the like. Transient transformation methods include, for example without limitation, microinjection, electroporation or pa rticle bombardment. Polynucleotides may be included in vectors, such as for example plasmid vectors or viral vectors.

[0285] Also provided herein are isolated cells and cell lines obtained by the above-described methods of engineering cells provided herein. In some embodiments, an isolated cell comprises at least one CAR as described above. In some embodiments, an isolated cell comprises a population of CARs, each CAR comprising different extracellular ligand-binding domains.

[0286] Also provided herein are isolated immune cells obtained according to any one of the methods described above. Any immune cell capable of expressing heterologous DNAs can be used for the purpose of expressing the CAR of interest. In some embodiments, the immune cell is a T cell. In some embodiments, an immune cell can be derived from, for example without limitation, a stem cell. The stem cells can be adult stem cells, non-human embryonic stem cells, more particularly non-human stem cells, cord blood stem cells, progenitor cells, bone marrow stem cells, induced pluripotent stem cells, totipotent stem cells or hematopoietic stem cells. Representative human cells are CD34+ cells. The isolated cell can also be a dendritic cell, killer dendritic cell, a mast cell, a NK-cell, a B-cell or a T cell selected from the group consisting of inflammatory T-lymphocytes, cytotoxic T-lymphocytes, regulatory T-lymphocytes or helper T-lymphocytes. In some embodiments, the cell can be derived from the group consisting of CD4+ T-lymphocytes and CD8+ T-lymphocytes.

[0287] In some embodiments, the engineered immune cells expressing at their cell surface membrane a CD70-specific CAR of the disclosure comprise a percentage of stem cell memory and central memory cells greater than 10%, 20%, 30%, 40%, 50%, or 60%. In some embodiments, the engineered immune cells expressing at their cell surface membrane a CD70-specific CAR of the disclosure comprise a percentage of stem cell memory and central memory cells of about 10% to about 60%, about 10% to about 50%, about 10% to about 40%,

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about 15% to about 50%, about 15% to about 40%, about 20% to about 60%, or about 20% to about 70%.

[0288] In some embodiments, the immune cell is an inflammatory T-lymphocyte that expresses any one of the CARs described herein. In some embodiments, the immune cell is a cytotoxic T-lymphocyte that expresses any one of the CARs described herein. In some embodiments, the immune cell is a regulatory T-lymphocyte that expresses any one of the CARs described herein. In some embodiments, the immune cell is a helper T-lymphocyte that expresses any one of the CARs described herein.

[0289] Prior to expansion and genetic modification, a source of cells can be obtained from a subject through a variety of non-limiting methods. Cells can be obtained from a number of non-limiting sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In some embodiments, any number of T cell lines available and known to those skilled in the art, may be used. In some embodiments, cells can be derived from a healthy donor, from a patient diagnosed with cancer or from a patient diagnosed with an infection. In some embodiments, cells can be part of a mixed population of cells which present different phenotypic characteristics.

[0290] Also provided herein are cell lines obtained from a transformed T cell according to any of the above-described methods. Also provided herein are modified cells resistant to an immunosuppressive treatment. In some embodiments, an isolated cell according to the disclosure comprises a polynucleotide encoding a CAR.

[0291] The immune cells of the disclosure can be activated and expanded, either prior to or after genetic modification of the T cells, using methods as generally described, for example without limitation, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7,172,869; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and U.S. Patent Application Publication No. 20060121005. T cells can be expanded in vitro or in vivo. Generally, the T cells of the disclosure can be expanded, for example, by contact with an agent that stimulates a CD3 TCR complex and a co-stimulatory molecule on the surface of the T cells to create an activation signal for the T cell. For example, chemicals such as calcium ionophore A23187, phorbol 12-myristate 13-acetate (PMA), or mitogenic lectins like phytohemagglutinin (PHA) can be used to create an activation signal for the T cell.

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[0292] In some embodiments, T cell populations may be stimulated in vitro by contact with, for example, an anti-CD3 antibody, or antigen-binding fragment thereof, or an anti-CD2 antibody immobilized on a surface, or by contact with a protein kinase C activator (*e.g.*, bryostatin) in conjunction with a calcium ionophore. For co-stimulation of an accessory molecule on the surface of the T cells, a ligand that binds the accessory molecule is used. For example, a population of T cells can be contacted with an anti-CD3 antibody and an anti-CD28 antibody, under conditions appropriate for stimulating proliferation of the T cells. The anti-CD3 antibody and an anti-CD28 antibody can be disposed on a bead or plate or other substrate. Conditions appropriate for T cell culture include an appropriate media (*e.g.*, Minimal Essential Media or RPMI Media 1640 or, X-vivo 5, (Lonza)) that may contain factors necessary for proliferation and viability, including serum (*e.g.*, fetal bovine or human serum), interleukin-2 (IL-2), insulin, IFN-γ, IL-4, IL-7, GM-CSF, IL-10, IL-2, IL-15, TGFp, and TNF, or any other additives for the growth of cells known to the skilled artisan. Other additives for the growth of cells include, but are not limited to, surfactant, plasmanate, and reducing agents such as N-acetyl- cysteine and 2-mercaptoethanoi. Media can include RPMI 1640, A1M-V, DMEM, MEM, a- MEM, F-12, X-Vivo 1, and X-Vivo 20, Optimizer, with added amino acids, sodium pyruvate, and vitamins, either serum-free or supplemented with an appropriate amount of serum (or plasma) or a defined set of hormones, and/or an amount of cytokine(s) sufficient for the growth and expansion of T cells (*e.g.*, IL-7 and/or IL-15). Antibiotics, *e.g.*, penicillin and streptomycin, are included only in experimental cultures, not in cultures of cells that are to be infused into a subject. The target cells are maintained under conditions necessary to support growth, for example, an appropriate temperature (*e.g.*, 37° C) and atmosphere (*e.g.*, air plus 5% CO_2). T cells that have been exposed to varied stimulation times may exhibit different characteristics

[0293] In some embodiments, the cells of the disclosure can be expanded by co-culturing with tissue or cells. The cells can also be expanded in vivo, for example in the subject's blood after administering the cell into the subject.

[0294] In some embodiments, an isolated cell according to the present disclosure comprises one disrupted or inactivated gene selected from the group consisting of CD52, CD70, GR, PD-1, CTLA-4, LAG3, Tim3, BTLA, BY55, TIGIT, B7H5, LAIR1, SIGLEC10, 2B4, HLA, TCRα and TCRβ and/or expresses a CAR, a multi-chain CAR and/or a pTα transgene. In some embodiments, an isolated cell comprises polynucleotides encoding polypeptides comprising a

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multi-chain CAR. In some embodiments, the isolated cell according to the present disclosure comprises two disrupted or inactivated genes selected from the group consisting of: CD52 and GR, CD52 and TCRα, CDR52 and TCRβ, CD70 and CD52, CD70 and TCRα, CD70 and TCRβ , GR and TCRα, GR and TCRβ, TCRα and TCRβ, PD-1 and TCRα, PD-1 and TCRβ, CTLA-4 and TCRα, CTLA-4 and TCRβ, LAG3 and TCRα, LAG3 and TCRβ, Tim3 and TCRα, Tim3 and TCRβ, BTLA and TCRα, BTLA and TCRβ, BY55 and TCRα, BY55 and TCRβ, TIGIT and TCRα, TIGIT and TCRβ, B7H5 and TCRα, B7H5 and TCRβ, LAIR1 and TCRα, LAIR1 and TCRβ, SIGLEC10 and TCRα, SIGLEC10 and TCRβ, 2B4 and TCRα, 2B4 and TCRβ and/or expresses a CAR, a multi-chain CAR and a pTα transgene.

[0295] In some embodiments, the isolated cell according to the present disclosure comprises three disrupted or inactivated genes selected from CD52, CD70 and TCRα or CD52, CD70 and TCRβ and/or expresses a CAR, a multi-chain CAR and a pTα transgene.

[0296] In some embodiments, TCR is rendered not functional in the cells according to the disclosure by disrupting or inactivating TCRα gene and/or TCRβ gene(s). In some embodiments, a method to obtain modified cells derived from an individual is provided, wherein the cells can proliferate independently of the major histocompatibility complex (MHC) signaling pathway. Modified cells, which can proliferate independently of the MHC signaling pathway, susceptible to be obtained by this method are encompassed in the scope of the present disclosure. Modified cells disclosed herein can be used in for treating patients in need thereof against Host versus Graft (HvG) rejection and Graft versus Host Disease (GvHD); therefore in the scope of the present disclosure is a method of treating patients in need thereof against Host versus Graft (HvG) rejection and Graft versus Host Disease (GvHD) comprising treating said patient by administering to said patient an effective amount of modified cells comprising disrupted or inactivated TCRα and/or TCRβ genes.

[0297] In some embodiments, the immune cells are engineered to be resistant to one or more chemotherapy drugs. The chemotherapy drug can be, for example, a purine nucleotide analogue (PNA), thus making the immune cell suitable for cancer treatment combining adoptive immunotherapy and chemotherapy. Exemplary PNAs include, for example, clofarabine, fludarabine, cyclophosphamide, and cytarabine, alone or in combination. PNAs are metabolized by deoxycytidine kinase (dCK) into mono-, di-, and tri-phosphate PNA. Their tri-phosphate forms compete with ATP for DNA synthesis, act as pro-apoptotic agents, and are potent inhibitors of ribonucleotide reductase (RNR), which is involved in

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trinucleotide production. Provided herein are CD70-specific CAR-T cells comprising an disrupted or inactivated dCK gene. In some embodiments, the dCK knockout cells are made by transfection of T cells using polynucleotides encoding specific TAL-nulcease directed against dCK genes by, for example, electroporation of mRNA. The dCK knockout CD70-specific CAR-T cells can be resistant to PNAs, including for example clorofarabine and/or fludarabine, and maintain T cell cytotoxic activity toward CD70-expressing cells.

[0298] In some embodiments, isolated cells or cell lines of the disclosure can comprise a pTα or a functional variant thereof. In some embodiments, an isolated cell or cell line can be further genetically modified by disrupting or inactivating the TCRα gene.

MONOCLONAL ANTIBODY-SPECIFIC EPITOPES

[0299] In some embodiments, the extracellular domain of any one of the CD70-specific CARs disclosed herein may comprise one or more epitopes specific for (*i.e.*, specifically recognized by) a monoclonal antibody. These epitopes are also referred to herein as mAb-specific epitopes. Exemplary mAb-specific epitopes are disclosed in International Patent Publication No. WO 2016/120126, which is incorporated herein in its entirety. In these embodiments, the extracellular domain comprises the VH and VL polypeptides that specifically bind to CD70 and one or more epitopes that bind to one or more monoclonal antibodies (mAbs). CARs comprising the mAb-specific epitopes can be single-chain or multi-chain.

[0300] The inclusion of eptiopes specific for monoclonal antibodies in the extracellular domain of the CARs described herein allows sorting and depletion of engineered immune cells expressing the CARs. In some embodiments, this feature also promotes recovery of endogenous CD70-expressing cells that were depleted by administration of engineered immune cells expressing the CARs.

[0301] Accordingly, in some embodiments, the present disclosure relates to a method for sorting and/or depleting the engineered immune cells endowed with the CARs comprising mAb-specific epitopes and a method for promoting recovery of endogenous CD70-expressing cells, such as bone marrow progeniotr cells.

[0302] Several epitope-monoclonal antibody couples can be used to generate CARs comprising monoclonal antibody specific epitopes; in particular, those already approved for medical use, such as CD20 epitope/rituximab as a non-limiting example.

[0303] The disclosure also encompasses methods for sorting the engineered immune cells endowed with the CD70-specific CARs expressing the mAb-specific epitope(s) and

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therapeutic methods where the activation of the engineered immune cells endowed with these CARs is modulated by depleting the cells using an antibody that targets the external ligand binding domain of said CARs.

Rituximab		
Mimotope	SEQ ID NO: 293	CPYSNPSLC
Palivizumab		
Epitope	SEQ ID NO: 660	NSELLSLINDMPITNDQKKLMSNN
Cetuximab		
Mimotope 1	SEQ ID NO: 603	CQFDLSTRRLKC
Mimotope 2	SEQ ID NO: 604	CQYNLSSRALKC
Mimotope 3	SEQ ID NO: 605	CVWQRWQKSYVC
Mimotope 4	SEQ ID NO: 606	CMWDRFSRWYKC
Nivolumab		
Epitope 1	SEQ ID NO: 607	SFVLNWYRMSPSNQTDKLAAFPEDR
Epitope 2	SEQ ID NO: 608	SGTYLCGAISLAPKAQIKE
QBEND-10		
Epitope 1	SEQ ID NO: 609	ELPTQGTFSNVSTNVS
Epitope 2	SEQ ID NO: 295	ELPTQGTFSNVSTNVSPAKPTTTA
Alemtuzumab		
Epitope	SEQ ID NO: 610	GQNDTSQTSSPS

[0304] In some embodiments, the CAR-T cell comprises a polynucleotide encoding a suicide polypeptide, such as for example RQR8. See, *e.g.*, WO2013153391A, which is hereby incorporated by reference in its entirety. In CAR-T cells comprising the polynucleotide, the suicide polypeptide is expressed at the surface of a CAR-T cell. In some embodiments, the suicide polypeptide comprises the amino acid sequence shown in SEQ ID NO: 291.

CPYSNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCSGGGGSP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLS LVITLYCNHRNRRRVCKCPRPVV (SEQ ID NO: 291).

[0305] The suicide polypeptide may also comprise a signal peptide at the amino terminus—for example, MGTSLLCWMALCLLGADHADA (SEQ ID NO: 611). In some embodiments, the suicide polypeptide comprises the amino acid sequence shown in SEQ ID NO: 292, which includes the signal sequence of SEQ ID NO: 611.

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MGTSLLCWMALCLLGADHADACPYSNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTT TACPYSNPSLCSGGGGSPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIY IWAPLAGTCGVLLLSLVITLYCNHRNRRRVCKCPRPVV (SEQ ID NO: 292).

[0306] In some embodiments, the suicide polypeptide comprises the amino acid sequence of SEQ ID NO: 611

[0307] When the suicide polypeptide is expressed at the surface of a CAR-T cell, binding of rituximab to the R epitopes of the polypeptide causes lysis of the cell. More than one molecule of rituximab may bind per polypeptide expressed at the cell surface. Each R epitope of the polypeptide may bind a separate molecule of rituximab. Deletion of CD70-specific CAR-T cells may occur in vivo, for example by administering rituximab to a patient. The decision to delete the transferred cells may arise from undesirable effects being detected in the patient which are attributable to the transferred cells, such as for example, when unacceptable levels of toxicity are detected.

[0308] In some embodiments, upon administration to a patient, engineered immune cells expressing at their cell surface any one of the CD70-specific CARs described herein may reduce, kill or lyse endogenous CD70-expressing cells of the patient. In one embodiment, a percentage reduction or lysis of CD70-expressing endogenous cells or cells of a cell line expressing CD70 by engineered immune cells expressing any one of the CD70-specific CARs described herein is at least about or greater than 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%. In one embodiment, a percentage reduction or lysis of CD70-expressing endogenous cells or cells of a cell line expressing CD70 by engineered immune cells expressing any one of the CD70-specific CARs described herein is about 5% to about 95%, about 10% to about 95%, about 10% to about 90%, about 10% to about 80%, about 10% to about 70%, about 10% to about 60%, about 10% to about 50%, about 10% to about 40%, about 20% to about 90%, about 20% to about 80%, about 20% to about 70%, about 20% to about 60%, about 20% to about 50%, about 25% to about 75%, or about 25% to about 60%. In one embodiment, the endogenous CD70-expressing cells are endogenous CD70-expressing bone marrow cells.

[0309] In one embodiment, the percent reduction or lysis of target cells, *e.g.*, a cell line expressing CD70, by engineered immune cells expressing at their cell surface membrane a CD70-specific CAR of the disclosure can be measured using the assay disclosed herein.

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Method for sorting CAR-positive immune cells

[0310] In one aspect, provided are methods for in vitro sorting of a population of immune cells, wherein a subset of the population of immune cells comprises engineered immune cells expressing any one of the CD70-specific CARs comprising epitopes specific for monoclonal antibodies described herein. The method comprises contacting the population of immune cells with a monoclonal antibody specific for the epitopes and selecting the immune cells that bind to the monoclonal antibody to obtain a population of cells enriched in engineered immune cells expressing CD70-specific CAR.

[0311] In some embodiments, said monoclonal antibody specific for said epitope is optionally conjugated to a fluorophore. In this embodiment, the step of selecting the cells that bind to the monoclonal antibody can be done by Fluorescence Activated Cell Sorting (FACS). In some embodiments, said monoclonal antibody specific for said epitope is optionally conjugated to a magnetic particle. In this embodiment, the step of selecting the cells that bind to the monoclonal antibody can be done by Magnetic Activated Cell Sorting (MACS).

[0312] In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of one or more of SEQ ID NO: 294 or 601-610 In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 609. In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 295. In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 609 and the antibody used to contact the population of immune cells is QBEND-10. In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 295 and the antibody used to contact the population of immune cells is QBEND-10.

[0313] In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 294. In some embodiments, the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 294 and the antibody used to contact the population of immune cells is Rituximab.

[0314] In some embodiments, the population of CAR-expressing immune cells obtained when using the method for in vitro sorting of immune cells described above, comprises at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% of CAR-expressing immune cells. In some embodiments, the population of CD70 CAR-expressing immune cells obtained when using

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the method for in vitro sorting of CAR-expressing immune cells described above, comprises at least 85% of CAR-expressing immune cells.

[0315] According to the disclosure, cells to be administered to the recipient may be enriched in vitro from the source population. Methods of expanding source populations are well known in the art, and may include selecting cells that express an antigen such as CD34 antigen, using combinations of density centrifugation, immuno-magnetic bead purification, affinity chromatography, and fluorescent activated cell sorting, known to those skilled in the art.

[0316] Flow cytometry is widely used in the art and is a method well known to one of ordinary skill to sort and quantify specific cell types within a population of cells. In general, flow cytometry is a method for quantitating components or structural features of cells primarily by optical means. Since different cell types can be distinguished by quantitating structural features, flow cytometry and cell sorting can be used to count and sort cells of different phenotypes in a mixture.

[0317] A flow cytometric analysis involves two basic steps: 1) labeling selected cell types with one or more labeled markers, and 2) determining the number of labeled cells relative to the total number of cells in the population.

[0318] The primary method of labeling cell types is by binding labeled antibodies to markers expressed by the specific cell type. The antibodies are either directly labeled with a fluorescent compound or indirectly labeled using, for example, a fluorescent- labeled second antibody which recognizes the first antibody.

[0319] In some embodiments, the method used for sorting immune cells expressing a CAR is the Magnetic- Activated Cell Sorting (MACS). Magnetic-activated cell sorting (MACS) is a method for separation of various cell populations depending on their surface antigens (CD molecules) by using superparamagnetic nanoparticles and columns. It takes a few simple steps to get pure cell populations. Cells in a single-cell suspension are magnetically labeled with microbeads. The sample is applied to a column composed of ferromagnetic spheres, which are covered with a cell-friendly coating allowing fast and gentle separation of cells. The unlabeled cells pass through while the magnetically labeled cells are retained within the column. The flow-through can be collected as the unlabeled cell fraction. After a short washing step, the column is removed from the separator, and the magnetically labeled cells are eluted from the column.

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[0320] In some embodiments, the mAb used in the method for sorting immune cells expressing the CAR is chosen from alemtuzumab, ibritumomab tiuxetan, muromonab-CD3, tositumomab, abciximab, basiliximab, brentuximab vedotin, cetuximab, infliximab, rituximab, bevacizumab, certolizumab pegol, daclizumab, eculizumab, efalizumab, gemtuzumab, natalizumab, omalizumab, palivizumab, ranibizumab, tocilizumab, trastuzumab, vedolizumab, adalimumab, belimumab, canakinumab, denosumab, golimumab, ipilimumab, ofatumumab, panitumumab, QBEND-10 and/or ustekinumab. In some embodiments, said mAb is rituximab. In another embodiment, said mAb is QBEND-10.

[0321] In some embodiments, the CAR-T cell comprises a selected epitope within the scFv having a specificity to be recognized by a specific antibody. See, *e.g.*, WO2016/120216, which is hereby incorporated by reference in its entirety. Such an epitope facilitates sorting and/or depleting the CAR-T cells. The epitope can be selected from any number of epitopes known in the art. In some embodiments, the epitope can be a target of a monoclonal antibody approved for medical use, such as, for example without limitation, the CD20 epitope recognized by rituximab. In some embodiments, the epitope comprises the amino acid sequence CPYSNPSLC (SEQ ID NO: 293)

[0322] In some embodiments, the epitope is located within the CAR. For example without limitation, the epitope can be located between the scFv and the hinge of a CAR. In some embodiments, two instances of the same epitope, separated by linkers, may be used in the CAR. For example, the polypeptide comprising the amino acid sequence shown in SEQ ID NO: 294 or in SEQ ID NO: 609 or SEQ ID NO: 295 can be used within a CAR, located between the light chain variable region and the hinge.

GSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGS (SEQ ID NO: 294)

ELPTQGTFSNVSTNVS (SEQ ID NO: 609)

ELPTQGTFSNVSTNVSPAKPTTTA (SEQ ID NO: 295)

[0323] In some embodiments, the extracellular binding domain of the CAR comprises the following sequence

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-;

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-;

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2;

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Epitope1-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-V_1-L_1-V_2;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$-;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$;

$(L)_x$-Epitope1-$(L)_x$-V_1-$(L)_x$-Epitope2-$(L)_x$-V_2; or,

$(L)_x$-Epitope1-$(L)_x$-V_1-$(L)_x$-Epitope2-$(L)_x$-V_2-$(L)_x$-Epitope3-$(L)_x$;

wherein,

V_1 is V_L and V_2 is V_H or V_1 is V_H and V_2 is V_L;

L_1 is a linker suitable to link the V_H chain to the V_L chain;

L is a linker comprising glycine and serine residues, and each occurrence of L in the extracellular binding domain can be identical or different to other occurrence of L in the same extracellular binding domain, which in embodiments comprises or is SGGGG (SEQ ID NO: 614), GGGGS (SEQ ID NO: 615) or SGGGGS (SEQ ID NO: 616), and,

x is 0 or 1or 2 and each occurrence of x is selected independently from the others; and,

Epitope 1, Epitope 2, Epitope 3 and Epitope 4 are mAb-specific epitopes and can be identical or different and wherein V_H is an heavy chain variable fragment and V_L is a light chain variable fragment. In some embodiments, Epitope 1, Epitope 2 and Epitope 4 are a mAb-specific epitope having an amino acid sequence of SEQ ID NO:293 and Epitope 3 is a mAb-specific epitope having an amino acid sequence of SEQ ID NO: 295.

[0324] In some embodiments, the extracellular binding domain of the CAR comprises the following sequence

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-;

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-;

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2;

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Epitope1-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-V_1-L_1-V_2;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope3-$(L)_x$-;

$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$-;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$;

V_1-$(L)_x$-Epitope1-$(L)_x$-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$;

$(L)_x$-Epitope1-$(L)_x$-V_1-$(L)_x$-Epitope2-$(L)_x$-V_2; or,

$(L)_x$-Epitope1-$(L)_x$-V_1-$(L)_x$-Epitope2-$(L)_x$-V_2-$(L)_x$-Epitope3-$(L)_x$;

wherein,

V_1 is V_L and V_2 is V_H or V_1 is V_H and V_2 is V_L;

L_1 is a linker suitable to link the V_H chain to the V_L chain;

L is a linker comprising glycine and serine residues, and each occurrence of L in the extracellular binding domain can be identical or different to other occurrence of L in the same extracellular binding domain, which in embodiments comprises or is SGGGG (SEQ ID NO: 614), GGGGS (SEQ ID NO: 615) or SGGGGS (SEQ ID NO: 616), and,

x is 0 or 1or 2 and each occurrence of x is selected independently from the others; and,

Epitope 1, Epitope 2, Epitope 3 and Epitope 4 are mAb-specific epitopes and can be identical or different and wherein V_H is an heavy chain variable fragment and V_L is a light chain variable fragment. In some embodiments, Epitope 1, Epitope 2 and Epitope 4 are a mAb-specific epitope having an amino acid sequence of SEQ ID NO:293 and Epitope 3 is a mAb-specific epitope having an amino acid sequence of SEQ ID NO: 609.

[0325] In some embodiments, the extracellular binding domain of the CAR comprises the following sequence

V_1-L_1-V_2-$(L)_x$-Epitope1-$(L)_x$-Epitope2-$(L)_x$-; or,

$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$- wherein V_1, V_2, L_1, L, x and Epitope 1, Epitope 2, Epitope 3 and Epitope 4 are as defined above.

[0326] In some embodiments, the extracellular binding domain of the CAR comprises the following sequence

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$(L)_x$-Epitope1-$(L)_x$-V_1-L_1-V_2-$(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4-$(L)_x$- wherein V_1, V_2, L_1, L, x are as defined above and wherein $(L)_x$-Epitope1-$(L)_x$ is GGGGSCPYSNPSLCSGGGGSGGGGS (SEQ ID NO: 617), $(L)_x$-Epitope2-$(L)_x$-Epitope3-$(L)_x$-Epitope4 is GSGGGGSCPYSNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLC (SEQ ID NO: 618) and

and V_1, V_2, L_1, L, x are as defined above.

[0327] In some embodiments, the epitope-specific antibody may be conjugated with a cytotoxic drug. It is also possible to promote CDC cytotoxicity by using engineered antibodies on which are grafted component(s) of the complement system. In some embodiments, activation of the CAR-T cells can be modulated by depleting the cells using an antibody which recognizes the epitope.

THERAPEUTIC APPLICATIONS

[0328] Isolated cells obtained by the methods described above, or cell lines derived from such isolated cells, can be used as a medicament. In some embodiments, such a medicament can be used for treating cancer. In some embodiments, the cancer is Renal Cell Carcinoma, Glioblastoma, glioma such as low grade glioma, Non-Hodgkin's Lymphoma (NHL), Hodgkin's Disease (HD), Waldenstrom's macroglobulinemia, Acute Myeloid Leukemia, Multiple Myeloma, diffuse large-cell lymphoma, follicular lymphoma or Non-Small Cell Lung Cancer.

[0329] In some embodiments, the cancer is of hematopoeietic origin, such as a lymphoma or leukemia. In some embodiments, the cancer is selected from the group consisting of multiple myeloma, malignant plasma cell neoplasm, Hodgkin's lymphoma, nodular lymphocyte predominant Hodgkin's lymphoma, Kahler's disease and Myelomatosis, plasma cell leukemia, plasmacytoma, B-cell prolymphocytic leukemia, hairy cell leukemia, B-cell non-Hodgkin's lymphoma (NHL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), chronic myeloid leukemia (CML), follicular lymphoma, Burkitt's lymphoma, marginal zone lymphoma, mantle cell lymphoma, large cell lymphoma, precursor B-lymphoblastic lymphoma, myeloid leukemia, Waldenstrom's macroglobulienemia, diffuse large B cell lymphoma, follicular lymphoma, marginal zone lymphoma, mucosa-associated lymphatic tissue lymphoma, small cell lymphocytic lymphoma, mantle cell lymphoma, Burkitt lymphoma, primary mediastinal (thymic) large B-

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cell lymphoma, lymphoplasmactyic lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma, splenic marginal zone lymphoma, intravascular large B-cell lymphoma, primary effusion lymphoma, lymphomatoid granulomatosis, T cell/histiocyte-rich large B-cell lymphoma, primary central nervous system lymphoma, primary cutaneous diffuse large B-cell lymphoma (leg type), EBV positive diffuse large B-cell lymphoma of the elderly, diffuse large B-cell lymphoma associated with inflammation, intravascular large B-cell lymphoma, ALK-positive large B-cell lymphoma, plasmablastic lymphoma, large B-cell lymphoma arising in HHV8-associated multicentric Castleman disease, B-cell lymphoma unclassified with features intermediate between diffuse large B-cell lymphoma and Burkitt lymphoma, B-cell lymphoma unclassified with features intermediate between diffuse large B-cell lymphoma and classical Hodgkin lymphoma, and other hematopoietic cells related cancer, e.g. ALL or AML.

[0330] In some embodiments, an isolated cell according to the disclosure, or cell line derived from the isolated cells, can be used in the manufacture of a medicament for treatment of a cancer in a patient in need thereof.

[0331] Also provided herein are methods for treating patients. In some embodiments the method comprises providing an immune cell of the disclosure to a patient in need thereof. In some embodiments, the method comprises a step of administering transformed immune cells of the disclosure to a patient in need thereof.

[0332] In some embodiments, T cells of the disclosure can undergo robust in vivo T cell expansion and can persist for an extended amount of time.

[0333] Methods of treatment of the disclosure can be ameliorating, curative or prophylactic. The method of the disclosure may be either part of an autologous immunotherapy or part of an allogenic immunotherapy treatment. The disclosure is particularly suitable for allogeneic immunotherapy. T cells from donors can be transformed into non-alloreactive cells using standard protocols and reproduced as needed, thereby producing CAR-T cells which may be administered to one or several patients. Such CAR-T cell therapy can be made available as an “off the shelf” therapeutic product.

[0334] Cells that can be used with the disclosed methods are described in the previous section. Treatment can be used to treat patients diagnosed with, for example, cancer. Cancers that may be treated include, for example without limitation, cancers that involve B lymphocytes, including any of the above-listed cancers. Types of cancers to be treated with the CARs and

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CAR-T cells of the disclosure include, but are not limited to certain leukemia or lymphoid malignancies. Adult tumors/cancers and pediatric tumors/cancers are also included. In some embodiments, the treatment can be in combination with one or more therapies against cancer selected from the group of antibodies therapy, chemotherapy, cytokines therapy, dendritic cell therapy, gene therapy, hormone therapy, laser light therapy and radiation therapy.

[0335] In some embodiments, treatment can be administered into patients undergoing an immunosuppressive treatment. Indeed, the methods of the disclosure, in some embodiments, rely on cells or population of cells, which have been made resistant to at least one immunosuppressive agent due to the inactivation of a gene encoding a receptor for such immunosuppressive agent. In this aspect, the immunosuppressive treatment should help the selection and expansion of the T cells according to the disclosure within the patient. The administration of the cells or population of cells according to the disclosure may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, infusion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient subcutaneously, intradermaliy, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous or intralymphatic injection or infusion, or intraperitoneally. In some embodiments, the cell compositions of the disclosure are administered by intravenous injection or infusion.

[0336] In some embodiments the administration of the cells or population of cells can comprise administration of, for example, about 10^4 to about 10^9 cells per kg body weight including all integer values of cell numbers within those ranges. In some embodiments the administration of the cells or population of cells can comprise administration of about 10^5 to about 10^6 cells per kg body weight including all integer values of cell numbers within those ranges. The cells or population of cells can be administered in one or more doses. In some embodiments, said effective amount of cells can be administered as a single dose. In some embodiments, said effective amount of cells can be administered as more than one dose over a period time. Timing of administration is within the judgment of managing physician and depends on the clinical condition of the patient. The cells or population of cells may be obtained from any source, such as the patient, a blood bank, or a donor. While individual needs vary, determination of optimal ranges of effective amounts of a given cell type for a particular disease or conditions within the skill of the art. An effective amount means an amount which provides a therapeutic or prophylactic benefit. The dosage administered will be dependent

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upon the age, health and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment and the nature of the effect desired. In some embodiments, an effective amount of cells or composition comprising those cells are administered parenterally. In some embodiments, administration can be an intravenous administration. In some embodiments, administration can be directly done by injection within a tumor.

[0337] In some embodiments, the methods involve (a) administering to a subject having a disease a first dose of allogeneic CAR-T cells. In some embodiments, the first dose contains about 1×10^4 cells, about 5×10^4 cells, about 1×10^5 cells, about 5×10^5 cells, about 1×10^6 cells, about 5×10^6 cells, about 6×10^6 cells, about 1×10^7 cells, about 6×10^7 cells, about 1×10^8, about 1.8×10^8 cells, or about 4.8×10^8 cells. In some embodiments, the methods further involve (b) administering to the subject a subsequent dose of CAR-T cells at a time point that is at least or more than about 5 weeks after and less than about 24 weeks after initiation of the administration in (a).

[0338] In some embodiments, a subject with relapsed/refractory disease (*e.g.*, relapsed/refractory RCC) is administered a first and subsequent dose of allogeneic CAR-T cells each contain about 6×10^6 cells, and the subsequent dose of CAR-T cells in (b) is administered about 99 days after initiation of the administration in (a).

[0339] In some embodiments, the methods further involve the administration of additional subsequent or subsequent doses, such that a first and multiple subsequent doses are administered, e.g., in accordance with the dosing amounts and timing schedules as specified for the first and subsequent doses. In some embodiments, the first of one or more subsequent doses is administered at a time that is at least or greater than 5 weeks after the initiation of the administration of the subsequent dose. In some embodiments, the administration of the first, subsequent, and subsequent doses includes administering at least three of the doses within at or about 5 weeks. In some embodiments, the subsequent dose is administered at about 16 weeks following the initiation of administration of the first dose, and an additional subsequent or subsequent dose is administered at week 17 following the initiation of administration of the first dose. In some embodiments, additional subsequent doses are administered at week 17 and/or week 34 following the initiation of administration of the first dose.

[0340] In some aspects, the time of administering the subsequent dose(s) is further one at which the subject does not exhibit an immune response, e.g., does not exhibit a detectable adaptive host immune response specific for the CAR-T said first (or prior) dose.

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[0341] In some embodiments, the time between the administration of the first dose (initial dose), e.g., the initiation of the administration of the first or prior dose, and the initiation of the administration of the subsequent dose (e.g., the initiation of the administration of the subsequent dose) is greater than about 4 weeks, e.g., greater than about 5, 6, 7, 8, or 9 days, e.g., greater than about 20 weeks, e.g., between about 9 and about 35 weeks, between about 14 and about 28 weeks, between 15 and 27 weeks, or between 16 weeks and about 18 weeks; and/or at or about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27 weeks. In some embodiments, administration of the subsequent dose (e.g., initiation thereof) is more than about 5 weeks after and less than about 24 weeks after administration of the first or prior dose (e.g., initiation thereof). In some embodiments, the administration of the subsequent dose is initiated 17 weeks following the initiation of the first dose. In some embodiments, the time between administration of the first and the subsequent dose (e.g., initiation thereof) or prior and next subsequent dose is greater than about 5 weeks and less than about 24 weeks, such as between 10 and 24 weeks, such as about 17 weeks. In some embodiments, the time between administration of the first and the subsequent dose (e.g., initiation thereof) is about 17 weeks.

[0342] In some embodiments of the disclosure, cells are administered to a patient in conjunction with (*e.g.*, before, simultaneously or following) any number of relevant treatment modalities, including but not limited to treatment with agents such as monoclonal antibody therapy, CCR2 antagonist (*e.g.*, INC-8761), antiviral therapy, cidofovir and interleukin-2, cytarabine (also known as ARA-C) or nataliziimab treatment for MS patients or efaliztimab treatment for psoriasis patients or other treatments for PML patients. In some embodiments, CD70-specific CAR-T cells are administered to a patient in conjunction with one or more of the following: an anti-PD-1 antibody (*e.g.*, nivolumab, pembrolizumab, or PF-06801591), an anti-PD-L1 antibody (*e.g.*, avelumab, atezolizumab, or durvalumab), an anti-OX40 antibody (*e.g.*, PF-04518600), an anti-4-1BB antibody (*e.g.*, PF-05082566), an anti-MCSF antibody (*e.g.*, PD-0360324), an anti-GITR antibody, and/or an anti-TIGIT antibody. In some embodiments, a CD70-specific CAR comprising the amino acid sequence shown in SEQ ID NO: 319 or 327 is administered to a patient in conjunction with anti-PD-L1 antibody avelumab. In further embodiments, the T cells of the disclosure may be used in combination with chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAMPATH, anti-CD3 antibodies or other antibody therapies, cytoxin, fludaribine,

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cyclosporin, FK506, rapamycin, mycoplienolic acid, steroids, FR901228, cytokines, and/or irradiation. These drugs inhibit either the calcium dependent phosphatase calcineurin (cyclosporine and FK506) or inhibit the p70S6 kinase that is important for growth factor induced signaling (rapamycin) (Henderson, Naya et al. 1991; Liu, Albers et al. 1992; Bierer, Hollander et al. 1993). In further embodiments, the T cells of the disclosure may be used in combination with Receptor Tyrosine Kinase inhibitors such as Midostaurin, Sunitinib and axitanib, mTOR inhibitors such as Rapamacyn and Everolimus, epigenetic modulators such as Vormostat, proteasome inhibitors such as Bortezomib, immunomodulatory agents such as lenalidomide, Hedgehog inhibitors such as Erismodegib and PF-04449913 or Isocitrate Dehydrogenase (IDH) inhibitors such as AG-120 and AG-221. In a further embodiment, the cell compositions of the disclosure are administered to a patient in conjunction with (*e.g.*, before, simultaneously or following) bone marrow transplantation, T cell ablative therapy using either chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, or antibodies such as OKT3 or CAMPATH, In some embodiments, the cell compositions of the disclosure are administered following B-cell ablative therapy such as agents that react with CD20, *e.g.*, Rituxan. For example, in some embodiments, subjects may undergo standard treatment with high dose chemotherapy followed by peripheral blood stem cell transplantation. In certain embodiments, following the transplant, subjects receive an infusion of the expanded immune cells of the disclosure. In some embodiments, expanded cells are administered before or following surgery.

[0343] In some embodiments, provided are methods for depleting CD70-specific CAR-expressing engineered immune cells from a subject adminstered with said cells. Depletion can be by inhibition or elimination.

[0344] In one aspect, a method for depleting engineered immune cells expressing a CD70-specific CAR comprising an epitope specific for a monoclonal antibody comprises contacting said engineered immune cell with a monoclonal antibody specific for the epitope.

[0345] In some embodiments, a method for depleting from a subject administered with engineered immune cells expressing a CD70-specific CAR comprising an epitope specific for a monoclonal antibody comprises administering to the subject a monoclonal antibody specific for the epitope. In these embodiments, administration of the monoclonal antibody specific for the epitope present in the extracellular domain of the CAR to the subject eliminates or inhibits the activity of engineered CAR-expressing immune cells from the subject. In one aspect,

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depletion of engineered CAR expressing immune cells allows for recovery of an endogenous population of CD70-expressing cells.

[0346] In one aspect, the disclosure relates to a method for promoting recovery of endogenous CD70-expressing cells in a subject administered with engineered immune cells expressing at cell surface a CD70-specific CAR comprising an epitope specific for a monoclonal antibody, the method comprising administering a monoclonal antibody specific for the epitope to the subject. In some embodiments, endogenous CD70-expressing cells are endogenous CD70-expressing bone marrow cells. In one aspect, the term "recovery" refers to increasing the number of endogenous CD70-expressing cells. The number of endogenous CD70-expressing cells may increase due to increase in proliferation of endogenous CD70-expressing cells and/or due to reduction in elimination of endogenous CD70-expressing cells by CAR expressing engineered immune cells. In some embodiments, administration of the monoclonal antibody to the subject depletes the CAR expressing engineered immune cells and increases the number of endogenous CD70-expressing cells, *e.g.*, endogenous CD70-expressing bone marrow progenitor cells, in the subject. In one embodiment, administration of the monoclonal antibody to the subject increases the number of endogenous CD70-expressing cells by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%, compared to the number of endogenous CD70-expressing cells prior to administration of the monoclonal antibody.

[0347] In one aspect, provided is a method for treating a CD70-mediated condition in a subject, the method comprising: (a) administering to the subject engineered immune cells expressing at cell surface CD70-specific CARs comprising one or more epitopes specific for one or more monoclonal antibodies; and (b) subsequently depleting the engineered immune cells from the subject by administering one or more monoclonal antibodies specific for the epitope to the subject.

[0348] In some embodiments, the mAbs used in the method for depleting CAR-expressing engineered immune cells are selected from alemtuzumab, ibritumomab tiuxetan, muromonab-CD3, tositumomab, abciximab, basiliximab, brentuximab vedotin, cetuximab, infliximab, rituximab, bevacizumab, certolizumab pegol, daclizumab, eculizumab, efalizumab, gemtuzumab, natalizumab, omalizumab, palivizumab, ranibizumab, tocilizumab, trastuzumab, vedolizumab, adalimumab, belimumab, canakinumab, denosumab, golimumab,

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ipilimumab, ofatumumab, panitumumab, QBEND-10, ustekinumab, and combinations thereof.

[0349] In some embodiments, said epitope specific for a monoclonal antibody (mAb-specific epitope) is a CD20 epitope or mimotope, *e.g.* SEQ ID NO: 609, SEQ ID NO: 294, or SEQ ID NO: 295, and the mAb specific for the epitope is rituximab.

[0350] In some embodiments, the step of administering a monoclonal antibody to the subject comprises infusing the subject with the monoclonal antibody. In some embodiments, the amount of epitope-specific mAb administered to the subject is sufficient to eliminate at least 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% of the CAR-expressing immune cell in the subject.

[0351] In some embodiments, the step of administering a monoclonal antibody to the subject comprises infusing the subject with 375mg/m2 of rituximab, once or several times weekly.

[0352] In some embodiments, when immune cells expressing a CAR comprising an mAb-specific epitope (CAR-expressing immune cells) are depleted in a CDC assay using epitope-specific mAb, the amount of viable CAR-expressing immune cells decreases, *e.g.* by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90%.

[0353] In some embodiments, a cytotoxic drug is coupled to the epitope-specific mAbs which are used to deplete CAR-expressing immune cells. By combining targeting capabilities of monoclonal antibodies with the cell-killing ability of cytotoxic drugs, antibody-drug conjugate (ADC) allows a sensitive discrimination between healthy and diseased tissue when compared to the use of the drug alone. Market approvals were received for several ADCs; the technology for making them -particularly on linkers- is abundantly presented in the following prior art (Payne, G. (2003) Cancer Cell 3:207-212; Trail et al (2003) Cancer Immunol. Immunother. 52:328-337; Syrigos and Epenetos (1999) Anticancer Research 19:605-614; Niculescu-Duvaz and Springer (1997) Adv. Drug Del. Rev. 26:151-172; U.S. Pat. No. 4,975,278).

[0354] In some embodiments, the epitope-specific mAb to be infused is conjugated beforehand with a molecule able to promote complement dependent cytotoxicity (CDC). Therefore, the complement system helps or complements the ability of antibodies to clear pathogens from the organism. When stimulated by one of several, is triggered an activation cascade as a massive amplification of the response and activation of the cell-killing membrane attack complex. Different molecule may be used to conjugate the mAb, such as glycans [Courtois,

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A, Gac-Breton, S., Berthou, C, Guezennec, J., Bordron, A. and Boisset, C. (2012), Complement dependent cytotoxicity activity of therapeutic antibody fragments is acquired by immunogenic glycan coupling, Electronic Journal of Biotechnology ISSN: 0717-3458; http://www.ejbiotechnology.info DOI: 10.2225/voll5-issue5).

KITS

[0355] The disclosure also provides kits for use in the instant methods. Kits of the disclosure include one or more containers comprising a polynucleotide encoding a CD70-specific CAR, or an engineered immune cell comprising a polynucleotide encoding a CD70-specific CAR as described herein, and instructions for use in accordance with any of the methods of the disclosure described herein. Generally, these instructions comprise a description of administration of the engineered immune cell for the above described therapeutic treatments. The kit may include one or more agents for lymphodepletion (*e.g.* alemtuzumab, cytoxan, fludarabine, cyclophosphamide, or temozolomide).

[0356] The instructions relating to the use of the engineered immune cells as described herein generally include information as to dosage, dosing schedule, and route of administration for the intended treatment. The containers may be unit doses, bulk packages (*e.g.*, multi-dose packages) or sub-unit doses. Instructions supplied in the kits of the disclosure are typically written instructions on a label or package insert (*e.g.*, a paper sheet included in the kit), but machine-readable instructions (*e.g.*, instructions carried on a magnetic or optical storage disk) are also acceptable. In some embodiments, the containers are identifiable (*e.g.*, by label, barcode, or radio-frequency identification (RFID)), trackable, or imprinted with a machine-readable container identifier.

[0357] The kits of this disclosure are in suitable packaging. Suitable packaging includes, but is not limited to, vials, bottles, jars, flexible packaging (*e.g.*, sealed Mylar or plastic bags), and the like. In some embodiments, the container (*e.g.*, plastic bag) is suitable for intravenous infusion. Also contemplated are packages for use in combination with a specific device, such as an inhaler, nasal administration device (*e.g.*, an atomizer) or an infusion device such as a minipump. A kit may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The container may also have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection

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needle). At least one active agent in the composition is a CD70-specific CAR. The container may further comprise a second pharmaceutically active agent.

[0358] Kits may optionally provide additional components such as buffers and interpretive information. Normally, the kit comprises a container and a label or package insert(s) on or associated with the container.

[0359] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the disclosure in any way. Indeed, various modifications of the disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

[0360] The deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Pfizer, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 U.S.C. Section 122 and the Commissioner's rules pursuant thereto (including 37 C.F.R. Section 1.14 with particular reference to 886 OG 638).

[0361] The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the disclosure in contravention of the rights granted under the authority of any government in accordance with its patent laws.

EXAMPLES

Example 1. Generation of CD70-specific CAR-T cells

[0362] The following codon-optimized CD70 CAR sequences listed in Table 5 below were, synthesized and subcloned into the following lentiviral vectors pLVX-EF1a-TurboGFP-P2A-

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CD70 CAR (Clontech) or pCLS-EF1a-BFP-P2A-CD70 CAR (Cellectis) using the XmaI (5') and MluI (3') restriction sites (thus cloning the CAR following the P2A site).

Table 5: Exemplary CD70-specific CARs

CAR	CAR Amino Acid Sequence	Components
31H1	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKK PGSSVKVSCKAS**GGTFSSY**GFSWVRQAPGQGLEW MGGI**IPIFGS**ANYAQKFQGRVTITADKSTSTVYME LISLRSEDTAVYYCAR**GGSSSPFAY**WGQGTLVTVS SGGGGSGGGGSGGGGSGGGGSDIVMTQNPLSSPVT LGQPASISC**RSSQSLVHSDGNTYLS**WLQQRPGQSP RLLIY**KISNRFS**GVPDRFSGSGAGTDFTLKISRVEA EDVGVYYC**MQATQFPLT**IGGGSKVEIKTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR (SEQ ID NO: 311)	CD8α signal peptide; 31H1 VH; GS linker; 31H1 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
63B2	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKK PGSSVKVSCKAS**GGTFSSY**GFSWVRQAPGQGLEW MGGI**IPIFGT**ANYAQKFQGRVTITADKSTSTVFME LISLRSEYTAVYYCAR**GGSSSPFAY**WGQGTLVTVS SGGGGSGGGGSGGGGSGGGGSDIVMTQTPLSSPVT LGQPASISC**RSSQSLVHSDGNTYLS**WLQQRPGQSP RLLIY**KISNRFS**GVPDRFSGSGAGTDFTLKISRVEA EDVGVYYC**MQATQFPLT**IGGGSKVEIK TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG	CD8α signal peptide; 63B2 VH; GS linker; 63B2 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD;

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CAR	CAR Amino Acid Sequence	Components
	CELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 312)	CD3ζ ISD
40E3	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKP SETLSLTCTVS**GGSISSY**YWNWIRQPPGKGLEWIG YI**YYSGS**TNYNPSLKSRVTISVDTSKNQFSLKLRSV TAADTAVYYCAR**DIRTW**GQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TC**RASQGISNYLA**WFQQKPGKAPKSLIY**AASSLQS** GVPSKFSGSGSGTDFTLTISSLQPEDFATYYC**QQYN SYPLT**FGGGTKVEIKTTTPAPRPPTPAPTIASQPLSL RPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCG VLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQ NQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 313)	CD8α signal peptide; 40E3 VH; GS linker; 40E3 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
42C3	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQP GGSLRLSCAAS**GFTFRNS**WMSWVRQAPGKGLEW VANI**KRDGSE**KYYVDSVKGRFTISRDNAKNSLYL QMNSLRAEDTAVYYCAR**DQTGSFDY**WGQGTLVT VSSGGGGSGGGGSGGGGSGGGGSDVVMTQSPLSL PVTLGQPASISC**RSSQSLVYSDENTYLN**WFQQRPG QSLRRLIY**QVSNRDS**GVPDRFSGSGSGTDFTLKISR VEAEDVGVYFC**MQGTYWPPT**FGGGTKVEIKTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK	CD8α signal peptide; 42C3 VH; GS linker; 42C3 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD;

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CAR	CAR Amino Acid Sequence	Components
	LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 314)	CD3ζ ISD
45F11	MALPVTALLLPLALLLHAARPQVQLRGSGPGLVKP SETLSLTCTVS**DDSISVY**YWSWIRQPAGKGLEWIG RV**YSSGN**INYNPSLESRVTMSVDTSKSRFSLNLSSV TAADTAVYYCAR**GLDAFDI**WGQGTMVTVSSGGG GSGGGGSGGGGSGGGGSEIVMTQSPATLSMSLGER ATLSC**RASQSVSSSLA**WYQQKPGQAPRLLIY**GAST RAT**GIPARFGGSGSGTEFTLTISSLQSEDFAVYYC**Q QYINWPH**FGGGTKVEIKTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAG TCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 315)	CD8α signal peptide; 45F11 VH; GS linker; 45F11 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
64F9	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQP GESLRLSCEVS**GFTFTSY**AMSWVRQVPGKGLEWV SII**SGVAFT**TYYADSVKGRFTISRDHSKNTLYLQMN GLRAEDTAVYYCVK**VDGEVY**WGQGTLVTVSSGG GGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGD RVTITC**QASQDISNYLN**WYQQKPGKAPKILIY**GAS NLET**GVPSRFSGSGSGTDFTFAISSLQPEDVATYYC **QQYDNFPIT**FGQGTRLEIKTTTPAPRPPTPAPTIASQ PLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA	CD8α signal peptide; 64F9 VH; GS linker; 64F9 VL; GS linker; CD8α hinge; CD8α TM domain;

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CAR	CAR Amino Acid Sequence	Components
	GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPA YQQGQNQLYNELNLGRREEYDVLDKRRGRDPEM GGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ ID NO: 316)	41BB ISD; CD3ζ ISD
72C2	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKK PGSSVKVSCEAS**GGTFI**<u>**TY**AIS</u>WVRQAPGQGLEW MG<u>GI**IPFFGT**ANYAQKFQG</u>RVTITADKSTSTASME LRSLRSEDTAMYYCAQ<u>**WELFFFDF**</u>WGQGTPVTVS SGGGGSGGGGSGGGGSGGGGSEIVMTQSPDTLSVS PGERAILSC<u>**RASQSVSSNLA**</u>WYQQKPGQAPRLLIY <u>**SASTRAS**</u>GIPARFSGSGSGTEFTLSISSLQSEDFAVY YC<u>**QQYDNWPPLT**</u>FGGGTKVEIKTTTPAPRPPTPAP TIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 317)	CD8α signal peptide; 72C2 VH; GS linker; 72C2 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
2F10	MALPVTALLLPLALLLHAARPAVQLVESGGGLVQP GGSLRLSCAAS**GFTFT**<u>**YY**SMN</u>WVRQAPGKGLEW VS<u>HI**SIRSST**IYFADSAKG</u>RFTISRDNAKNSLYLQM NSLRDEDTAVYYCAR<u>**GSGWYGDYFDY**</u>WGQGTL <u>VTVSS</u>GGGGSGGGGSGGGGSGGGGSEIVLTQSPGT LSLSPGERATLSC<u>**RASQSVSSSYLA**</u>WYQQQPGQAP RLLIY<u>**GASSRAT**</u>GIPDRFSGSGSGTDFTLTISRLEPE DFAIYYC<u>**QQYGSSPLT**</u>FGGGTKVEIK	CD8α signal peptide; 2F10 VH; GS linker; 2F10 VL; GS linker; CD8α hinge;

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CAR	CAR Amino Acid Sequence	Components
	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 318)	CD8α TM domain; 41BB ISD; CD3ζ ISD
4F11	MALPVTALLLPLALLLHAARPQVTLKESGPVLVKP TETLTLTCTVS**GFSLSNARM**GVTWIRQPPGKALE WLAHI**FSNDE**KSYSTSLKSRLTISKDTSKTQVVLTM TNMDPVDTATYYCAR**IRDYYDISSYYDY**WGQGTL VSVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPS AMSASVGDRVTITC**RASQDISNYLA**WFQQKPGKV PKRLIY**AASSLQS**GVPSRFSGSGSGTEFTLTISSLLPE DFATYYC**LQLNSFPFT**FGGGTKVEIN TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH TRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR (SEQ ID NO: 319)	CD8α signal peptide; 4F11 VH; GS linker; 4F11 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
10H10	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQP GGSLRLSCAVS**GFTFSNH**NIHWVRQAPGKGLEWIS YI**SRSSST**IYYADSVKGRFTISRDNAKNSLYLQMNS LRDEDTAVYYCAR**DHAQWYGMDV**WGQGTTVTV SSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSVSA SVGDRVTITC**RASQGISSWLA**WYQQKPGKAPKVL	CD8α signal peptide; 10H10 VH; GS linker; 10H10 VL;

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CAR	CAR Amino Acid Sequence	Components
	IY**AASSLQS**GVPSRFSGSGSGTDFTLTISSLQPEDFA TYYC**QQAFSFPFT**FGPGTKVDIKTTTPAPRPPTPAP TIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR (SEQ ID NO: 320)	GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
17G6	MALPVTALLLPLALLLHAARPEVQLVESGGGLVQP GGSLRLSCVAS**GFTFSSY**WMSWVRQAPGKGLEW VASI**KQDGSE**KYYVDSVKGRFTISRDNAKNSVYL QMNSLRAEDTGVYYCAR**EGVNWGWRLYWHFD L**WGRGTLVTVSSGGGGSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINC**KSSQSVLYSYNNKN YVA**WYQQKPGQPPNLLIF**WASTRES**GVPDRFSGS GSGTDFTLTISSLQAEDVAVYYC**QQYYSTLT**FGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVIT LYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR (SEQ ID NO: 321)	CD8α signal peptide; 17G6 VH; GS linker; 17G6 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
65E11	MALPVTALLLPLALLLHAARPEVQVVESGGGLVQP GGSLRLSCAAS**GFTFSSY**SMNWVRQAPGKGLEWV SHS**SISRGN**IYFADSVKGRFTISRDNAKNSLYLQMN SLRDEDTAVYYCAR**GSGWYGDYFDY**WGQGTLVT	CD8α signal peptide; 65E11 VH; GS linker;

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CAR	CAR Amino Acid Sequence	Components
	VSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLS LSPGERVTLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDF AVYYC**QQYGSSPLT**FGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIY IWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRS ADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR (SEQ ID NO: 322)	65E11 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P02B10	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQP GGSLRLSCAAS**GFAFSNY**AMSWVRQAPGKGLEW VSAI**RGGGGS**TYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR**DFISGTWYPDY**WGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQPP SASGTPGQRVTISC**SGSSSNIGSNYVY**WYQQLPGT APKLLIY**RNNQRPS**GVPDRFSGSKSGTSASLAISGL RSEDEADYYC**AAWDDSLSGVV**FGGGTKLTVLTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR (SEQ ID NO: 323)	CD8α signal peptide; P02B10 VH; GS linker; P02B10 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P07D03	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYRFTSY**WIGWVRQMPGKGLEW	CD8α signal peptide;

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CAR	CAR Amino Acid Sequence	Components
	MGSI**YPDDSD**TRYSPSFQGQVTISADKSISTAYLQW SSLKASDTAMYYCAS**STVDYPGYSYFDY**WGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQPP SASGTPGQRVTISC**SGSRSNIGSNYVY**WYQQLPGT APKLLIY**RNNQRPS**GVPDRFSGSKSGTSASLAISGL RSEDEADYYC**ASWDGSLSAVV**FGTGTKLTVLTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR (SEQ ID NO: 324)	P07D03 VH; GS linker; P07D03 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P08A02	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYTFTNY**WIAWVRQMPGKGLEW MGII**YPDGSD**TRYSPSFQGQVTISADKSISTAYLQW SSLKASDTAMYYCAR**DITSWYYGEPAFDI**WGQGT LVTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQ PPSASGTPGQRVTISC**SGSSSNIGSNYVY**WYQQLPG TAPKLLIY**RNNQRPS**GVPDRFSGSKSGTSASLAISG LRSEDEADYYC**ATWDDSLGSPV**FGTGTKLTVLTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR (SEQ ID NO: 325)	CD8α signal peptide; P08A02 VH; GS linker; P08A02 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD

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CAR	CAR Amino Acid Sequence	Components
P08E02	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYSFTSS**WIGWVRQMPGKGLEWM GII**YPGDSD**TRYSPSFQGQVTISADKSISTAYLQWSS LKASDTAMYYCAK**GLSQAMTGFGFDY**WGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSELDIQMTQS PSSLSASVGDRVTITC**RASQSISRYLN**WYQQKPGK APKLLIY**AASILQT**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYYC**QQSYSTTMWT**FGQGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR (SEQ ID NO: 326)	CD8α signal peptide; P08E02 VH; GS linker; P08E02 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P08F08	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYGFTSY**WIGWVRQMPGKGLEW MGII**HPDDSD**TKYSPSFQGQVTISADKSISTAYLQW SSLKASDTAMYYCAS**SYLRGLWGGYFDY**WGQGT LVTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQ PPSASGTPGQRVTISC**SGSSSNIGSNYVN**WYQQLPG TAPKLLIY**GDYQRPS**GVPDRFSGSKSGTSASLAISG LRSEDEADYYC**ATRDDSLSGSVV**FGTGTKLTVLTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD	CD8α signal peptide; P08F08 VH; GS linker; P08F08 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD

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CAR	CAR Amino Acid Sequence	Components
	TYDALHMQALPPR (SEQ ID NO: 327)	
P08G02	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYTFPSS**WIGWVRQMPGKGLEWM GII**YPDTSH**TRYSPSFQGQVTISADKSISTAYLQWSS LKASDTAMYYCAR**ASYFDRGTGYSSWWMDV**WG QGTLVTVSSGGGGSGGGGSGGGGSGGGGSELDIQ MTQSPSSLSASVGDRVTITC**RASQSIYDYLH**WYQQ KPGKAPKLLIY**DASNLQS**GVPSRFSGSGSGTDFTLT ISSLQPEDFATYYC**QQSYTTPLFT**FGQGTKVEIKTT TPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR (SEQ ID NO: 328)	CD8α signal peptide; P08G02 VH; GS linker; P08G02 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P12B09	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQP GGSLRLSCAAS**GFTFSQY**SMSWVRQAPGKGLEWV SAI**SGGGVS**TYYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAS**DISDSGGSHWYFDY**WGQG TLVTVSSGGGGSGGGGSGGGGSGGGGSELDIQMT QSPSSLSASVGDRVTITC**RASQYIGRYLN**WYQQKR GKAPKLLIH**GATSLAS**GVPSRFSGSGSGTDFTLTISS LQPEDFATYYC**QQSYSTTSPT**FGQGTKVEIKTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV	CD8α signal peptide; P12B09 VH; GS linker; P12B09 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD

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CAR	CAR Amino Acid Sequence	Components
	LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 329)	
P12F02	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQP GGSLRLSCAAS**GFTFSSY**AMSWVRQAPGKGLEWV STI**SGTGGT**TYYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAK**VRAGIDPTASDV**WGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQPP SASGTPGQRVTISC**SGSTSNIGRNYVY**WYQQLPGT APKLLIY**RTNQRPS**GVPDRFSGSKSGTSASLAISGL RSEDEADYYC**AAWDDSLSGRV**FGTGTKLTVLTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR (SEQ ID NO: 330)	CD8α signal peptide; P12F02 VH; GS linker; P12F02 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P12G07	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQP GGSLRLSCAAS**GFTFNNF**AMSWVRQAPGKGLEW VSGI**SGSGDN**TYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK**DRDIGLGWYSYYLDV**W GQGTLVTVSSGGGGSGGGGSGGGGSGGGGSELQS VLTQPPSASGTPGQRVTISC**SGSSSNIGSNYVY**WYQ QLPGTAPKPLIY**MNNQRPS**GVPDRFSGSKSGTSAS LAISGLRSEDEADYYC**AAWDDSLSAVV**FGTGTKL TVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGA VHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK	CD8α signal peptide; P12G07 VH; GS linker; P12G07 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD;

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CAR	CAR Amino Acid Sequence	Components
	RGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR (SEQ ID NO: 331)	CD3ζ ISD
P13F04	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKK PGSSVKVSCKAS**GGTFSSY**AISWVRQAPGQGLEW MGE**IIPIFGT**ASYAQKFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAR**AGWDDSWFDY**WGQGTLVT VSSGGGGSGGGGSGGGGSGGGGSELQSVLTQPPSA SGTPGQRVTISC**SGSNSNIGTNYVS**WYQQLPGTAP KLLIY**RSSRRPS**GVPDRFSGSKSGTSASLAISGLRSE DEADYYC**AAWDGSLSGHWV**FGTGTKLTVLTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 332)	CD8α signal peptide; P13F04 VH; GS linker; P13F04 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD
P15D02	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYSFA**S**Y**WIGWVRQMPGKGLEWM GVI**YPGTSE**TRYSPSFQGQVTISADKSISTAYLQWS SLKASDTAMYYCAK**GLSASASGYSFQY**WGQGTL VTVSSGGGGSGGGGSGGGGSGGGGSELDIQMTQS PSSLSASVGDRVTITC**RASQSIDTYLN**WYQQKPGK APKLLIY**SASSLHS**GVPSRFSGSGSGTDFTLTISSLQ PEDFATYYC**QQSYSTTAWT**FGQGTKVEIKTTTPAP	CD8α signal peptide; P15D02 VH; GS linker; P15D02 VL; GS linker; CD8α hinge;

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CAR	CAR Amino Acid Sequence	Components
	RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR (SEQ ID NO: 333)	CD8α TM domain; 41BB ISD; CD3ζ ISD
P16C05	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKP GESLKISCKGS**GYSFTDY**WIGWVRQMPGKGLEW MGMI**SPGGST**TIYRPSFQGQVTISADKSISTAYLQW SSLKASDTAMYYCAR**EMYTGGYGGSWYFDY**WG QGTLVTVSSGGGGSGGGGSGGGGSGGGGSELDIQ MTQSPSSLSASVGDRVTITC**RASQSIGQSLN**WYQQ KPGKAPKLLIY**GASSLQS**GVPSRFSGSGSGTDFTLT ISSLQPEDFATYYC**QQSYSTPIT**FGQGTKVEIKTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR (SEQ ID NO: 334)	CD8α signal peptide; P16C05 VH; GS linker; P16C05 VL; GS linker; CD8α hinge; CD8α TM domain; 41BB ISD; CD3ζ ISD

[0363] CARs comprising ScFv based on 10A1, 10E2, 11A1, 11C1, 11D1, 11E1, 12A2, 12C4, 12C5, 12D3, 12D6, 12D7, 12F5, 12H4, 8C8, 8F7, 8F8, 9D8, 9E10, 9E5, 9F4 or 9F8 sequences are also prepared and comprise sequences shown in SEQ ID NO: 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600 and 601.

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Example 2: Jurkat screen for in vitro characterization of anti-CD70 CARs

[0364] Jurkat cells are an immortalized human T cell line and much like primary T cells, express CD70 upon activation or transduction. Hence, these cells were chosen for transduction with CD70 CARs to study their activation profile. Jurkat cells modified using CRISPR/Cas9 to knockout CD70 ("KO Jurkat") or parental Jurkat ("WT Jurkat") were transduced with CD70 CARs. Their auto-activation profile was determined by comparing the percentage of CD69 expression on WT Jurkat (auto-activation and target-dependent activation since WT Jurkat express target *i.e.*, CD70, upon transduction) versus that on KO Jurkat (auto-activation alone, in the absence of target, *i.e.*, CD70) by flow cytometry. Clones that showed target-specific activation and minimal auto-activation were then selected based on the "Activation ratio" (please see below for definition of the term). Auto-activation is a term used to describe the target-independent clustering and activation of CARs. CAR auto-activation can range from minimal/none to high and is thought to be an inherent characteristic or tendency of the scFv to aggregate and cluster. Auto-activation leads to chronic signaling and can lead to T cell differentiation, exhaustion, and decreased cytolytic potential. Screening and elimination of highly auto-activating CARs is an essential step in optimal CAR identification. Ideal CARs have minimal auto-activation.

[0365] Binding of CARs to recombinant antigen is one way to characterize CARs and bin them into unique groups. Strong binding can be an indication that a CAR is highly expressed on the cell surface and has a moderate to high affinity for its target antigen. Low or minimal binding can indicate low expression and/or weaker affinity. CARs with high and low binding should be further characterized, as optimal affinity and cell-surface expression are unknown.

Materials and methods:

CRISPR/Cas9 knockout of CD70 in Jurkat cells

[0366] Jurkat cells were transfected with CD70-targeting guide RNA vectors containing Cas9 and GFP obtained from DNA 2.0 using Lipofectamine 3000 (Invitrogen). Forty-eight hours after transfection, fluorescence activated single cell sorting was performed to select GFP+ CD70- cells. Individual clones were then expanded and genomic DNA was obtained for PCR by crude cell lysis. PCR products were sequenced to identify clones with indels or frameshifts indicating CD70 knockout.

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Jurkat cell transduction with CD70 CARs

[0367] HEK293T cells were plated at 0.5 million cells per mL in 2mL of DMEM (Gibco) supplemented with 10% FBS (Hyclone or JR Scientific) per well of a 6-well plate on Day 0. On Day 1, the lentivirus was prepared by mixing together lentiviral packaging vectors 1.5ug psPAX2, 0.5ug pMD2G, and 2ug of the appropriate transfer CAR vector containing GFP tag in 250uL Opti-MEM (Gibco) per well of the 6-well plate ("DNA mix"). 10uL Lipofectamine 2000 (Invitrogen) in 250uL Opti-MEM was incubated at room temperature for 5 minutes and then added to the DNA mix. The virus was incubated at room temperature for 20 minutes and the total volume of 500uL was slowly added to the sides of the wells containing HEK293T. On Day 2, the media from each well of the 6-well plate was replaced with 2mL per well of Jurkat cell media, *i.e.*, RPMI (Gibco) supplemented with 10% FBS. On Day 3, Jurkat cells (KO or WT) were resuspended at 0.5 million cells per mL in 2mL of RPMI supplemented with 10% FBS per well of a 6-well plate. The lentiviral supernatants from HEK293T cells were harvested and passed through a 0.45 micron filter (EMD Millipore) to remove cell debris, and then added to the Jurkat cells. On Day 6, transduction efficiency was determined by detecting GFP signal via flow cytometry. Cells were expanded into larger flasks as needed using RPMI supplemented with 10% FBS.

Activation profile and ability to bind CD70 protein

[0368] On Day 5, transduced cells were stained with human anti-CD69 antibody conjugated to PE-Cy7 and acquired on a flow cytometer to obtain percentage of CD69+ population for each CAR. Cells were also incubated with recombinant biotinylated human CD70 protein, stained with streptavidin conjugated to PE, and acquired on a flow cytometer to determine protein binding. Activation ratios (WT activation/KO activation) and protein binding were used to rank CARs.

Table 6

CAR	**CD69+ in WT (%)**	**CD69+ in KO (%)**	**Activation ratio (WT/KO)**	**Type of activation**	**Protein binding (%)**
31H1	37.2	16.1	2.31	Auto	1.75
63B2	11.1	1.85	6	Target	0.02
40E3	59.2	28.3	2.09	Auto	0.65

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42C3	30.8	5.86	5.25	Target	1.48
45F11	16.4	2.46	6.67	Target	1.29
64F9	25.2	6.48	3.89	Target	6.24
72C2	7.85	1.27	6.18	Target	0.09
2F10	22.2	2.86	7.76	Target	0.00
4F11	27.6	2.32	11.90	Target	47.10
10H10	32.8	4.48	7.32	Target	17.90
17G6	78.7	11.5	6.84	Target	37.60
65E11	11.4	1.36	8.38	Target	0.05

[0369] Activation ratio and protein binding of hybridoma CARs were determined in the Jurkat screen and used for *in vitro* characterization of CARs. Activation ratio was determined by calculating the ratio of the percentage of CD69 expression on WT Jurkat cells transduced with CD70 CAR (WT) to that on CD70 knockout Jurkat cells transduced with CD70 CAR (KO). A higher activation ratio indicates target-dependent activation. Protein binding was determined by binding to recombinant biotinylated hCD70 protein and detected using streptavidin conjugated to phycoerythrin (PE) dye via flow cytometry. Protein binding values indicate the percentage of CD3+ CAR T cells that bind to human CD70 protein.

Table 7

CAR	**%CD69+ in WT (%)**	**CD69+ in KO (%)**	**Activation ratio (WT/KO)**	**Type of activation**	**Protein binding (%)**
P02B10	22.50	8.01	2.81	Target	77.90
P07D03	14.40	4.73	3.04	Target	0.68
P08A02	67.60	4.69	14.41	Target	20.70
P08E02	43.70	13.30	3.29	Target	57.10
P08F08	34.90	10.20	3.42	Target	35.90
P08G02	54.70	25.90	2.11	Auto	77.80
P12B09	52.10	12.00	4.34	Target	5.74
P12F02	34.80	2.91	11.96	Target	2.39
P12G07	64.90	5.60	11.59	Target	15.50

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P13F04	43.20	10.00	4.32	Target	37.50
P15D02	33.60	12.90	2.60	Target	62.00
P16C05	59.80	26.50	2.26	Auto	70.80

[0370] **Table 7**: Activation ratio and protein binding of phage CARs were determined in the Jurkat screen. Activation ratio was used for *in vitro* characterization of CARs. Activation ratio was determined by calculating the ratio of the percentage of CD69 expression on WT Jurkat cells transduced with CD70 CAR (WT) to that on CD70 knockout Jurkat cells transduced with CD70 CAR (KO). A higher activation ratio indicates target-dependent activation. Protein binding was determined by binding to recombinant biotinylated hCD70 protein and detected using streptavidin conjugated to phycoerythrin (PE) dye via flow cytometry. Protein binding values indicate the percentage of CD3+ CAR T cells that bind to human CD70 protein.

[0371] CARs that showed minimal auto-activation, *i.e.*, minimal expression of CD69 when transduced in CD70 KO Jurkat, were considered more desirable compared to those that are highly activated even in the absence of target since this could lead to a more exhausted CAR phenotype. Similarly, CARs with higher human CD70 protein binding were considered to be more desirable as this indicated proper expression and folding of the CARs on the surface.

Example 3: Primary T cell screen for in vitro characterization of phage and hybridoma CARs

[0372] Primary human T cells were transduced with CD70 CARs to determine transduction efficiencies, CD70-expression on T cells in culture, and T cell subsets. Transduced CAR T cells were then frozen for use in functional assays.

[0373] Transduction efficiency of CAR constructs can vary greatly between different clones. Greater transduction efficiency leads to increased CAR T cells numbers and a more efficient production process, while CARs with low transduction efficiency may not be suitable for large scale production. High transduction efficiency is, in some embodiments, advantageous.

[0374] T cells have a range of phenotypes or subsets, indicative of differentiation state and antigen exposure. Cell surface marks help identify T cell subsets and the marker, CD62L is generally found on naïve, stem-cell memory, and central memory T cells. These cells are less differentiated relative to other subsets such as effector memory and effector T cells, and thus CAR T cells with higher percentages of CD62L positive cells are, in some embodiments, advantageous.

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[0375] CD70 surface expression also varies between different tranduced CARs with some CAR T cells expressing 20-40% CD70 due to activation and transduction of T cells and others expressing none.

Materials and methods:

Primary T cell isolation

[0376] T cells were purified from buffy coat samples obtained from Stanford University using Ficoll gradient density medium (Ficoll Paque PLUS / GE Healthcare Life Sciences). The PBMC layer was recovered and T cells were purified using a commercially available T cell isolation kit (Miltenyi Biotec).

T cell transduction with CD70 CARs

[0377] HEK293T cells were plated at 0.5 million cells per mL in 2mL of DMEM (Gibco) supplemented with 10% FBS (Hyclone or JR Scientific) per well of a 6-well plate on Day 0. On Day 1, the lentivirus was prepared by mixing together lentiviral packaging vectors 1.5ug psPAX2, 0.5ug pMD2G, and 2ug of the appropriate transfer CAR vector containing GFP tag in 250uL Opti-MEM (Gibco) per well of the 6-well plate ("DNA mix"). 10uL Lipofectamine 2000 (Invitrogen) in 250uL Opti-MEM was incubated at room temperature for 5 minutes and then added to the DNA mix. The virus was incubated at room temperature for 20 minutes and the total volume of 500uL was slowly added to the sides of the wells containing HEK293T. Purified T cells were activated in X-Vivo-15 medium (Lonza) supplemented with 100IU/mL human IL-2 (Miltenyi Biotec), 10% FBS (Hyclone or JR Scientific), and human T activation CD2/CD3/CD28 beads at a bead:cell ratio 1:2 (Miltenyi Biotec). On Day 2, the media from each well of the 6-well plate was replaced with 2mL per well of T cell transduction media, *i.e.*, X-Vivo-15 supplemented with 10% FBS. On Day 3, T cells were resuspended at 0.5 million cells per mL in 2mL of T cell transduction media per well of a 6-well plate. The lentiviral supernatants from HEK293T cells were harvested and passed through a 0.45 micron filter (EMD Millipore) to remove cell debris, and then added to the T cells along with 100IU/mL human IL-2. On Day 6, transduction efficiency was determined by detecting GFP signal via flow cytometry. Cells were expanded into larger flasks or G-Rex vessels (Wilson Wolf) as needed using T cell expansion media, *i.e.*, X-Vivo-15 supplemented with 5% human AB serum (Gemini Bio).

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CD70 expression and T cell subsets of CAR T cells

[0378] On Day 13 post-activation, transduced CAR T cells were stained with anti-human CD70 antibody conjugated to PE and anti-human CD62L antibody conjugated to BV605, and acquired on a flow cytometer to obtain percentage of CD70+ and CD62L+ populations for each CAR. Expanded CAR T cells were then frozen in FBS containing 10% DMSO (Sigma Aldrich) for future use in functional assays.

Table 8

CAR	**CAR+ (%)**	**CD70+ (%)**	**CD62L+ (%)**
31H1	58.7	16.0	53.4
63B2	4.1	30.0	76.3
40E3	60.0	31.3	54.5
42C3	51.5	35.9	58.9
45F11	26.8	33.6	78.8
64F9	57.3	27.3	79.1
72C2	32.2	32.2	83.2
2F10	1.1	27.9	32.3
4F11	89.3	0.1	78.0
10H10	37.4	1.7	49.0
17G6	71.7	0.2	69.0
65E11	56.9	5.0	76.1
P02B10	74.2	43.9	73.5
P07D03	81.0	17.7	76.1
P08A02	22.3	0.81	27.6
P08E02	48.1	1.25	35.6
P08F08	89.2	17.0	78.6
P08G02	66.9	1.22	58.8
P12B09	49.7	3.19	25.7
P12F02	59.8	12.8	27.1
P12G07	26.2	3.90	23.1

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P13F04	6.47	6.78	32.9
P15D02	78.8	0.37	26.0
P16C05	60.3	11.8	34.4

[0379] **Table 8**: CAR T cell phenotype at day 13 post-activation was used for *in vitro* characterization of phage and hybridoma CARs. CAR+ population was determined by gating on CD3+ cells; CD70-expressing population was determined by gating on live CD3+ cells; CD62L-expressing population was determined by gating on live CD3+ CAR+ CD8+ cells.

[0380] CAR constructs tested showed varying levels of transduction efficiency. Clones that resulted in low transduction efficiencies were considered less desirable since they would be less suitable for large scale production. The CAR T cell products also showed different phenotype (as measured by CD62L expression) and varying levels of CD70 expression on the surface. In general, CAR T cells that expressed higher levels of CD62L were considered more desirable since these are likely less differentiated.

Example 4: Stress test with phage CARs

[0381] CAR T cells were generated and frozen from 12 different scFvs from the phage library as described in the previous example. These CAR T cells were then thawed and mixed with Raji target cells that are known to express CD70 at an effector:target (E:T) ratio of 1:1 in RPMI supplemented with 10% FBS. Raji cells were added to the CAR T cells every 2 days thereafter in order to maintain an E:T ratio of 1:1. Percentage lysis of target cells and fold expansion of effector CAR T cells were determined at each time-point.

[0382] Stress test is a screening assay that involves repeated exposure of CAR T cells to their target causing the CARs to undergo proliferation and in certain cases, differentiation and exhaustion. The stress test was used to select optimal clones with high target cell lysis and proliferative abilities after several rounds of exposure to target cells.

Materials and methods:

[0383] On Day 0, CAR T cells derived from 12 different scFvs from the phage library were thawed and mixed with Raji cells at and E:T ratio of 1:1. On Day 2, 200uL of cells from the assay were mixed with 50uL of cell counting beads (CountBright, Invitrogen) and acquired on the flow cytometer. The counting beads were used to determine the total number of GFP+ CAR T cells (gated on CD3+) and Raji cells (gated on CD3-) for each CAR treatment. Based

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on the total CAR T cell count, the number of Raji cells required to maintain E:T ratio of 1:1 was calculated and added to the respective well of the assay. This process was repeated on Day 5 and Day 7. Percentage lysis of target cells was calculated at each time-point by calculating the percentage of live Raji cells for each CAR treatment and then normalizing to non-transduced control. Fold expansion of CAR T cells over the number of CAR T cells plated on Day 0 was calculated at each time-point.

[0384] Optimal clones were those with highest target cell lysis and best fold expansion at the end of the assay on Day 7, for example P08F08.

Table 9

CAR	**Serial Killing Assay**					
	Target cell lysis (%)			**CAR T cell fold expansion**		
	Day 2	Day 5	Day 7	Day 2	Day 5	Day 7
P02B10	61.6	-42.9	-12.0	1.56	0.97	0.49
P07D03	**80.2**	**48.9**	**26.9**	**1.63**	**6.11**	**10.33**
P08A02	91.8	12.5	6.9	0.69	1.69	2.65
P08E02	98.8	37.6	-5.7	0.50	0.45	1.06
P08F08	**75.9**	**30.2**	**57.8**	**1.52**	**11.47**	**24.35**
P08G02	**98.9**	**49.9**	**27.4**	**0.75**	**0.56**	**3.05**
P12B09	85.4	11.3	5.4	0.76	2.53	3.34
P12F02	82.8	-53.7	-46.3	2.18	0.96	0.26
P12G07	94.8	36.4	9.1	0.87	1.13	1.58
P13F04	**89.3**	**44.8**	**41.3**	**2.15**	**3.61**	**5.67**
P15D02	**98.7**	**54.6**	**28.6**	**1.12**	**1.29**	**3.78**
P16C05	92.7	18.9	-10.7	1.31	3.13	3.72

[0385] **Table 9**: Target cell lysis and CAR T cell fold expansion in a stress test were used for *in vitro* characterization of phage CARs. CAR T cell phenotype was determined at day 13 post-activation and the cells were then frozen on day 14. Stress test was performed using thawed CAR T cells with target Raji cells at an E:T ratio of 1:1. Target cells lysis was determined via flow cytometry by gating on CD3- target cells 2, 5, and 7 days after co-culturing with CAR T

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cells. CAR T cell fold expansion was determined using cell counting beads and calculating the number of cells on days 2, 5, and 7 relative to the number of cells added at the beginning of the assay. CARs highlighted in **bold** show high target cells lysis and fold expansion.

Example 5: Repeat of stress test with optimal CARs generated from a second donor

[0386] CAR T cells were generated and frozen from 4 scFvs (P07D03, P08F08, P08G02, P15D02) from the phage library and 2 scFvs from the hybridoma library (4F11, 17G6) as described in Example 3. These CAR T cells were then thawed and mixed with Raji target cells that are known to express CD70 at an effector:target (E:T)ratio of 1:1 in RPMI supplemented with 10% FBS. Raji cells were added to the CAR T cells every 2 days thereafter in order to maintain an E:T ratio of 1:1. Percentage lysis of target cells and fold expansion of effector CAR T cells were determined at each time-point.

[0387] All clones performed well in terms of target cell lysis. Standout performers based on fold expansion were P08F08 and 4F11.

Table 10

CAR	**CAR+ (%)**	**CD70+ (%)**	**CD62L+ (%)**	**Serial Killing Assay**					
				Target cell lysis (%)			**CAR T cell fold expansion**		
				Day 2	Day 5	Day 7	Day 2	Day 5	Day 7
P07D03	48.8	3.2	63.4	95.1	98.1	98.7	1.2	8.1	11.8
P08F08	**66.9**	**2.8**	**58.3**	**96.2**	**97.8**	**98.0**	**1.4**	**12.3**	**15.8**
P08G02	37.9	0.1	35.0	98.6	97.2	99.5	0.9	2.4	5.7
P15D02	88.4	0.2	28.4	98.8	97.7	98.8	0.8	4.1	12.2
4F11	**88.3**	**0.3**	**54.4**	**98.3**	**96.9**	**97.3**	**0.9**	**6.0**	**15.5**
17G6	34.8	0.2	28.3	98.7	94.3	90.0	0.5	0.8	2.4

[0388] **Table 10**: Target cell lysis and CAR T cell fold expansion in a stress test were used for *in vitro* characterization of optimal CARs. CAR T cell phenotype was determined at day 14 post-activation and the cells were then frozen on the same day. Stress test was performed using thawed CAR T cells with target Raji cells at an E:T ratio of 1:1. Target cells lysis was determined via flow cytometry by gating on CD3- target cells 2, 5, and 7 days after co-

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culturing with CAR T cells. CAR T cell fold expansion was determined using cell counting beads and calculating the number of cells on days 2, 5, and 7 relative to the number of cells added at the beginning of the assay. CARs highlighted in **bold** show high target cells lysis and fold expansion.

Example 6: Dose-dependent CAR T *in vivo* efficacy in an RCC S.C. tumor model

[0389] CAR T cells were generated from 4F11 scFv as described in Example 3. NOD scid gamma (NSG) mice were implanted with 786-O tumors subcutaneously and once the tumors attained a volume of 200mm^3, the mice were treated with 4F11 CAR T cells at different doses intravenously via tail vein injection to determine the optimal CAR T dose. 786-O cells are available from ATCC® as CRL-1932™. The 4F11 CAR T was highly efficacious in vivo and caused complete tumor regression at the 5x10^6 CAR T dose.

Materials and methods:

[0390] Fifty NOD scid gamma (NSG) mice were shaved and prepared for subcutaneous tumor implant on the right flank. 786-O tumor cells that are known to express CD70 were expanded in RPMI supplemented with 10% FBS. On Day 0, 786-O cells were resuspended in serum-free RPMI at the required concentration to inject 5 million cells per animal. Tumor cells were injected in 100uL of serum-free RPMI combined with 100uL Matrigel (Corning) per animal subcutaneously. Day 0 baseline body weights were recorded for all animals immediately after tumor implant. Tumors were measured twice a week starting on Day 9 using Digimatic Calipers (Mitutoyo) and body weights recorded. On Day 14, when the tumors attained 200mm^3 (standard error 8.39) 40 tumor-bearing mice were randomized to 4 groups of 10 mice each. 4F11 CAR T cells were thawed in RPMI supplemented with 10% FBS and resuspended in serum-free RPMI at the required concentration to inject 1, 3, or 5 million CAR+ T cells per animal (calculated based on 4F11 transduction efficiency 57.2%). Number of non-transduced T cells (NTD) required to maintain equal number of total T cells in each group were calculated and added to respective samples. CAR T cells or non-transduced T cell control were injected in 200uL of serum-free RPMI per animal intravenously via tail vein. Tumors were measured and body weights recorded twice a week till Day 43 when the NTD group reached the study end-point (1500mm^3 tumor volume).

[0391] Tumor volumes (mean and error SEM) were plotted on GraphPad Prism and statistics were calculated using one-way ANOVA with repeated measures (see FIGs. 1 and 2). While

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tumors were completely eliminated with the 5 million CAR+ dose, the 1 million CAR+ dose showed no efficacy as compared with the NTD group. Thus, the 3 million CAR+ dose was chosen as the optimal dose for future *in vivo* studies.

Example 7: *In vivo* comparison of CD70 CARs with or without CD70 TALEN knockout in 786-O cells

[0392] 4F11 and P08F08 CAR T cells were generated as described in Example 1 with or without CD70 TALEN DNA electroporation on Day 6 post-activation. NSG mice were implanted with 786-O tumors subcutaneously and once the tumors attained a volume of 200mm^3, the mice were treated with CAR T cells intravenously via tail vein injection to determine the CAR and condition with most optimal efficacy. P08F08 CAR T cells were highly efficacious in vivo and caused complete tumor regression at the 3x10^6 CAR T dose regardless of CD70 knockout (KO). 4F11 CAR T cells showed good efficacy when CD70 was knocked out but merely controlled tumor growth in the absence of CD70 knockout. These results suggest that CD70 knock out can improve the activity CD70 CARs.

Materials and methods:

[0393] Seventy-five NSG mice were shaved and prepared for subcutaneous tumor implant on the right flank. 786-O tumor cells that are known to express CD70 were expanded in RPMI supplemented with 10% FBS. On Day 0, 786-O cells were resuspended in serum-free RPMI at the required concentration to inject 5 million cells per animal. Tumor cells were injected in 100uL of serum-free RPMI combined with 100uL Matrigel (Corning) per animal subcutaneously. Day 0 baseline body weights were recorded for all animals immediately after tumor implant. Tumors were measured twice a week starting on Day 7 using Digimatic Calipers (Mitutoyo) and body weights recorded. On Day 20, when the tumors attained 200mm^3 (standard error 9.69), 60 tumor-bearing mice were randomized to 6 groups of 10 mice each. On Day 21, CAR T cells were thawed in RPMI supplemented with 10% FBS and resuspended in serum-free RPMI at 3 million CAR+ T cells per animal (calculated based on individual transduction efficiencies). Number of NTD cells required to maintain equal percentage of CAR+ T cells as well as equal number of total T cells in each group were calculated and added to respective samples. CAR T cells or NTD control were injected in 200uL of serum-free RPMI per animal intravenously via tail vein. Tumors were measured

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and body weights recorded twice a week till Day 56 when the NTD group reached the study end-point (1500mm^3 tumor volume) (See FIGs. 3 and 4).

[0394] Tumor volumes (mean and error SEM) were plotted on GraphPad Prism and statistics were calculated using one-way ANOVA with repeated measures. P08F08 CAR T groups, both with or without CD70 knockout, caused complete tumor regression at the 3 million CAR+ dose. 4F11 CAR T group with CD70 knockout also caused complete rumor regression at the 3 million CAR+ dose. However, 4F11 CAR T group without CD70 knockout did not cause complete regression.

[0395] In FIGs. 3 and 4, statistical significance over corresponding NTD control are indicated to the right of the legend (for example, P08F08 with CD70 KO over NTD with CD70 KO) Statistical significance of each CAR group with CD70 KO over corresponding CAR group without CD70 KO are indicated to the left of the legend. Statistics represent RM one-way ANOVA with Dunnett's post-hoc test (ns $p>0.05$, *$p<0.05$, **$p<0.01$, ***$p<0.001$, **** $p<0.0001$).

Example 8: *In vivo* comparison of CD70 CARs with or without CD70 TALEN knockout in ACHN metastasis model

[0396] 4F11 and P08F08 CAR T cells from Example 7 were further tested in ACHN cells, a renal cell cancer (RCC)-derived cell line. ACHN cells are described in Simmons et al. Animal Models of Bone Metastasis. *Veterinary Pathology* 52:827-841, 834 (2015). NSG mice were each implanted with 1 million ACHN tumor cells intravenously and 15 days post-tumor cell injection, the mice were treated with CAR T cells intravenously via tail vein injection to determine the CAR and condition with most optimal efficacy. 4F11 CAR T cells dosed at 3 million CAR+ cells per mouse were efficacious across all 3 donors tested regardless of CD70 knockout (KO). P08F08 CAR T cells showed little to no efficacy and were only tested in the absence of CD70 knockout.

Materials and methods:

[0397] Forty-five NSG mice were prepared for intravenous tumor injection via tail vein. ACHN tumor cells that are known to express CD70 were expanded in MEM supplemented with 10% FBS. On Day 0, ACHN tumor cells were resuspended in serum-free MEM at the required concentration to inject 1 million cells per animal. ACHN tumor cells were injected in 200uL of serum-free MEM intravenously. Day 4 baseline body weights were recorded for all

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animals. Tumor flux was measured twice a week starting on Day 7 using bioluminence (IVIS Spectrum Imager™ from PerkinElmer™; auto-exposure with a maximum exposure time of 120 seconds), and body weights were recorded. On Day 20, when the tumors attained 200mm^3 (standard error 9.69), 20 tumor-bearing mice were randomized to 4 groups of 5 mice each. On Day 15, CAR T cells were thawed in MEM supplemented with 10% FBS and resuspended in serum-free MEM at 3 million CAR+ T cells per animal (calculated based on individual transduction efficiencies). Number of NTD cells required to maintain equal percentage of CAR+ T cells as well as equal number of total T cells in each group were calculated and added to respective samples. CAR T cells or NTD control were injected in 200uL of serum-free MEM per animal intravenously via tail vein. Tumor flux was measured and body weights recorded twice a week till Day 35-49 when the NTD group reached the study end-point (> 20% body weight loss) (See FIGs. 5a, 5b and 5c).

[0398] Bioluminescence (mean and error SEM) were plotted on GraphPad Prism and statistics were calculated using one-way ANOVA with repeated measures. 4F11 CAR T groups, both with or without CD70 knockout, showed anti-tumor efficacy at the 3 million CAR+ dose. P08F08 CAR T group without CD70 knockout showed little to no efficacy at the 3 million CAR+ dose.

Example 9: Activity of CD70-specific CAR T cells expressing CD20 epitopes

Part A: *In vitro* activity

[0399] CD70-specific CAR T cells expressing CD20 epitopes are effective against 786-0 target cells in cell-killing assay

[0400] Six CD70-specific CAR formats were designed (FIG. 6A-6F). Sequences of the constructed CARs are as shown in Tables 11A-11F:

Table 11A

Format	Clone Name	Full Amino Sequence	Seq ID NO:

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No Epitope (FIG. 6A)	4F11	MALPVTALLLPLALLLHAARPQVTLKESGPVLVKPTETLTLTCT VSGFSLSNARMGVTWIRQPPGKALEWLAHIFSNDEKSYSTSLKS RLTISKDTSKTQVVLTMTNMDPVDTATYYCARIRDYYDISSYYD YWGQGTLVSVSSGGGGSGGGGSGGGGSDIQMTQSPSAMSASV GDRVTITCRASQDISNYLAWFQQKPGKVPKRLIYAASSLQSGVP SRFSGSGSGTEFTLTISSLLPEDFATYYCLQLNSFPFTFGGGTKVE INTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	619
	4F11-2	MALPVTALLLPLALLLHAARPQVTLKESGPVLVKPTETLTLTCT VSGFSLSNARMGVTWIRQPPGKALEWLAHIFSNDEKSYSTSLKS RLTISKDTSKTQVVLTMTNMDPVDTATYYCARIRDYYDISSYYD YWGQGTLVSVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSA MSASVGDRVTITCRASQDISNYLAWFQQKPGKVPKRLIYAASSL QSGVPSRFSGSGSGTEFTLTISSLLPEDFATYYCLQLNSFPFTFGG GTKVEINTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQ GQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR	672
	P08F08	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLKISCK GSGYGFTSYWIGWVRQMPGKGLEWMGIIHPDDSDTKYSPSFQG QVTISADKSISTAYLQWSSLKASDTAMYYCASSYLRGLWGGYF DYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQP PSASGTPGQRVTISCSGSSSNIGSNYVNWYQQLPGTAPKLLIYGD YQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCATRDDSLS GSVVFGTGTKLTVLTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR	327
	10A1	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCT VSGGSISYYYWTWIRQPPGKGLEWIGHIYYSGSTNYNPSLKSRV TISIDTSKNLFSLKLSSVTAADTAVYYCARAEGSIDAFDFWGQGT MVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGD RVTITCRASQSISTWLAWYQQKPGKAPKVLIYKASSLESGVPSR FSGSGSGTEFILTINSLQPDDFASYYCQQYKSYSHTFGQGTKLEI KTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	580

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	11C1	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLNCT VSGGSISYYYWTWIRQPPGKGLEWIGHVIYSGTTNYNPSLKSRV TISVDTSKNQFSLKLNSVTAADTAVYYCVRAEGSlDAFDLWGQ GTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSILSASV GDRVTITCRASQSVSSWLAWYQQKPGKAPKVLIYKASSLESGV PSRFSGTGSGTEFTLTISSLQSDDFATYYCQQYNTYSHTFGQGTK LEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDF ACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQ LYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR	583
	11E1	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPLQTLSLTCT VSGGSISSdgYYWSWIRQNPGKGLEWIGYMYYSGSTYYNPSLKS RVTISVDTSKNQFSLKLRSVTAADTAVYYCTRDFGWYFDLWGR GTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASV GDSITITCRASQDIDNYLAWYQQKTGKVPKVLIYAASALQSGVP SRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSGPRTFGQGTK VEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR	585
	12A2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQSLSLTCS VSGGSVSSdgYYWSWIRQHPGKGLEWIGYIYYRRITDYNPSLKS RVNISLDTSKNQFSLKLSSVTAADTAVYYCARDFGWYFDLWGR GTLVAVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASV GDRVTITCRASQDISNYLTWYQQKPGRVPEVLIYAASALQSGVP SRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSAPRTFGQGTK VEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD FACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQN QLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR	586
	12C5	MALPVTALLLPLALLLHAARPEVELVESGGGMVQPGRSLRLSC AASGFTFSDYGMHWVRQAPGMGLEWVTVIWYDGSnKYYADS VKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCARDEVGfvGAF DIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSF LSASVGDRVIITCRASQGINSHLAWYQQKPGKAPKLLIYYASTLP SGVPSRFSGSGSGTEFTLTVTSLQPEDFATYYCQQLNHYPITFGQ GTRLDINTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQ GQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR	588

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	12C6	MALPVTALLLPLALLLHAARPEVELVESGGGMVQPGRSLRLSC AASGFTFSDYGMHWVRQAPGMGLEWVTVIWYDGSnKYYADS VKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCARDEVGfvGAF DIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPSF LSASVGDRVIITCRASQGINSHLAWYQQKPGKAPKLLIYYASTLP SGVPSRFSGSGSGTEFTLTVTSLQPEDFATYYCQQLNHYPITFGQ GTRLEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQ GQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR	673
	8F8	MALPVTALLLPLALLLHAARPQVQLQESGPGLVQPSETLSLTCT VSGGSISYYYWSWIRQPPGKGLEWIGNINYMGNTIYNPSLKSRV TISVDTSKDQFSLKLTSVSAADTAVYYCVRAEGSlDAFDFWGQG TLVAVSLGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG DRVTITCRASQSISSWLAWYQQKPGKAPKVLIYKASNLESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSCTFGQGTKLE IKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	596

Table 11B

Format	Clone Name	Full Amino Sequence	Seq ID NO:
SR2 (FIG. 6B)	4F11-SR2	MALPVTALLLPLALLLHAARPQVTLKESGPVLVKPTETLTLTCT VSGFSLSNARMGVTWIRQPPGKALEWLAHIFSNDEKSYSTSLKS RLTISKDTSKTQVVLTMTNMDPVDTATYYCARIRDYYDISSYY DYWGQGTLVSVSSGGGGSGGGGSGGGGSDIQMTQSPSAMSAS VGDRVTITCRASQDISNYLAWFQQKPGKVPKRLIYAASSLQSGV PSRFSGSGSGTEFTLTISSLLPEDFATYYCLQLNSFPFTFGGGTKV EINGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	620
	4F11-2-SR2	MALPVTALLLPLALLLHAARPQVTLKESGPVLVKPTETLTLTCT VSGFSLSNARMGVTWIRQPPGKALEWLAHIFSNDEKSYSTSLKS RLTISKDTSKTQVVLTMTNMDPVDTATYYCARIRDYYDISSYY DYWGQGTLVSVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPS AMSASVGDRVTITCRASQDISNYLAWFQQKPGKVPKRLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLLPEDFATYYCLQLNSFPFTFG GGTKVEINGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGG STTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL	674

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	
	P08F08-SR2	MALPVTALLLPLALLLHAARPEVQLVQSGAEVKKPGESLKISCK GSGYGFTSYWIGWVRQMPGKGLEWMGIIHPDDSDTKYSPSFQG QVTISADKSISTAYLQWSSLKASDTAMYYCASSYLRGLWGGYF DYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSELQSVLTQP PSASGTPGQRVTISCSGSSSNIGSNYVNWYQQLPGTAPKLLIYGD YQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCATRDDSL SGSVVFGTGTKLTVLGSGGGGSCPYSNPSLCSGGGGSCPYSNPS LCSGGGGSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHT RGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK QPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQ QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR	621
	10A1-SR2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLTCT VSGGSISYYYWTWIRQPPGKGLEWIGHIYYSGSTNYNPSLKSRV TISIDTSKNLFSLKLSSVTAADTAVYYCARAEGSlDAFDFWGQG TMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG DRVTITCRASQSISTWLAWYQQKPGKAPKVLIYKASSLESGVPS RFSGSGSGTEFILTINSLQPDDFASYYCQQYKSYSHTFGQGTKLE IKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTPAP RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	622
	11C1-SR2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSETLSLNCT VSGGSISYYYWTWIRQPPGKGLEWIGHVIYSGTTNYNPSLKSRV TISVDTSKNQFSLKLNSVTAADTAVYYCVRAEGSlDAFDLWGQ GTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSILSASV GDRVTITCRASQSVSSWLAWYQQKPGKAPKVLIYKASSLESGV PSRFSGTGSGTEFTLTISSLQSDDFATYYCQQYNTYSHTFGQGTK LEIKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	623

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
	11E1-SR2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPLQTLSLTCT VSGGSISSdgYYWSWIRQNPGKGLEWIGYMYYSGSTYYNPSLKS RVTISVDTSKNQFSLKLRSVTAADTAVYYCTRDFGWYFDLWGR GTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASV GDSITITCRASQDIDNYLAWYQQKTGKVPKVLIYAASALQSGVP SRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSGPRTFGQGTK VEIKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	624
	12A2-SR2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVKPSQSLSLTCS VSGGSVSSdgYYWSWIRQHPGKGLEWIGYIYYRRITDYNPSLKS RVNISLDTSKNQFSLKLSSVTAADTAVYYCARDFGWYFDLWGR GTLVAVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASV GDRVTITCRASQDISNYLTWYQQKPGRVPEVLIYAASALQSGVP SRFSGSGSGTDFTLTISSLQPEDVATYYCQNYNSAPRTFGQGTK VEIKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	625
	12C5-SR2	MALPVTALLLPLALLLHAARPEVELVESGGGMVQPGRSLRLSC AASGFTFSDYGMHWVRQAPGMGLEWVTVIWYDGSnKYYADS VKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCARDEVGfvGA FDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPS FLSASVGDRVIITCRASQGINSHLAWYQQKPGKAPKLLIYYAST LPSGVPSRFSGSGSGTEFTLTVTSLQPEDFATYYCQQLNHYPITF GQGTRLDINGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGG GSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQ LYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR	626
	12C6-SR2	MALPVTALLLPLALLLHAARPEVELVESGGGMVQPGRSLRLSC AASGFTFSDYGMHWVRQAPGMGLEWVTVIWYDGSnKYYADS VKGRFTISRDNSKNTVFLQMNSLRAEDTAVYYCARDEVGfvGA FDIWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDIQLTQSPS FLSASVGDRVIITCRASQGINSHLAWYQQKPGKAPKLLIYYAST LPSGVPSRFSGSGSGTEFTLTVTSLQPEDFATYYCQQLNHYPITF GQGTRLEIKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGG GSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQ LYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE	675

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR	
	8F8-SR2	MALPVTALLLPLALLLHAARPQVQLQESGPGLVQPSETLSLTCT VSGGSISYYYWSWIRQPPGKGLEWIGNINYMGNTIYNPSLKSRV TISVDTSKDQFSLKLTSVSAADTAVYYCVRAEGSlDAFDFWGQG TLVAVSLGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG DRVTITCRASQSISSWLAWYQQKPGKAPKVLIYKASNLESGVPS RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSCTFGQGTKLE IKGSGGGGSCPYSNPSLCSGGGGSCPYSNPSLCSGGGGSTTTPAP RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	627

Table 11C

Format	Clone Name	Full Amino Sequence	Seq ID NO:
RSRQR (FIG. 6C)	4F11-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQ PPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMT NMDPVDTATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGS GGGGSGGGGSDIQMTQSPSAMSASVGDRVTITCRASQDISNYLA WFQQKPGKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLLP EDFATYYCLQLNSFPFTFGGGTKVEINGSGGGGSCPYSNPSLCSG GGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	628
	4F11-2-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQ PPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMT NMDPVDTATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGS GGGGSGGGGSGGGGSDIQMTQSPSAMSASVGDRVTITCRASQD ISNYLAWFQQKPGKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTL TISSLLPEDFATYYCLQLNSFPFTFGGGTKVEINGSGGGGSCPYS NPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCT TTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI	676

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR	
	P08F08-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSEVQLVQSGAEVKKPGESLKISCKGSGYGFTSYWIGWVRQM PGKGLEWMGIIHPDDSDTKYSPSFQGQVTISADKSISTAYLQWSS LKASDTAMYYCASSYLRGLWGGYFDYWGQGTLVTVSSGGGGS GGGGSGGGGSGGGGSELQSVLTQPPSASGTPGQRVTISCSGSSS NIGSNYVNWYQQLPGTAPKLLIYGDYQRPSGVPDRFSGSKSGTS ASLAISGLRSEDEADYYCATRDDSLSGSVVFGTGTKLTVLGSGG GGSCPYSNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPY SNPSLCTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRG LDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQG QNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR	629
	10A1-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVQLQESGPGLVKPSETLSLTCTVSGGSISYYYWTWIRQPP GKGLEWIGHIYYSGSTNYNPSLKSRVTISIDTSKNLFSLKLSSVTA ADTAVYYCARAEGSlDAFDFWGQGTMVTVSSGGGGSGGGGSG GGGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISTWLAW YQQKPGKAPKVLIYKASSLESGVPSRFSGSGSGTEFILTINSLQPD DFASYYCQQYKSYSHTFGQGTKLEIKGSGGGGSCPYSNPSLCSG GGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	630
	11C1-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVQLQESGPGLVKPSETLSLNCTVSGGSISYYYWTWIRQPP GKGLEWIGHVIYSGTTNYNPSLKSRVTISVDTSKNQFSLKLNSVT AADTAVYYCVRAEGSlDAFDLWGQGTMVTVSSGGGGSGGGGS GGGGSGGGGSDIQMTQSPSILSASVGDRVTITCRASQSVSSWLA WYQQKPGKAPKVLIYKASSLESGVPSRFSGTGSGTEFTLTISSLQ SDDFATYYCQQYNTYSHTFGQGTKLEIKGSGGGGSCPYSNPSLC SGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPAP RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	631
	11E1-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVQLQESGPGLVKPLQTLSLTCTVSGGSISSdgYYWSWIRQ NPGKGLEWIGYMYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLR SVTAADTAVYYCTRDFGWYFDLWGRGTLVTVSSGGGGSGGGG	632

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		SGGGGSGGGGSDIQMTQSPSSLSASVGDSITITCRASQDIDNYLA WYQQKTGKVPKVLIYAASALQSGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCQNYNSGPRTFGQGTKVEIKGSGGGGSCPYSNPSL CSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	
	12A2-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVQLQESGPGLVKPSQSLSLTCSVSGGSVSSdgYYWSWIRQ HPGKGLEWIGYIYYRRITDYNPSLKSRVNISLDTSKNQFSLKLSS VTAADTAVYYCARDFGWYFDLWGRGTLVAVSSGGGGSGGGG SGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLT WYQQKPGRVPEVLIYAASALQSGVPSRFSGSGSGTDFTLTISSLQ PEDVATYYCQNYNSAPRTFGQGTKVEIKGSGGGGSCPYSNPSLC SGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPAP RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	633
	12C5-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSEVELVESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQ APGMGLEWVTVIWYDGSnKYYADSVKGRFTISRDNSKNTVFLQ MNSLRAEDTAVYYCARDEVGfvGAFDIWGQGTMVTVSSGGGG SGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGI NSHLAWYQQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTL TVTSLQPEDFATYYCQQLNHYPITFGQGTRLDINGSGGGGSCPY SNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLC TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR	634
	12C6-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSEVELVESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQ APGMGLEWVTVIWYDGSnKYYADSVKGRFTISRDNSKNTVFLQ MNSLRAEDTAVYYCARDEVGfvGAFDIWGQGTMVTVSSGGGG SGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGI NSHLAWYQQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTL TVTSLQPEDFATYYCQQLNHYPITFGQGTRLEIKGSGGGGSCPY SNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLC TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK	677

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR	
	8F8-RSRQR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCSGGGGSGG GGSQVQLQESGPGLVQPSETLSLTCTVSGGSISYYYWSWIRQPP GKGLEWIGNINYMGNTIYNPSLKSRVTISVDTSKDQFSLKLTSVS AADTAVYYCVRAEGSlDAFDFWGQGTLVAVSLGGGGSGGGGS GGGGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLA WYQQKPGKAPKVLIYKASNLESGVPSRFSGSGSGTEFTLTISSLQ PDDFATYYCQQYNSYSCTFGQGTKLEIKGSGGGGSCPYSNPSLC SGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCTTTPAP RPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R	635

Table 11D

Format	Clone Name	Full Amino Sequence	Seq ID NO:
RSR (FIG. 6D)	4F11-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVT LKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQPPGKAL EWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMTNMDPVD TATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGSGGGGSG GGGSDIQMTQSPSAMSASVGDRVTITCRASQDISNYLAWFQQKP GKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLLPEDFATY YCLQLNSFPFTFGGGTKVEINGGGGSCPYSNPSLCGGGGSTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	636
	4F11-2-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVT LKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQPPGKAL EWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMTNMDPVD TATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGSGGGGSG GGGSGGGGSDIQMTQSPSAMSASVGDRVTITCRASQDISNYLA WFQQKPGKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLLP EDFATYYCLQLNSFPFTFGGGTKVEINGGGGSCPYSNPSLCGGG GSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFA CDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	678
	P08F08-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVQ LVQSGAEVKKPGESLKISCKGSGYGFTSYWIGWVRQMPGKGLE WMGIIHPDDSDTKYSPSFQGQVTISADKSISTAYLQWSSLKASDT	637

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		AMYYCASSYLRGLWGGYFDYWGQGTLVTVSSGGGGSGGGGS GGGGSGGGGSELQSVLTQPPSASGTPGQRVTISCSGSSSNIGSNY VNWYQQLPGTAPKLLIYGDYQRPSGVPDRFSGSKSGTSASLAIS GLRSEDEADYYCATRDDSLSGSVVFGTGTKLTVLGGGGSCPYS NPSLCGGGGSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAV HTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAY QQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR	
	10A1-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPSETLSLTCTVSGGSISYYYWTWIRQPPGKGLEWI GHIYYSGSTNYNPSLKSRVTISIDTSKNLFSLKLSSVTAADTAVY YCARAEGSlDAFDFWGQGTMVTVSSGGGGSGGGGSGGGGSGG GGSDIQMTQSPSTLSASVGDRVTITCRASQSISTWLAWYQQKPG KAPKVLIYKASSLESGVPSRFSGSGSGTEFILTINSLQPDDFASYY CQQYKSYSHTFGQGTKLEIKGGGGSCPYSNPSLCGGGGSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	638
	11C1-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPSETLSLNCTVSGGSISYYYWTWIRQPPGKGLEW IGHVIYSGTTNYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAV YYCVRAEGSlDAFDLWGQGTMVTVSSGGGGSGGGGSGGGGSG GGGSDIQMTQSPSILSASVGDRVTITCRASQSVSSWLAWYQQKP GKAPKVLIYKASSLESGVPSRFSGTGSGTEFTLTISSLQSDDFATY YCQQYNTYSHTFGQGTKLEIKGGGGSCPYSNPSLCGGGGSTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	639
	11E1-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPLQTLSLTCTVSGGSISSdgYYWSWIRQNPGKGLE WIGYMYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLRSVTAADT AVYYCTRDFGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSG GGGSDIQMTQSPSSLSASVGDSITITCRASQDIDNYLAWYQQKT GKVPKVLIYAASALQSGVPSRFSGSGSGTDFTLTISSLQPEDVAT YYCQNYNSGPRTFGQGTKVEIKGGGGSCPYSNPSLCGGGGSTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	640
	12A2-	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ	641

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
	RSR	LQESGPGLVKPSQSLSLTCSVSGGSVSSdgYYWSWIRQHPGKGL EWIGYIYYRRITDYNPSLKSRVNISLDTSKNQFSLKLSSVTAADT AVYYCARDFGWYFDLWGRGTLVAVSSGGGGSGGGGSGGGGS GGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLTWYQQK PGRVPEVLIYAASALQSGVPSRFSGSGSGTDFTLTISSLQPEDVAT YYCQNYNSAPRTFGQGTKVEIKGGGGSCPYSNPSLCGGGGSTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR	
	12C5-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVEL VESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQAPGMGLE WVTVIWYDGSNKYYADSVKGRFTISRDNSKNTVFLQMNSLRAE DTAVYYCARDEVGFVGAFDIWGQGTMVTVSSGGGGSGGGGSG GGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGINSHLAWY QQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTLTVTSLQPE DFATYYCQQLNHYPITFGQGTRLDINGGGGSCPYSNPSLCGGGG STTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	642
	12C6-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVEL VESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQAPGMGLE WVTVIWYDGSNKYYADSVKGRFTISRDNSKNTVFLQMNSLRAE DTAVYYCARDEVGFVGAFDIWGQGTMVTVSSGGGGSGGGGSG GGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGINSHLAWY QQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTLTVTSLQPE DFATYYCQQLNHYPITFGQGTRLEIKGGGGSCPYSNPSLCGGGG STTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFAC DIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQL YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR	679
	8F8-RSR	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVQPSETLSLTCTVSGGSISYYYWSWIRQPPGKGLEWI GNINYMGNTIYNPSLKSRVTISVDTSKDQFSLKLTSVSAADTAV YYCVRAEGSlDAFDFWGQGTLVAVSLGGGGSGGGGSGGGGSG GGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP GKAPKVLIYKASNLESGVPSRFSGSGSGTEFTLTISSLQPDDFAT YYCQQYNSYSCTFGQGTKLEIKGGGGSCPYSNPSLCGGGGSTTT PAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQ EEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ	643

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Format	Clone Name	Full Amino Sequence	Seq ID NO:
		ALPPR	

Table 11E

Format	Clone Name	Full Amino Sequence	Seq ID NO:
RSR-short (FIG. 6E)	4F11-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVT LKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQPPGKAL EWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMTNMDPVD TATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGSGGGGSG GGGSDIQMTQSPSAMSASVGDRVTITCRASQDISNYLAWFQQKP GKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLLPEDFATY YCLQLNSFPFTFGGGTKVEINGGGGSCPYSNPSLCTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGT CGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	644
	4F11-2-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVT LKESGPVLVKPTETLTLTCTVSGFSLSNARMGVTWIRQPPGKAL EWLAHIFSNDEKSYSTSLKSRLTISKDTSKTQVVLTMTNMDPVD TATYYCARIRDYYDISSYYDYWGQGTLVSVSSGGGGSGGGGSG GGGSGGGGSDIQMTQSPSAMSASVGDRVTITCRASQDISNYLA WFQQKPGKVPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLLP EDFATYYCLQLNSFPFTFGGGTKVEINGGGGSCPYSNPSLCTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	680
	P08F08-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVQ LVQSGAEVKKPGESLKISCKGSGYGFTSYWIGWVRQMPGKGLE WMGIIHPDDSDTKYSPSFQGQVTISADKSISTAYLQWSSLKASDT AMYYCASSYLRGLWGGYFDYWGQGTLVTVSSGGGGSGGGGS GGGGSGGGGSELQSVLTQPPSASGTPGQRVTISCSGSSSNIGSNY VNWYQQLPGTAPKLLIYGDYQRPSGVPDRFSGSKSGTSASLAIS GLRSEDEADYYCATRDDSLSGSVVFGTGTKLTVLGGGGSCPYS NPSLCTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGL DFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQG QNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR	645

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	10A1-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPSETLSLTCTVSGGSISYYYWTWIRQPPGKGLEWI GHIYYSGSTNYNPSLKSRVTISIDTSKNLFSLKLSSVTAADTAVY YCARAEGSlDAFDFWGQGTMVTVSSGGGGSGGGGSGGGGSGG GGSDIQMTQSPSTLSASVGDRVTITCRASQSISTWLAWYQQKPG KAPKVLIYKASSLESGVPSRFSGSGSGTEFILTINSLQPDDFASYY CQQYKSYSHTFGQGTKLEIKGGGGSCPYSNPSLCTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGT CGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	646
	11C1-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPSETLSLNCTVSGGSISYYYWTWIRQPPGKGLEW IGHVIYSGTTNYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAV YYCVRAEGSlDAFDLWGQGTMVTVSSGGGGSGGGGSGGGGSG GGGSDIQMTQSPSILSASVGDRVTITCRASQSVSSWLAWYQQKP GKAPKVLIYKASSLESGVPSRFSGTGSGTEFTLTISSLQSDDFATY YCQQYNTYSHTFGQGTKLEIKGGGGSCPYSNPSLCTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAG TCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	647
	11E1-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPLQTLSLTCTVSGGSISSDGYYWSWIRQNPGKGL EWIGYMYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLRSVTAAD TAVYYCTRDFGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGS GGGGSDIQMTQSPSSLSASVGDSITITCRASQDIDNYLAWYQQK TGKVPKVLIYAASALQSGVPSRFSGSGSGTDFTLTISSLQPEDVA TYYCQNYNSGPRTFGQGTKVEIKGGGGSCPYSNPSLCTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPL AGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	648
	12A2-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVKPSQSLSLTCSVSGGSVSSDGYYWSWIRQHPGKGL EWIGYIYYRRITDYNPSLKSRVNISLDTSKNQFSLKLSSVTAADT AVYYCARDFGWYFDLWGRGTLVAVSSGGGGSGGGGSGGGGS GGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLTWYQQK PGRVPEVLIYAASALQSGVPSRFSGSGSGTDFTLTISSLQPEDVAT YYCQNYNSAPRTFGQGTKVEIKGGGGSCPYSNPSLCTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	649

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	12C5-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVEL VESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQAPGMGLE WVTVIWYDGSNKYYADSVKGRFTISRDNSKNTVFLQMNSLRAE DTAVYYCARDEVGFVGAFDIWGQGTMVTVSSGGGGSGGGGSG GGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGINSHLAWY QQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTLTVTSLQPE DFATYYCQQLNHYPITFGQGTRLDINGGGGSCPYSNPSLCTTTP APRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIW APLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR	650
	12C6-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSEVEL VESGGGMVQPGRSLRLSCAASGFTFSDYGMHWVRQAPGMGLE WVTVIWYDGSNKYYADSVKGRFTISRDNSKNTVFLQMNSLRAE DTAVYYCARDEVGFVGAFDIWGQGTMVTVSSGGGGSGGGGSG GGGSGGGGSDIQLTQSPSFLSASVGDRVIITCRASQGINSHLAWY QQKPGKAPKLLIYYASTLPSGVPSRFSGSGSGTEFTLTVTSLQPE DFATYYCQQLNHYPITFGQGTRLEIKGGGGSCPYSNPSLCTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP PR	681
	8F8-RSR-short	MALPVTALLLPLALLLHAARPGGGGSCPYSNPSLCGGGGSQVQ LQESGPGLVQPSETLSLTCTVSGGSISYYYWSWIRQPPGKGLEWI GNINYMGNTIYNPSLKSRVTISVDTSKDQFSLKLTSVSAADTAV YYCVRAEGSlDAFDFWGQGTLVAVSLGGGGSGGGGSGGGGSG GGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP GKAPKVLIYKASNLESGVPSRFSGSGSGTEFTLTISSLQPDDFAT YYCQQYNSYSCTFGQGTKLEIKGGGGSCPYSNPSLCTTTPAPRP PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLA GTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR	651

[0401] Testing was performed on: NTD control; the RSRQR format (shown above and schematically in FIG. 6C) of a 4F11 CAR; the SR2 format (shown above and schematically in FIG. 6B) of a P08F08 CAR; the R2S format (shown above and schematically in FIG. 6F) of a P08F08 CAR; and the RSR-short format (shown above and schematically in FIG. 6E) of a P08F08 CAR.

[0402] CAR T cells were generated that express each of the CAR formats. These CAR T cells were then thawed and mixed with 786-0 target cells that are known to express CD70 at an effector:target (E:T) ratio of 3:1, 1:1, 1:3, or 1:9 (or 0 control) in RPMI supplemented with

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10% FBS. Percentage lysis of target cells and fold expansion of effector CAR T cells were determined (FIG. 7).

[0403] Percentage lysis of target cells was calculated at each time-point by calculating the percentage of live 786-0 cells for each CAR treatment and then normalizing to no treatment control. Fold expansion of CAR T cells over the number of CAR T cells plated on Day 0 was calculated at each time-point.

[0404] These results demonstrate that CD70-specific CAR-T cells expressing CD20 epitopes can kill target cells effectively at 3:1, 1:1, 1:3, and 1:9 E:T ratios, and ratios therebetween, as well as potentially at ratios outside 3:1 to 1:9 range not test in this experiment.

Part B: Sensitivity to Rituximab *In Vivo*

[0405] Depletion of CD70-specific CAR T cells following rituximab administration allows recovery of CD70-expressing lymphocytes in NSG mice

[0406] The ability of the anti-CD20 antibody rituximab to mediate depletion of CD70-specific CAR T cells expressing CD20 epitopes and facilitate lymphocytes recovery is tested in mice. In this experiment, mice are treated with T cells expressing either a CD70-specific CAR that can bind to mouse CD70 protein on the surface of lymphocytes (α-mouse CD70 CAR Ts) and comprising a CD20 epitope recognized by rituximab or a control CAR, with negligible binding to mouse FLT3 protein. Flow cytometry analysis of lymphocytes is used to demonstrate CAR T cell cytotoxic activity against CD70-expressing lymphocytes, seen as a reduction of lymphocytes compared to mice that received control CAR T cells or to untreated mice. After confirmation of CAR T cell killing activity, mice are given rituximab for four consecutive days and circulating residual CAR T cells are enumerated by flow cytometry at day 13. The CD70-specific CAR T cells in the blood of these mice are depleted compared to the control group, which do not receive rituximab. Finally, flow cytometry analysis of lymphocytes demonstrates that only the mice that received rituximab (day 20) shows lymphocytes recovery.

[0407] This experiment demonstrates that rituximab-dependent depletion of CD70-specific CAR T cells that express CD20 epitopes mitigates damage to CD70-expressing tissues, allowing for rapid lymphocyte recovery.

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Example 10: Activity of CD70-specific CAR T cells

[0408] Target cell killing was assessed using the same assay and similar experimental parameters to those described in Example 9, Part A. The tested cells lines were 786-0, ACHN, and REH (a human acute lymphocytic leukemia cell line). REH cell line shows the best differentiation of CD70-specific CAR T cells and hence will be used to rank scFvs in all future experiements. FIGs. 8A-8D show cell killing of 786-0 (FIG. 8A), ACHN (FIG. 8B), or REH (FIG. 8C) cells using CD70-specific CAR T cells where the CAR extracellular domain comprises the scFvs indicated in the legend (FIG. 8D). The naked CAR format was used for all experiments.

[0409] Table 12 provides the underlying data for FIGs. 8A-8D and additionally the measured percentage positive cells for fluorescently labeled anti-CD70 antibody, CD25 and 4-1BB (activation markers); the stem memory T cell (TSCM) percentage, the BFP percentage (CAR+) before going into the cytotoxicity assay.

Table 12

Clone	%Lysis REH	%Lysis ACHN	%Lysis 786-O	%CD70 D9 (gated on CAR)	%CD25 4-1BB D9 (gated on CAR)	%Tscm D14 (gated on CAR)	%BFP CAR D14
12D6	98.5	75.4	84.6	0.7	15.1	17.2	77.4
8F8	98.1	84.7	94.8	0.0	26.1	28.9	70.5
12H4	97.7	65.8	80.5	0.1	16.9	31.5	83.8
12A2	97.5	76.1	89.3	3.9	6.2	46.5	73.2
12C5	97.5	81.7	91.6	0.0	31.1	24.7	88.2
10A1	97.2	77.0	88.3	0.1	21.5	31.4	73.5
11E1	96.8	84.7	94.5	0.2	34.8	20.4	54.8
12D3	96.0	63.8	75.4	7.5	14.2	35.0	71.0
4F11	96.0	73.4	85.6	4.3	44.0	15.7	36.3
12D7	95.7	84.9	92.7	1.2	48.5	5.4	43.1
11C1	95.6	76.9	90.0	0.5	31.8	30.3	57.9
11A1	73.5	46.0	64.6	2.4	7.0	41.6	82.5
9E10	71.7	77.1	90.0	68.2	21.7	25.2	63.9
8C8	70.7	80.7	90.2	76.6	12.9	26.3	57.6
10E2	59.2	41.5	36.9	52.0	6.4	28.1	34.8
P08F08	45.8	78.0	94.5	30.6	7.8	48.4	43.1
8F7	38.6	39.3	55.4	46.4	3.0	32.3	63.5
12F5	21.7	14.5	16.2	50.9	7.1	29.9	44.7
9E5	13.9	7.0	11.9	13.1	1.3	77.0	63.9
11D1	12.7	-4.4	7.3	32.3	2.0	50.4	58.5
9F8	12.5	8.9	32.6	20.5	1.3	59.4	67.5
9F4	10.4	1.1	8.4	20.8	1.6	63.8	35.7
9D8	5.2	24.6	76.2	29.3	4.6	46.8	70.8

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NTD	3.3	7.6	12.0				

[0410] FIG. 9A shows the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled 786-O target cells (CAR T cells were transferred to a 96-well plate containing fresh targets every 2-3 days). The E:T ratio was 3:1. The CARs were expressed in cells from donor D503. Similar to the results described in Example 4, target cell lysis in the stress test were used for *in vitro* characterization of CAR scFvs.

[0411] FIG. 9B shows the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled ACHN target cells (CAR T cells were transferred to a 96-well plate containing fresh targets every 2-3 days). The E:T ratio was 10:1. The CARs were expressed in cells from donor D503. Similar to the results described in Example 4, target cell lysis in the stress test were used for *in vitro* characterization of CAR scFvs.

[0412] FIG. 9C shows the efficacy of CD70-specific CARs upon repeated exposure to luciferase-labeled REH target cells ($2x10^6$ cells added at indicated time-points). The E:T ratio was 1:5. The CARs were expressed in cells from donor D503. Similar to the results described in Example 4, target cell lysis in the stress test were used for *in vitro* characterization of CAR scFvs.

[0413] FIG. 10 shows the efficacy of CD70-specific CARs in various formats (as mentioned in example 9 Part A) upon repeated exposure to luciferase-labeled REH target cells ($2x10^6$ cells added at indicated time-points). The E:T ratio was 1:5. Similar to the results described in Example 4, target cell lysis in the stress test were used for *in vitro* characterization of CAR scFvs.

Example 11: *In vivo* comparison of CD70 CARs in ACHN metastasis model

[0414] CAR T cells containing different CD70 scFvs were generated and tested in ACHN cells, a renal cell cancer (RCC)-derived cell line. ACHN cells are described in Simmons et al. Animal Models of Bone Metastasis. *Veterinary Pathology* 52:827-841, 834 (2015). NSG mice were each implanted with 1 million ACHN tumor cells intravenously and 15 days post-tumor cell injection, the mice were treated with CAR T cells intravenously via tail vein injection to determine the CAR and condition with most optimal efficacy. 12C5 CAR T cells dosed at 3 million CAR+ cells per mouse showed the best efficacy.

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Materials and methods:

[0415] Forty-five NSG mice were prepared for intravenous tumor injection via tail vein. ACHN tumor cells that are known to express CD70 were expanded in MEM supplemented with 10% FBS. On Day 0, ACHN tumor cells were resuspended in serum-free MEM at the required concentration to inject 1 million cells per animal. ACHN tumor cells were injected in 200uL of serum-free MEM intravenously. Day 4 baseline body weights were recorded for all animals. Tumor flux was measured twice a week starting on Day 7 using bioluminence (IVIS Spectrum Imager™ from PerkinElmer™; auto-exposure with a maximum exposure time of 120 seconds), and body weights were recorded. On Day 20, when the tumors attained 200mm^3 (standard error 9.69), 35 tumor-bearing mice were randomized to 7 groups of 5 mice each. On Day 15, CAR T cells were thawed in MEM supplemented with 10% FBS and resuspended in serum-free MEM at 3 million CAR+ T cells per animal (calculated based on individual transduction efficiencies). Number of NTD cells required to maintain equal percentage of CAR+ T cells as well as equal number of total T cells in each group were calculated and added to respective samples. CAR T cells or NTD control were injected in 200uL of serum-free MEM per animal intravenously via tail vein. Tumor flux was measured and body weights recorded twice a week till Day 32 when the NTD group reached the study end-point (~ 20% body weight loss) (See FIG. 11).

[0416] Bioluminescence (mean and error SEM) were plotted on GraphPad Prism and statistics were calculated using one-way ANOVA with repeated measures. 12C5 CAR T group showed anti-tumor efficacy at the 3 million CAR+ dose.

Example 12: Expression levels of CD70 on patient-derived RCC samples and lysis of patient-derived RCC samples by CD70-specific CAR T cells

[0417] Primary RCC patient samples were obtained from Conversant Bio (frozen dissociated tumor cells) or from CHTN Western/NDRI (fresh tumor fragments which were then dissociated in house using Miltenyi MACS human tumor dissociation kit and GentleMACS). Primary tumor cells were maintained in RPMI supplemented with 20% FBS. To determine cell surface expression of CD70 protein in these cells along with relevant RCC cell lines, we performed flow cytometry and receptor quantification using anti-CD70 antibody conjugated to Phycoerythrin at a 1:1 ratio. Cell surface receptors were calculated using Quantibrite beads from BD Biosciences and antibody binding capacity (ABC) values were calculated as per manufacturer's recommendation. CD70-specific CAR T cells were generated as previously

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described and their cytotoxicity against primary RCC cells and ACHN RCC cell line was assessed using the same assay and similar experimental parameters to those described in Example 9, Part A.

Results

[0418] It was confirmed that primary RCC cells express CD70 across ABC values ranging from ~2,000 CD70 receptors per cell (receptors/cell) to ~25,000 receptors/cell (FIG. 12B) with expression on RCC cell lines ranging from ~25,000 receptors/cell to ~400,000 receptors/cell (FIG. 12A). We also confirmed that cells expressing 7,000 CD70 receptors per cell (receptors/cell) (FIG. 13B), 24,000 receptors/cell (FIG. 13A), or 40,000 receptors/cell (FIG. 13C) are effectively killed by CD70-specific CAR T cells, where the CAR is generated from either the 4F11 or P08F08 scFv.

Example 13: Expression levels of CD70 on various hematological tumor cell lines and lysis of these cells by CD70-specific CAR T cells

[0419] The potential to target CD70 across a range of heme tumors including lymphomas, leukemias, and myeloma was characterized. Characterization included expression analysis of both CD70 RNA and cell surface protein in multiple malignancies, followed by efficacy of CAR T cells against cell lines.

Results

[0420] Analysis of RNA expression across acute myeloid leukemia (AML), acute lymphoblastic leukemia (ALL), non-Hodkins lymphoma (NHL), and multiple myeloma (MM cell) lines using The Cancer Genome Atlas (TCGA) shows that CD70 expression can be observed across all 4 cancer types indicating the potential utility of targeting these cancers with CD70 CAR T cells. To determine cell surface expression of CD70 protein in these cancers, we performed flow cytometry and receptor quantification on a panel of cell lines originating from the selected tumor types. Cell surface protein expression patterns were similar to RNA analyses confirming that CD70 expression was broadly observed in cell lines from all tumor types (FIG. 14A). Next we generated CD70-specific CAR T cells to test their efficacy in an *in vitro* cytotoxicity assay against the same cell lines. CD70 CAR T cells exhibited robust specific activity against target cells expressing the CD70 antigen (FIG. 14B). Various cell lines can be killed by a CD70-specific CAR (FIG. 14B), indicating that CD70-specific CARs can kill even cells that expression CD70 at a low level. This demonstrates that the activity of

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the CD70-specific CARs is not restricted to particular cell types. Finally, we showed that these CARs are effective against the MM1S cell line in the *in vivo* assay performed as in Example 7 (FIGs. 15A and 15B). MM1S is a multiple-myeloma cell line expressing a moderate number of CD70 receptors per cell (FIG. 14A). In conclusion, it was observed that CD70 has a broad expression profile across a range of hematological malignancies. Using CD70 CAR T cells either alone or in combination with the other heme targets offers opportunity to target or prevent tumor antigen escape in a wide range of hematologic malignancies.

Example 14: Determination of kinetics and affinity of human CD70/CD70 antibodies interactions at 37°C

[0421] This example determines the binding kinetics and/or affinity of various anti-CD70 antibodies toward human CD70. ScFvs were generated by cloning the variable regions of the anti-CD70 antibodies flanking a $(GGGGS)_4$ linker (SEQ ID NO: 602) then part of the hinge and Fc from a modified human IgG2 sequence resulting in a scFv-Fc fusion which was expressed using Expi293 then purified by Protein A affinity chromatography. Recombinant human CD70 was generated by fusing an AviTag™, a polyhistidine tag and a trimerization domain from chicken tenascin to the N-terminus of the human CD70 extracellular domain (ECD) which was expressed using Expi293 then purified by immobilized metal affinity chromatography (IMAC) followed by size exclusion chromatography (SEC) as needed.

[0422] The antibody binding kinetics were determined by surface plasmon resonance (Biacore 8K, GE Healthcare Bio-Sciences, Pittsburg PA) at 37°C in HBS-T+ (0.01 M HEPES pH 7.4, 0.15 M NaCl, 0.05% v/v Tween20, 1 mg/mL BSA). Recombinant human CD70 diluted in HBS-T+ was captured on a C1 chip immobilized with an anti-AviTag™ antibody. Purified anti-CD70 scFv-Fc fusions were serially diluted into HBS-T+, injected at 30 uL/min for 2-4 min, dissociation monitored for 10 min then the surface regenerated with 75 mM phosphoric acid between injections. Buffer cycles were collected for each anti-CD70 scFv-Fc fusion for double-referencing purposes (double-referencing as described in Myszka, D.G. Improving biosensor analysis. *J. Mol. Recognit.* **12**, 279-284 (1999)). Kinetic association rates (k_{on}) and dissociation rates (k_{off}) were obtained simultaneously by fitting the double-referenced sensorgrams globally to a 1:1 Langmuir with mass transport model using Biacore 8K Evaluation Software (GE Healthcare Bio-Sciences, Pittsburg PA) then used to calculate an

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equilibrium dissociation constant (K_D) from the kinetic rate constants ($K_D = k_{off}/k_{on}$). The data was fit to a 1:1 steady state affinity model using Biacore 8K Evaluation Software to determine a steady state equilibrium dissociation constant (SS K_D) as needed.

[0423] The binding kinetics and affinity parameters for the tested anti-CD70 antibodies are shown in Table 13. The antibodies shown in Table 13 share the same scFv sequence as the CARs shown in Tables 5 and 11 having the same name.

Table 13

	scFv format				
	k_a (1/Ms)	k_d (1/s)	$t_{1/2}$ (min)	K_D (nM)	SS KD (nM)
10A1	5.77E+05	7.73E-04	14.9	1.3	
10H10	4.62E+04	3.20E-03	3.6	69.3	
11C1	2.24E+05	1.86E-04	62.2	0.8	
11E1	5.78E+05	1.00E-03	11.6	1.7	
12A2	-	-	-	Ambiguous	
12C4	1.56E+06	4.55E-04	25.3	0.3	
12D6	7.12E+04	1.94E-03	5.9	27.3	
12D7	4.41E+05	7.55E-04	15.3	1.7	
17G6	-	-	-	Weak binding	
4F11	8.25E+05	1.60E-03	7.2	1.9	
8C8	1.03E+05	1.59E-03	7.3	15.4	
8F8	3.48E+05	7.93E-04	14.6	2.3	
9E10	8.25E+05	2.12E-03	5.4	2.6	
P02B10	-	-	-		355
P07D03	-	-	-		1070
P08A02	-	-	-		1200
P08E02	8.23E+05	4.38E-03	2.6	5.3	
P08F08	1.44E+06	1.53E-02	0.8	10.7	
P08G02	2.39E+04	7.88E-03	1.5	330	
P12B09	3.30E+05	1.35E-03	8.6	4.1	
P12F02	2.75E+05	1.55E-03	7.4	5.7	
P12G07	-	-	-	Weak binding	
P13F04	9.77E+04	2.00E-02	0.6	205	
P15D02	2.86E+05	<8.05E-	>136	<0.3	
P16C05	-	-	-	Weak binding	

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[0424] Although the disclosed teachings have been described with reference to various applications, methods, kits, and compositions, it will be appreciated that various changes and modifications can be made without departing from the teachings herein and the claimed invention below. The foregoing examples are provided to better illustrate the disclosed teachings and are not intended to limit the scope of the teachings presented herein. While the present teachings have been described in terms of these exemplary embodiments, the skilled artisan will readily understand that numerous variations and modifications of these exemplary embodiments are possible without undue experimentation. All such variations and modifications are within the scope of the current teachings.

[0425] All references cited herein, including patents, patent applications, papers, text books, and the like, and the references cited therein, to the extent that they are not already, are hereby incorporated by reference in their entirety. In the event that one or more of the incorporated literature and similar materials differs from or contradicts this application, including but not limited to defined terms, term usage, described techniques, or the like, this application controls.

[0426] The foregoing description and Examples detail certain specific embodiments of the disclosure and describes the best mode contemplated by the inventors. It will be appreciated, however, that no matter how detailed the foregoing may appear in text, the invention may be practiced in many ways and the invention should be construed in accordance with the appended claims and any equivalents thereof.

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The claims defining the invention are as follows:

1. A method for treating a CD70-mediated condition in a subject, the method comprising:

(i) administering to the subject engineered immune cells expressing at their cell surface CD70-specific CARs and

(ii) subsequently depleting the engineered immune cells from the subject by administering one or more monoclonal antibodies specific for the epitope to the subject wherein:

the CAR comprises an extracellular ligand-binding domain, a first transmembrane domain, and an intracellular signaling domain, wherein the extracellular ligand-binding domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70, and

the CAR further comprises one or more epitopes specific for one or more monoclonal antibodies;

or the method comprising:

(iii) in a subject to whom have been administered engineered immune cells expressing at cell surface CD70-specific CARs, depleting the engineered immune cells from the subject by administering one or more monoclonal antibodies specific for the epitope to the subject; wherein:

the CAR comprises an extracellular ligand-binding domain, a first transmembrane domain, and an intracellular signaling domain, wherein the extracellular ligand-binding domain comprises a single chain Fv fragment (scFv) binding to the extracellular domain of CD70, and

the CAR further comprises one or more epitopes specific for one or more monoclonal antibodies;

and further wherein the scFv comprises:

(a) a heavy chain variable (VH) region comprising three CDRs from the VH region shown in SEQ ID NO: 18 and a light chain variable (VL) region comprising three CDRs from the VL region shown in SEQ ID NO: 17; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, a combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

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(b) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 371; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 370; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(c) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 339; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 338; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(d) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 343; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 342; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(e) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 345; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 344; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(f) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 349; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 348; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(g) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 351; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 350; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(h) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 355; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 354; wherein each CDR is defined in accordance with the Kabat definition, the

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Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(i) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 357; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 356; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(j) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 359; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 358; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(k) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 361; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 360; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR; or

(l) a VH region comprising three CDRs from the VH region shown in SEQ ID NO: 365; and a VL region comprising three CDRs from the VL region shown in SEQ ID NO: 364; wherein each CDR is defined in accordance with the Kabat definition, the Chothia definition, the combination of the Kabat definition and the Chothia definition, the AbM definition, or the contact definition of CDR.

2. The method of claim 1, wherein the extracellular binding domain of the CAR comprises a mAb-specific epitope comprising the amino acid sequence of one or more of SEQ ID NO: 294 or 601-610.
3. The method of claim 2, wherein the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 609.
4. The method of claim 1, wherein the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 295.
5. The method of claim 4, wherein the one or more antibodies is QBEND-10.
6. The method of claim 2, wherein the extracellular binding domain of the CAR comprises a mAb-specific epitope of SEQ ID NO: 294.
7. The method of claim 6, wherein the one or more antibodies is rituximab.

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8. The method of claim 1, wherein the CAR comprises an epitope specific for a monoclonal antibody selected from alemtuzumab, ibritumomab tiuxetan, muromonab-CD3, tositumomab, abciximab, basiliximab, brentuximab vedotin, cetuximab, infliximab, rituximab, bevacizumab, certolizumab pegol, daclizumab, eculizumab, efalizumab, gemtuzumab, natalizumab, omalizumab, palivizumab, ranibizumab, tocilizumab, trastuzumab, vedolizumab, adalimumab, belimumab, canakinumab, denosumab, golimumab, ipilimumab, ofatumumab, panitumumab, QBEND-10 and ustekinumab.
9. The method of claim 8, wherein the CAR comprises an epitope specific for rituximab.
10. The method of claim 8, wherein the CAR comprises an epitope specific for QBEND-10.
11. The method of any claim 1, wherein the CAR comprises an epitope specific for the amino acid sequence of SEQ ID NO: 293.
12. The method of any one of the preceding claims, wherein the epitope is located between the scFv and the hinge of the CAR.
13. The method claim 12, wherein the epitope comprises the amino acid sequence of SEQ ID NO: 294, SEQ ID NO: 609 or SEQ ID NO: 295 and the epitope is located between the light chain variable region and the hinge.
14. The method of any one of the preceding claims, wherein the CAR comprises two copies of the same epitope, separated by one or more linkers.
15. The method of claim 14, wherein the one or more linkers each comprise one or more copies of the amino acid sequence of SEQ ID NOs: 614, 615 or 616.
16. The method of any one of the preceding claims, wherein the epitope-specific antibody is conjugated with a cytotoxic drug.
17. The method of any one of the preceding claims, wherein the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 97, 98, or 99; a VH CDR2 comprising the amino acid sequence shown in SEQ ID NO: 100 or 101; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 102; and the VL region comprises a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 217; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 218; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 219.
18. The method of claim 17, wherein the VH region comprises the amino acid sequence shown in SEQ ID NO: 18 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 17.
19. The method of any one of claims 1-16, wherein the VH region comprises a VH CDR1 comprising the amino acid sequence shown in SEQ ID NO: 478, 479 or 480; a VH CDR2

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comprising the amino acid sequence shown in SEQ ID NO: 481 or 482; and a VH CDR3 comprising the amino acid sequence shown in SEQ ID NO: 483; and a light chain variable region (VL) comprising the following CDRs: a VL CDR1 comprising the amino acid sequence shown in SEQ ID NO: 562; a VL CDR2 comprising the amino acid sequence shown in SEQ ID NO: 563; and a VL CDR3 comprising the amino acid sequence shown in SEQ ID NO: 564.

20. The method of claim 19, wherein the VH region comprises the amino acid sequence shown in SEQ ID NO: 371 and the VL region comprises the amino acid sequence shown in SEQ ID NO: 370.
21. The method of any one of the preceding claims, wherein the intracellular signaling domain comprises a CD3ζ signalling domain.
22. The method of any one of the preceding claims, wherein the intracellular signaling domain comprises a 4-1BB domain.
23. The method of any one of the preceding claims, wherein the stalk domain is selected from the group consisting of: a human CD8α hinge, an IgG1 hinge, and an FcγRIIIα hinge.

FIG. 1

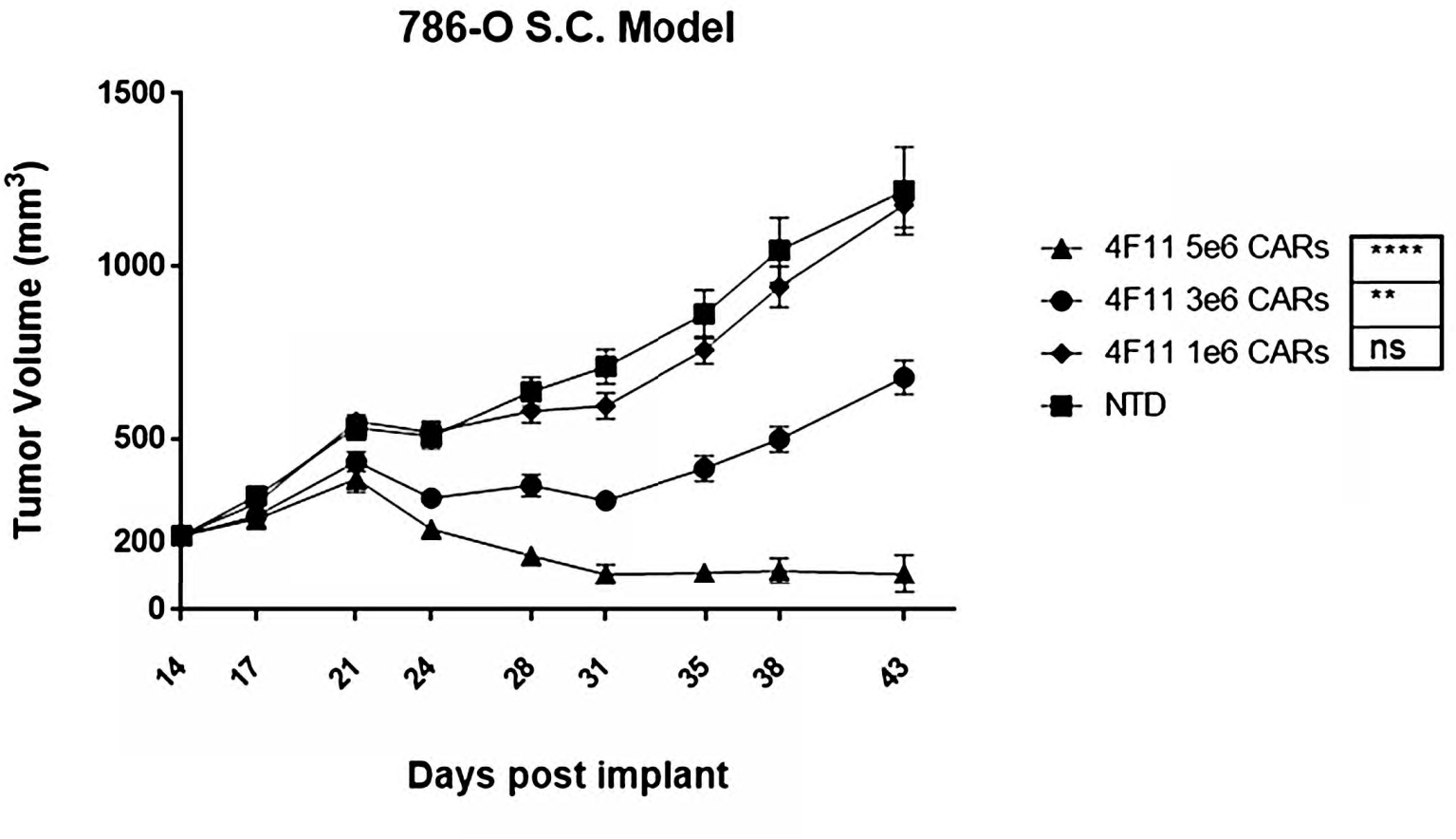
786-O S.C. Model
Tumor Volume (mm3)
1500
1000
500
200
0
14
17
21
24
28
31
35
38
43
Days post implant
4F11 5e6 CARs
4F11 3e6 CARs
4F11 1e6 CARs
NTD
****
**
ns

FIG. 2

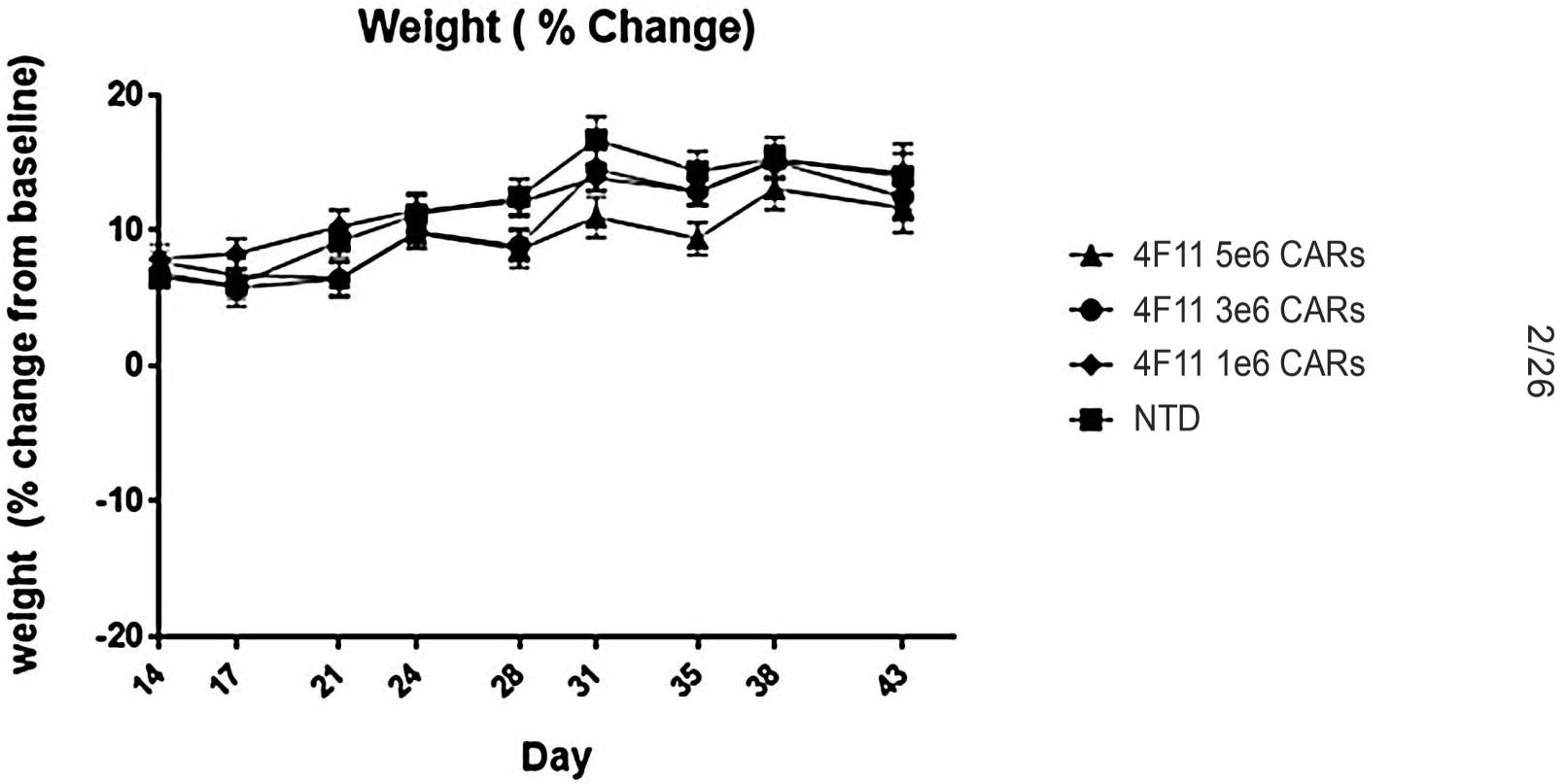
Weight (% Change)
welght (% change from baseline)
20
10
0
-10
-20
14
17
21
24
28
31
35
38
43
Day
4F11 5e6 CARs
4F11 3e6 CARs
4F11 1e6 CARs
NTD

FIG. 3

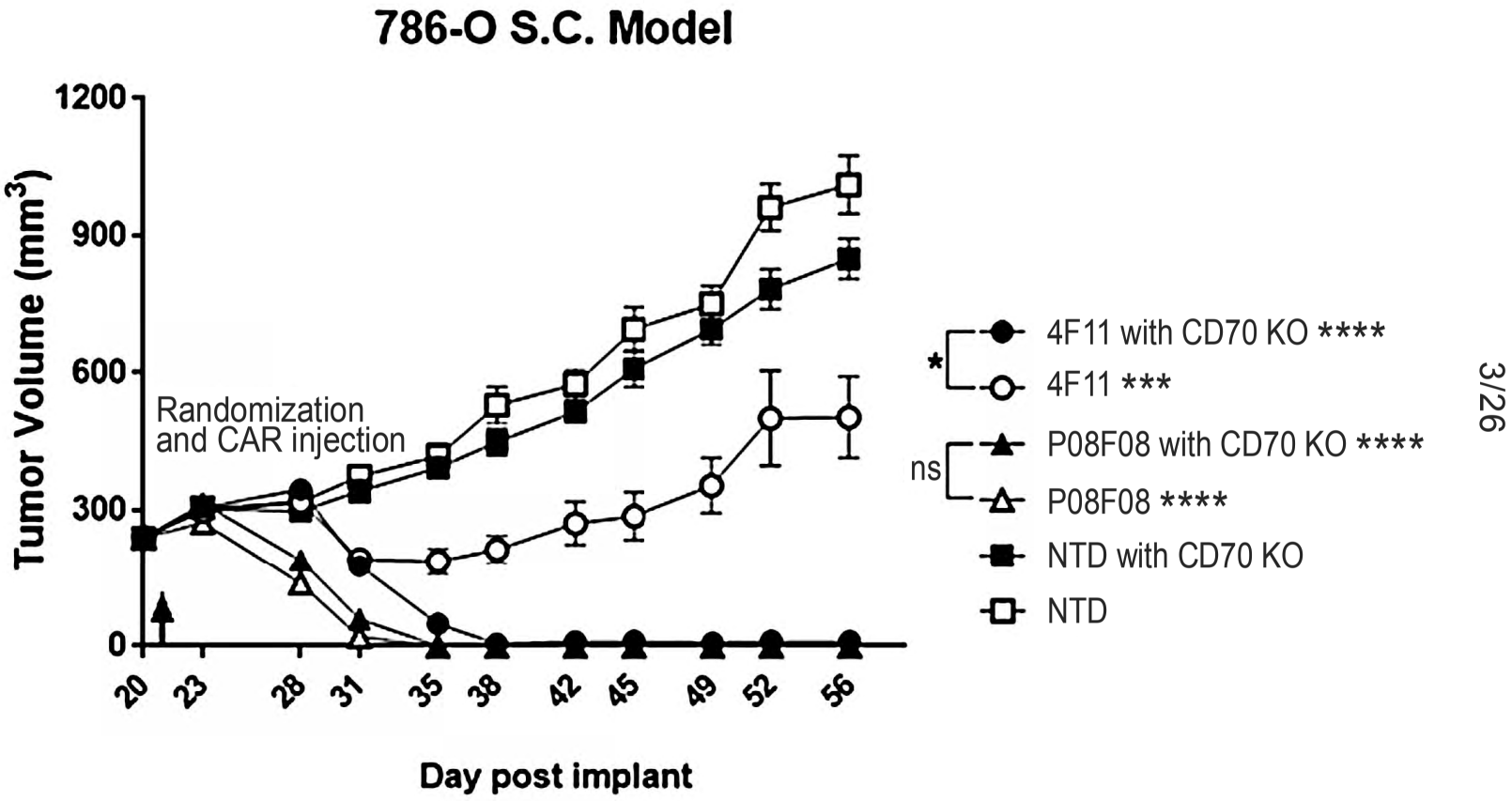
786-O S.C. Model
Tumor Volume (mm3)
1200
900
600
300
0
Randomization
and CAR injection
20
23
28
31
35
38
42
45
49
52
56
Day post implant
*
ns
4F11 with CD70 KO ****
4F11 ***
P08F08 with CD70 KO ****
P08F08 ****
NTD with CD70 KO
NTD

FIG. 4

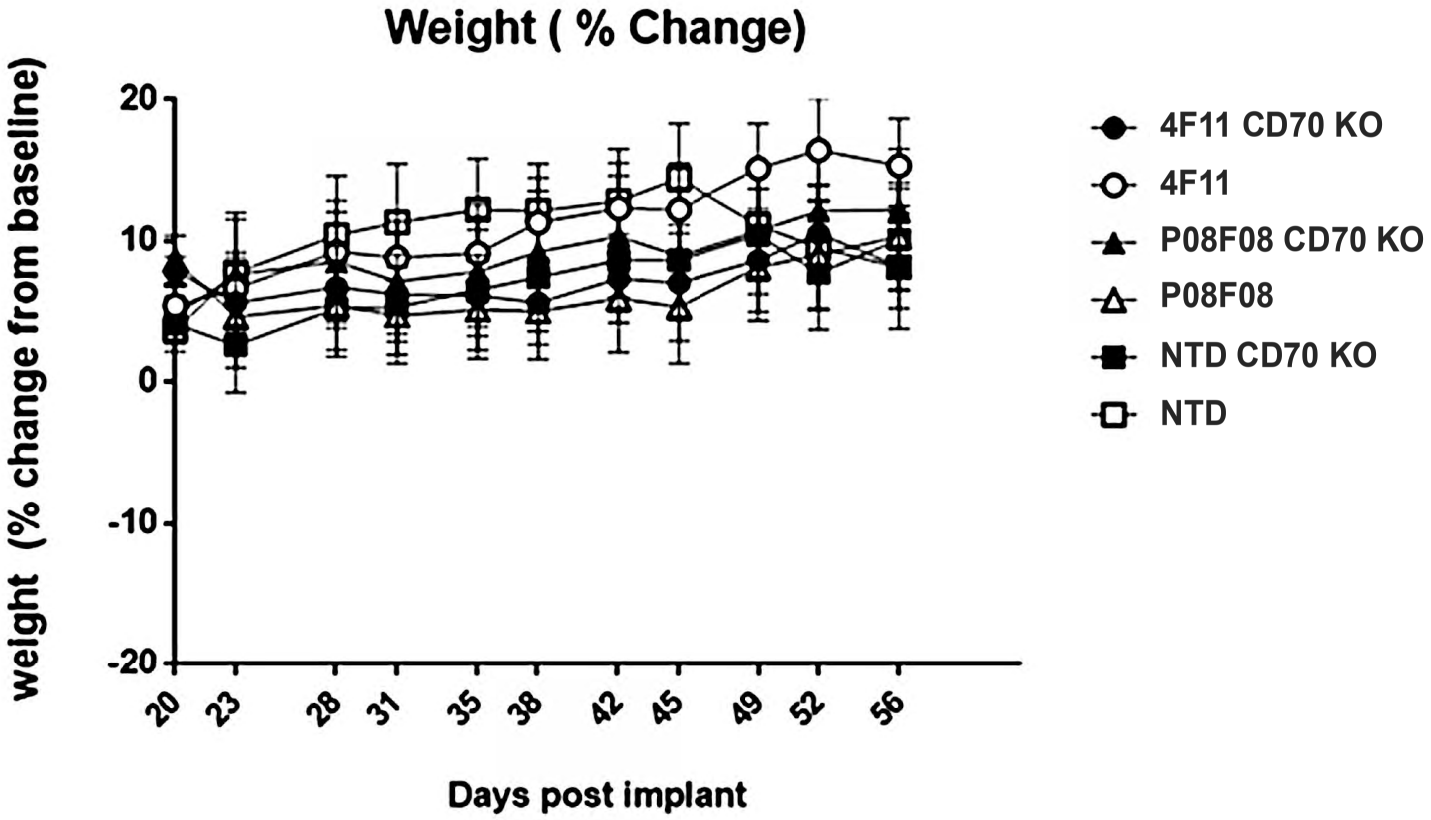
Weight (% Change)
weight (% change from baseline)
20
10
0
-10
-20
20
23
28
31
35
38
42
45
49
52
56
Days post implant
4F11 CD70 KO
4F11
P08F08 CD70 KO
P08F08
NTD CD70 KO
NTD

FIG. 5A

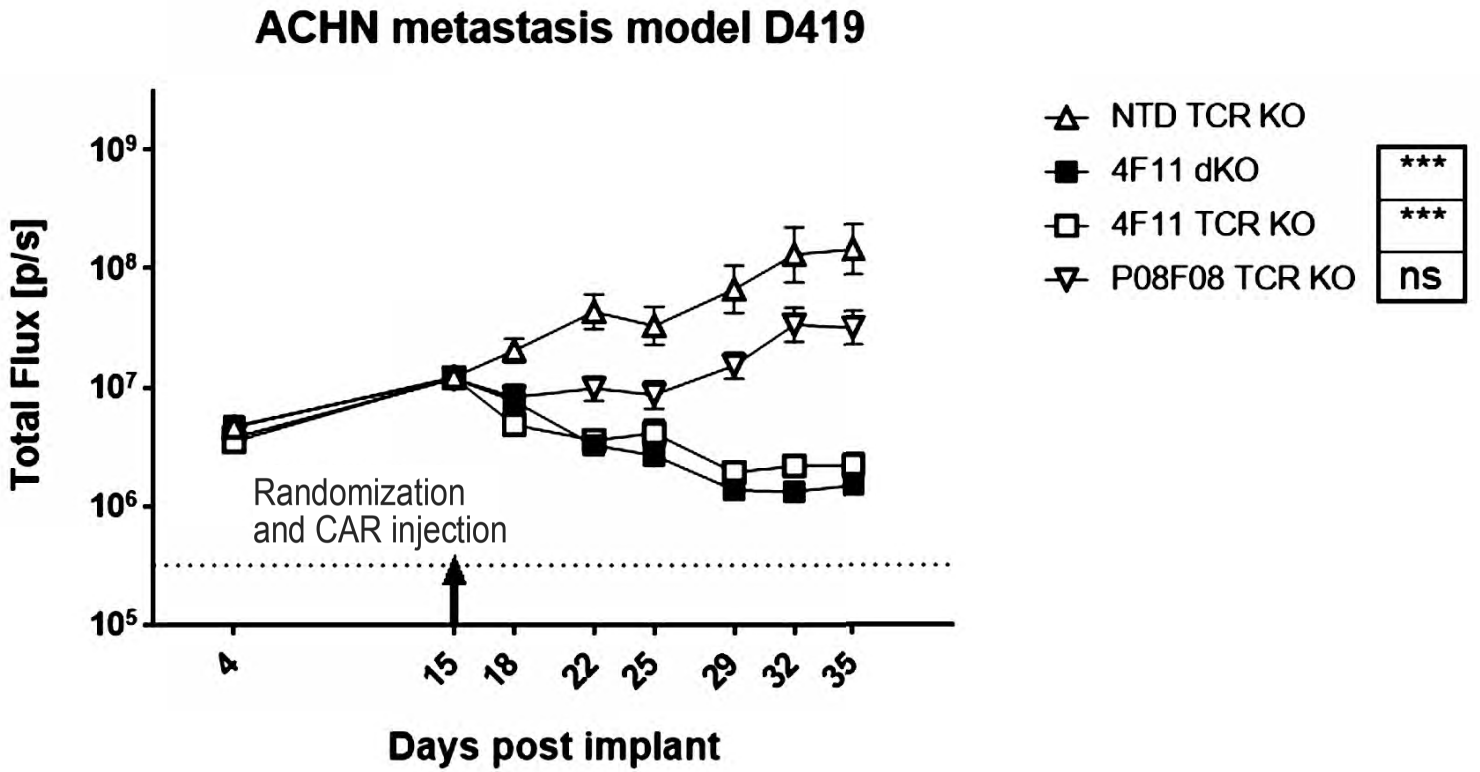
ACHN metastasis model D419
Total Flux [p/s]
10^9
10^8
10^7
10^6
10^5
Randomization
and CAR injection
4
15
18
22
25
29
32
35
Days post implant
NTD TCR KO
4F11 dKO
4F11 TCR KO
P08F08 TCR KO
***
***
ns

FIG. 5B

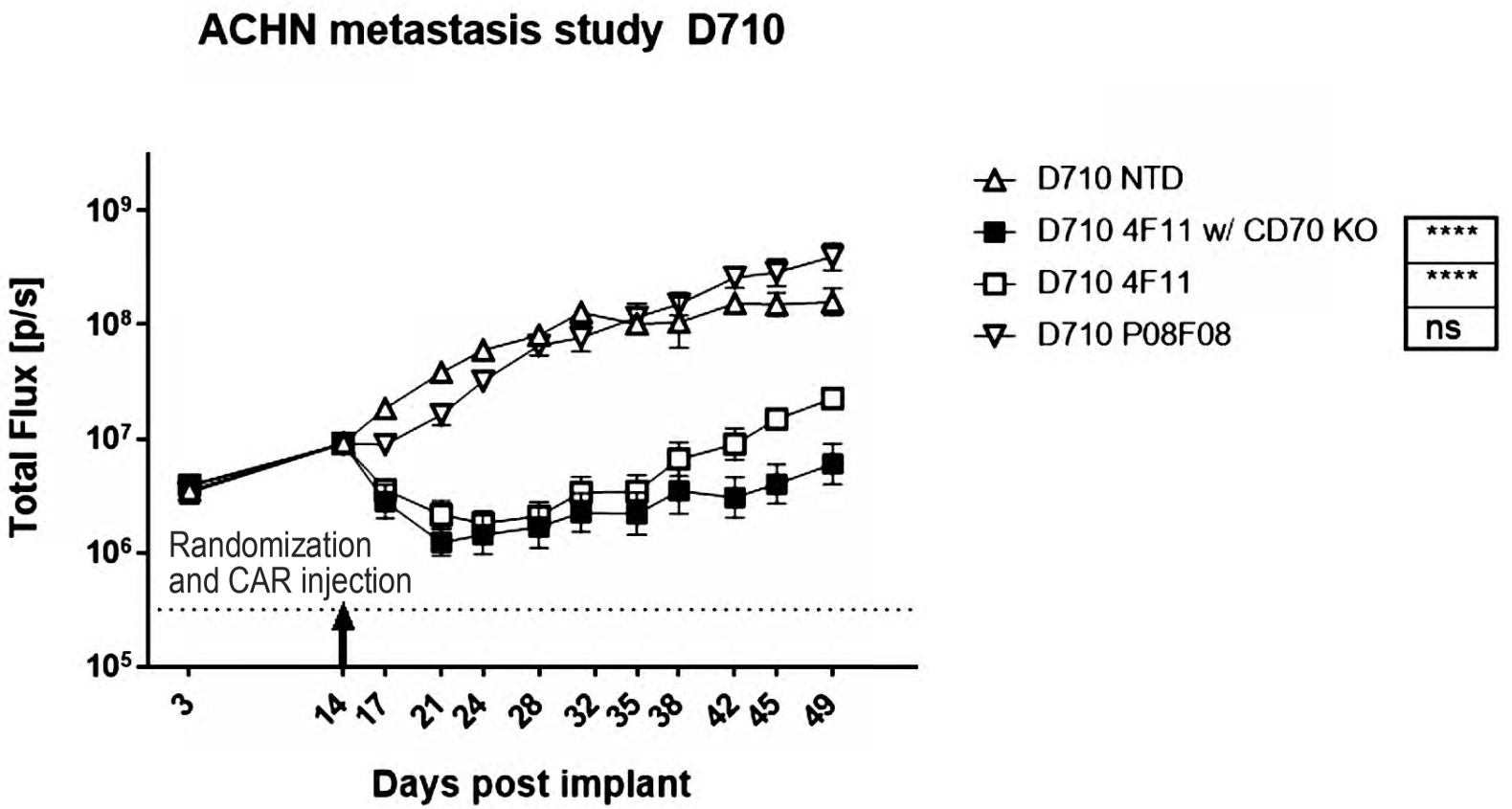
ACHN metastasis study D710
Total Flux [p/s]
10^9
10^8
10^7
10^6
10^5
Randomization
and CAR injection
3
14
17
21
24
28
32
35
38
42
45
49
Days post implant
D710 NTD
D710 4F11 w/ CD70 KO
D710 4F11
D710 P08F08
****
****
ns

FIG. 5C

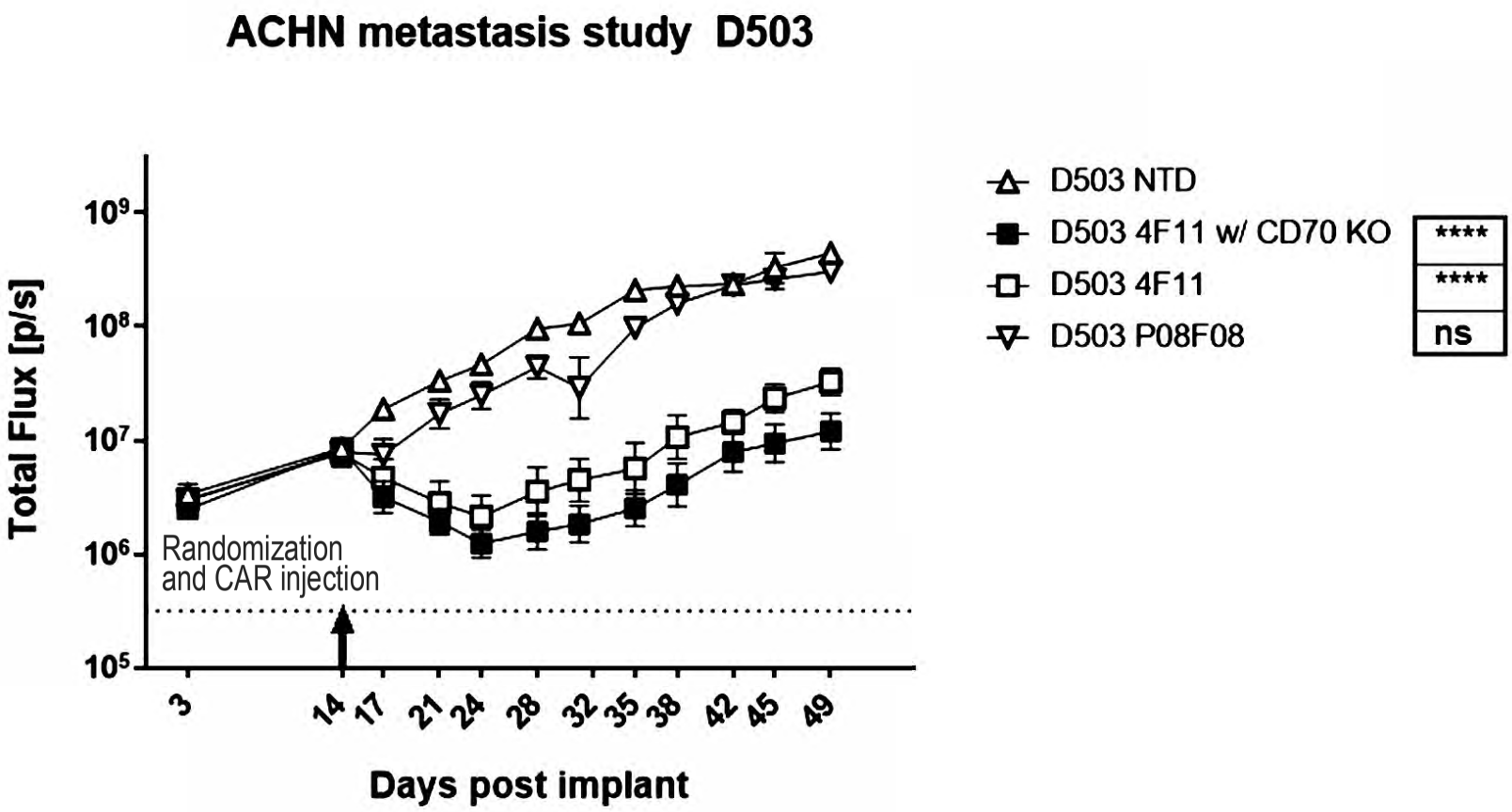
ACHN metastasis study D503
Total Flux [p/s]
10^9
10^8
10^7
10^6
10^5
Randomization
and CAR injection
3
14
17
21
24
28
32
35
38
42
45
49
Days post implant
D503 NTD
D503 4F11 w/ CD70 KO
D503 4F11
D503 P08F08
****
****
ns

FIG. 6A

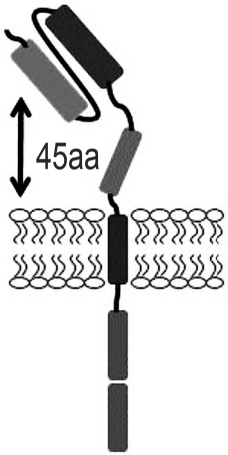

FIG. 6B

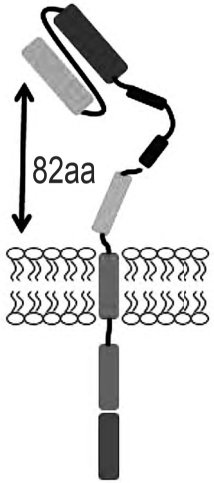

FIG. 6C

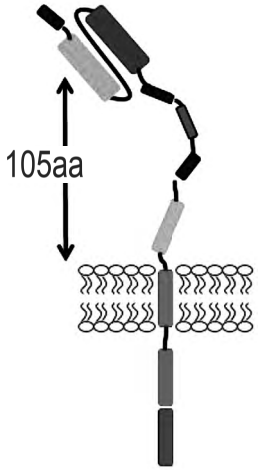

FIG. 6D

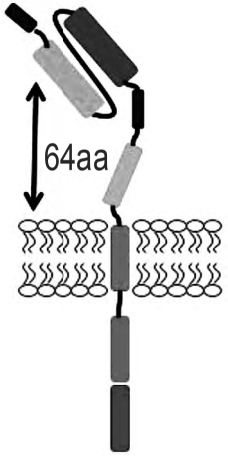

FIG. 6E

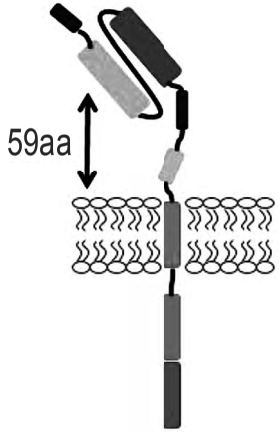

FIG. 6F

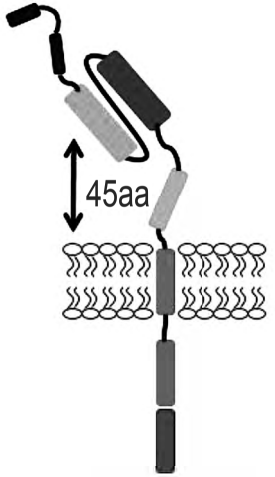

FIG. 7

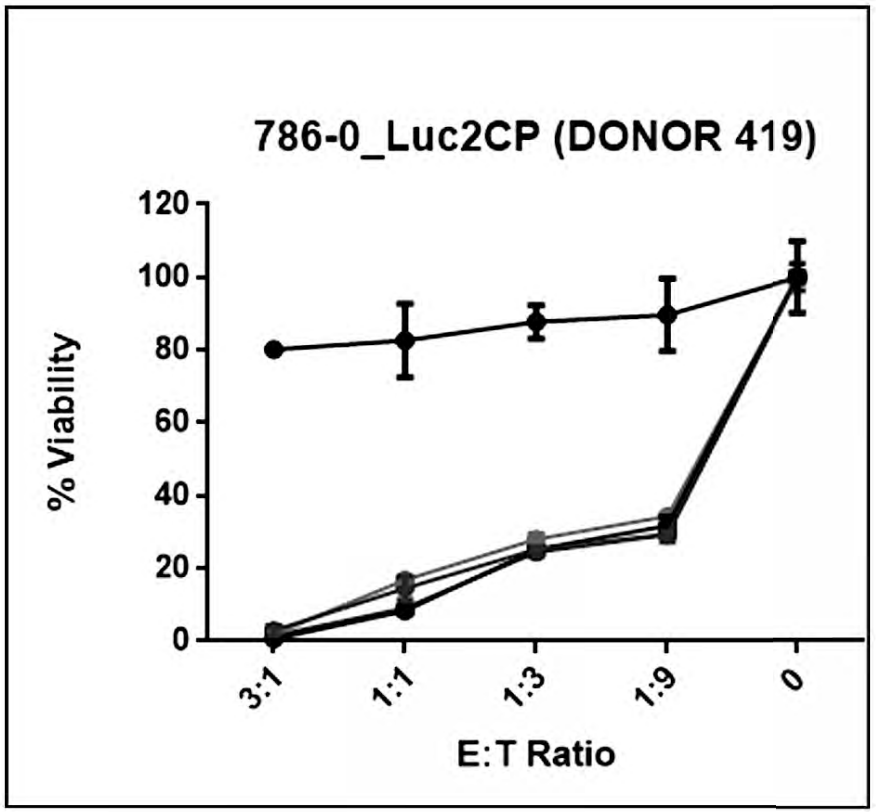
786-0_Luc2CP (DONOR 419)
% Viability
120
100
80
60
40
20
0
3:1
1:1
1:3
1:9
0
E:T Ratio
NTD
4F11 RSRQR
P08F08 SR2
P08F08 R2S
P08F08 RSR-short

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FIG. 8A

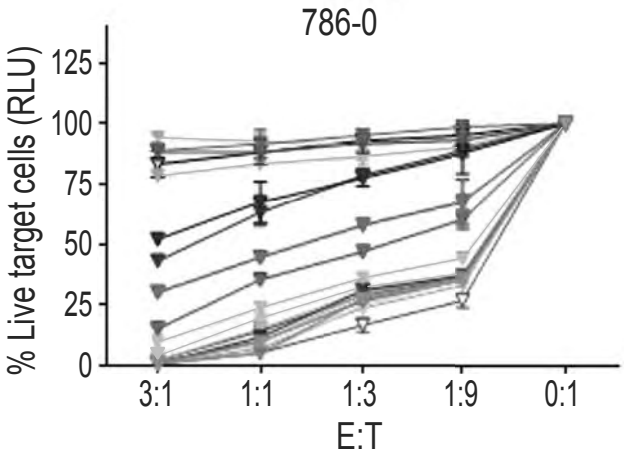

FIG. 8B

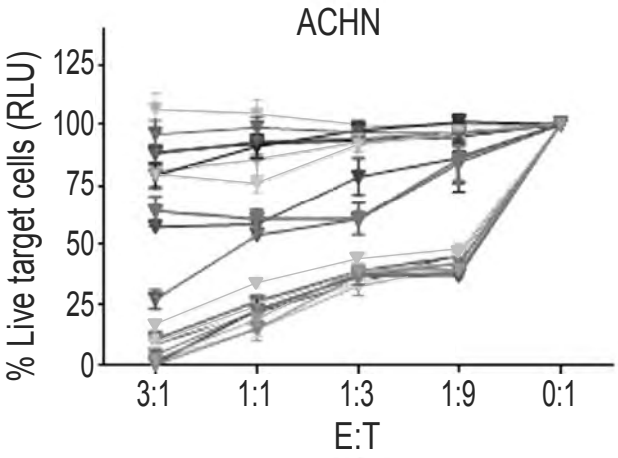

FIG. 8C

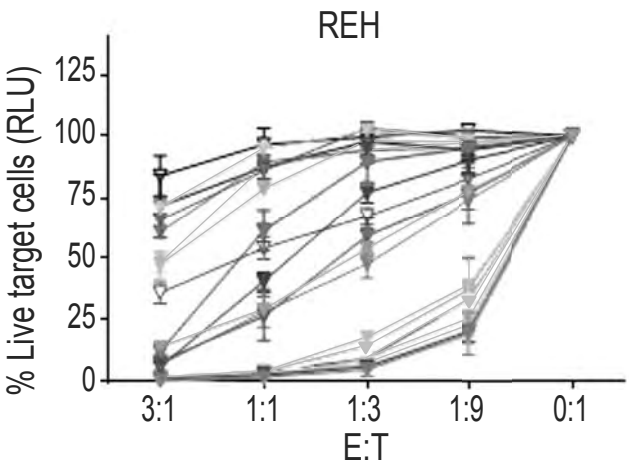

FIG. 8D



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FIG. 9A

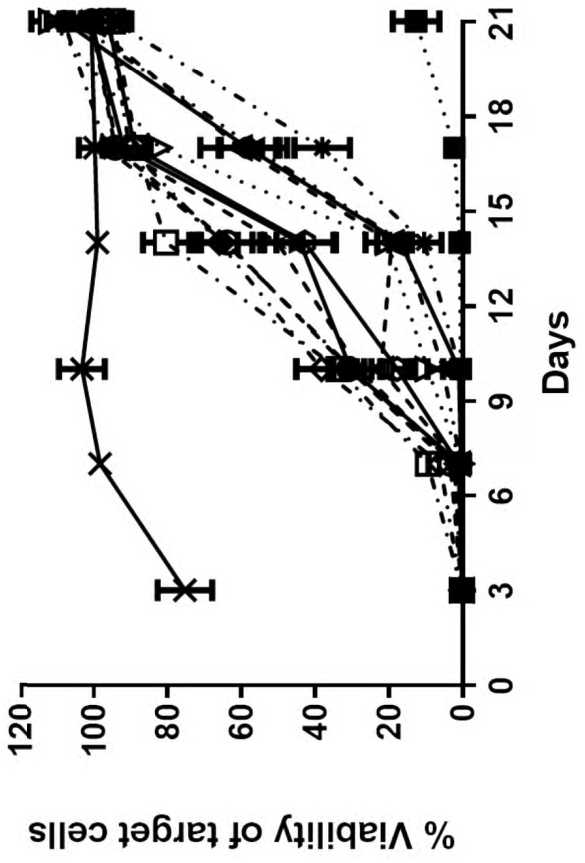


FIG. 9B

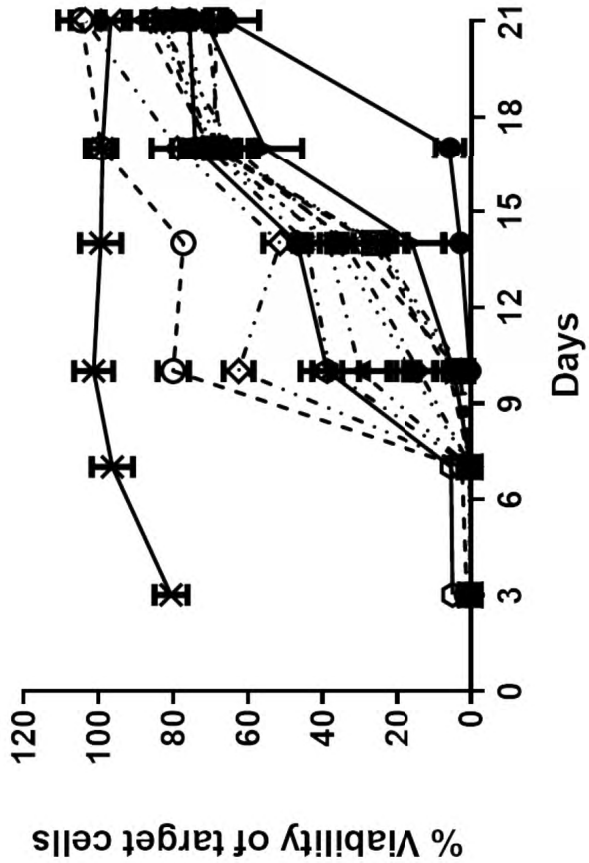


FIG. 9C

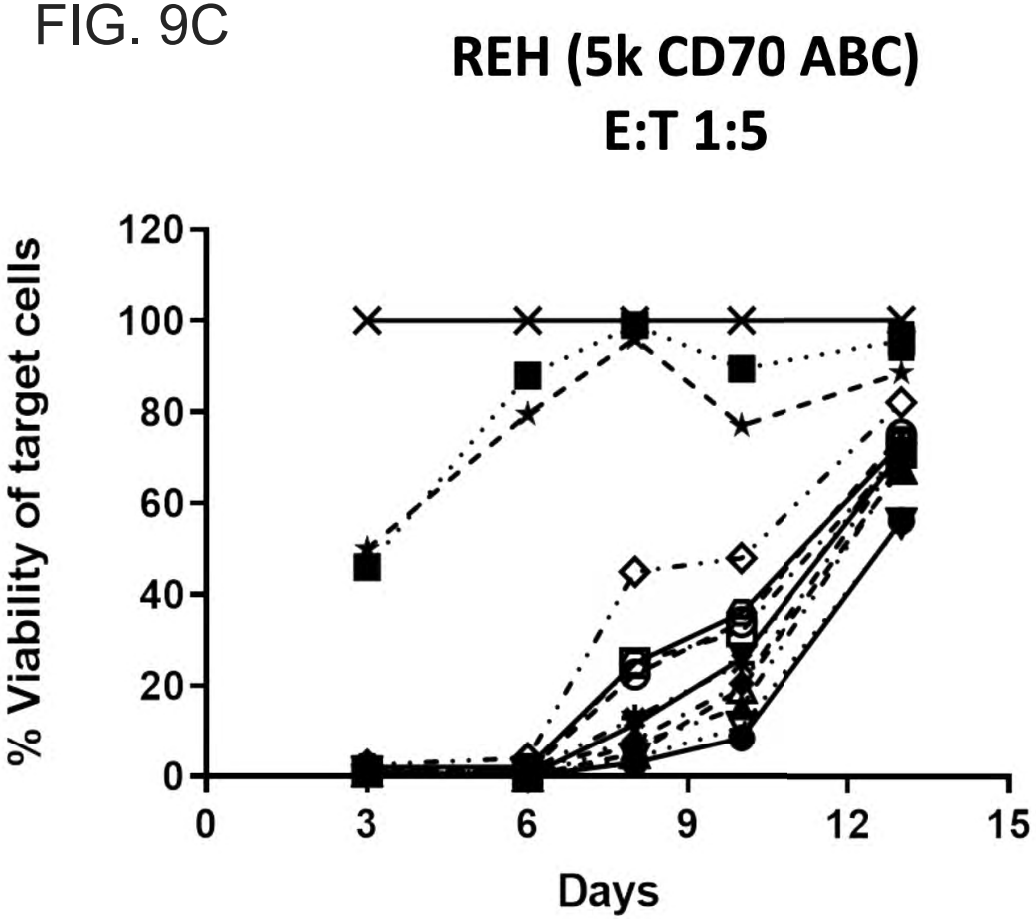
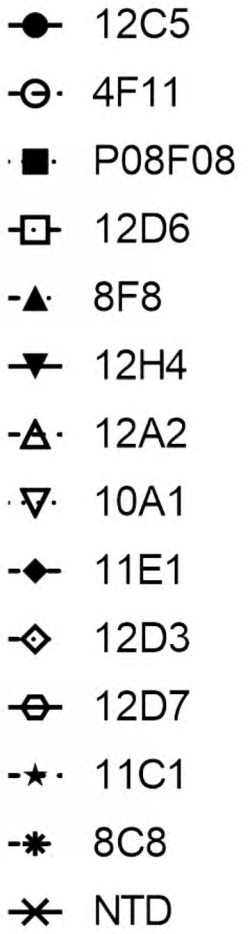

REH (5k CD70 ABC)
E:T 1:5
% Viability of target cells
120
100
80
60
40
20
0
0
3
6
9
12
15
Days

FIG. 9D


12C5
4F11
P08F08
12D6
8F8
12H4
12A2
10A1
11E1
12D3
12D7
11C1
8C8
NTD

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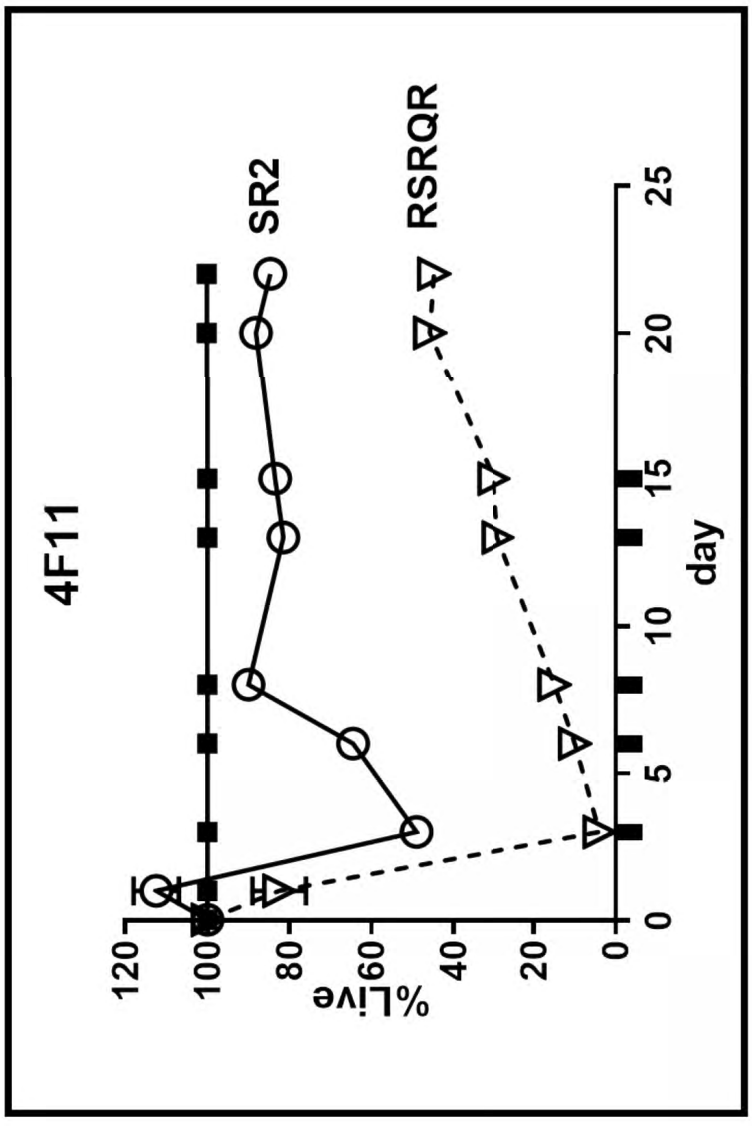

FIG. 10

FIG. 10 (contd.)

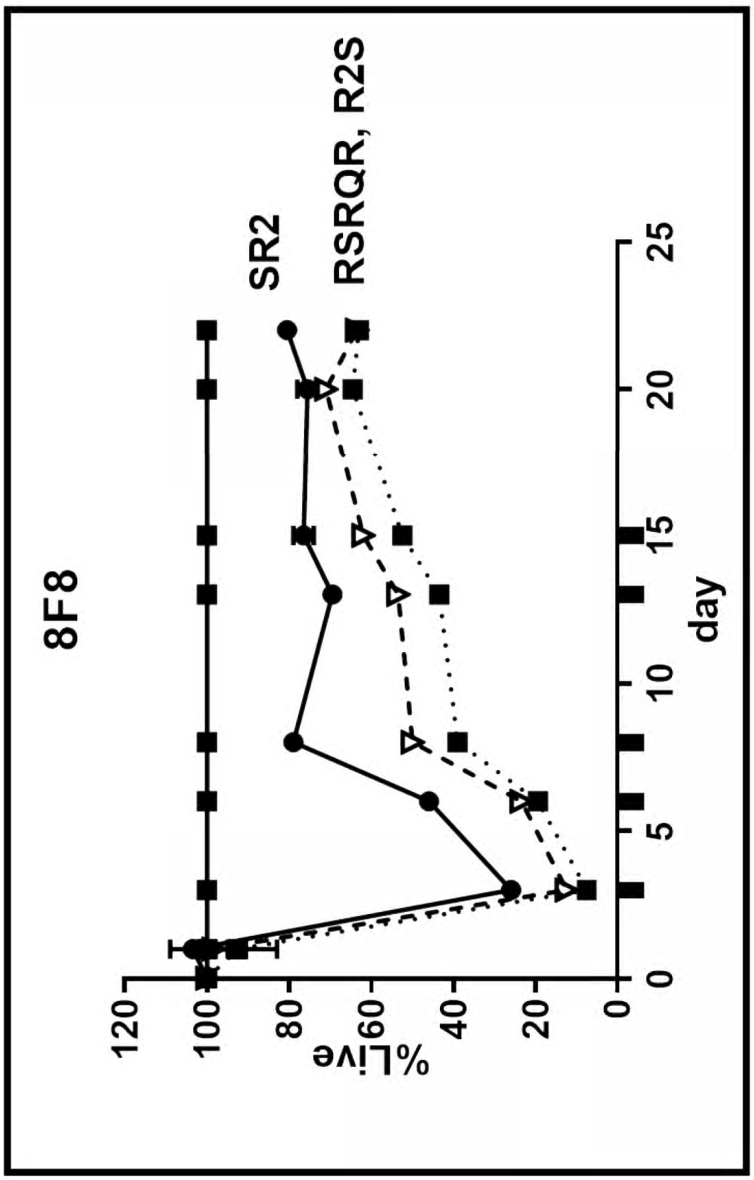

FIG. 10 (contd.)

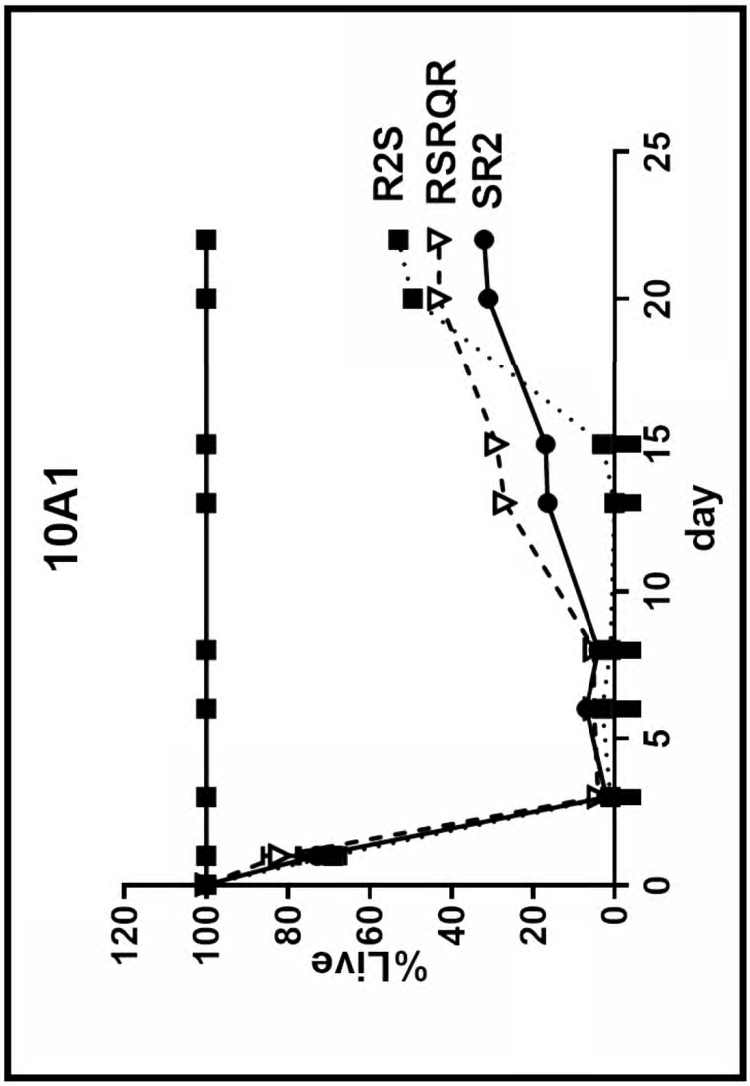

FIG. 10 (contd.)

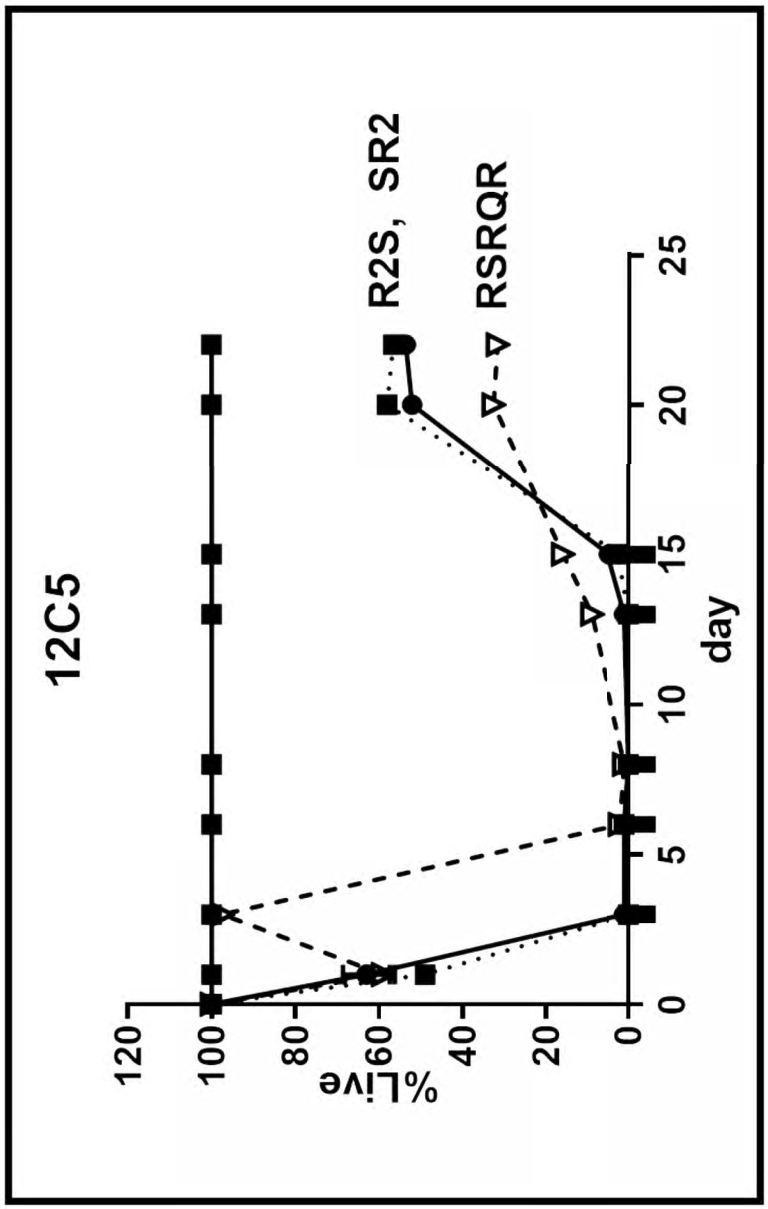

FIG. 11

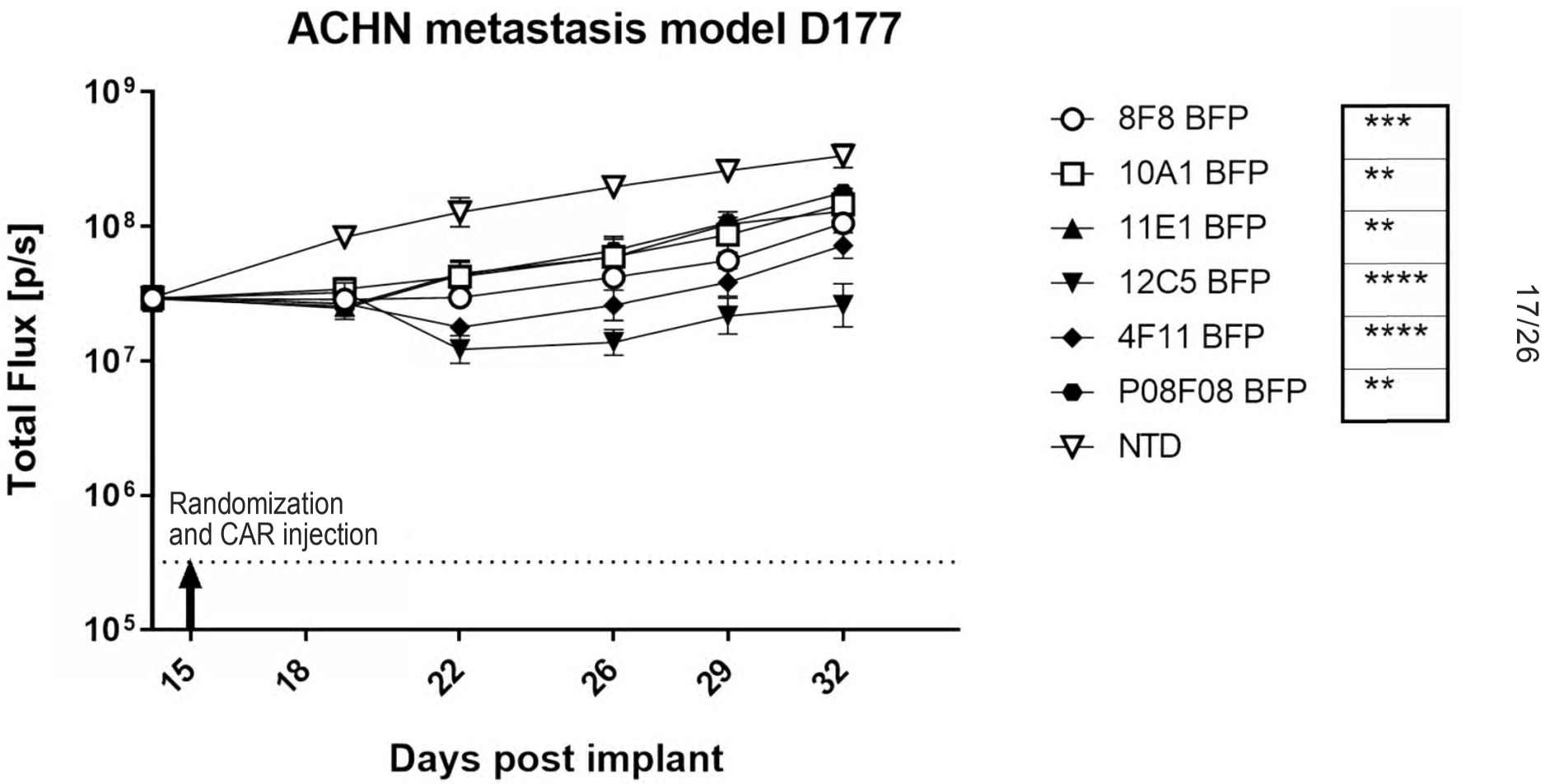
ACHN metastasis model D177
Total Flux [p/s]
10^9
10^8
10^7
10^6
10^5
Randomization
and CAR injection
15
18
22
26
29
32
Days post implant
8F8 BFP
10A1 BFP
11E1 BFP
12C5 BFP
4F11 BFP
P08F08 BFP
NTD
***
**
**
****
****
**

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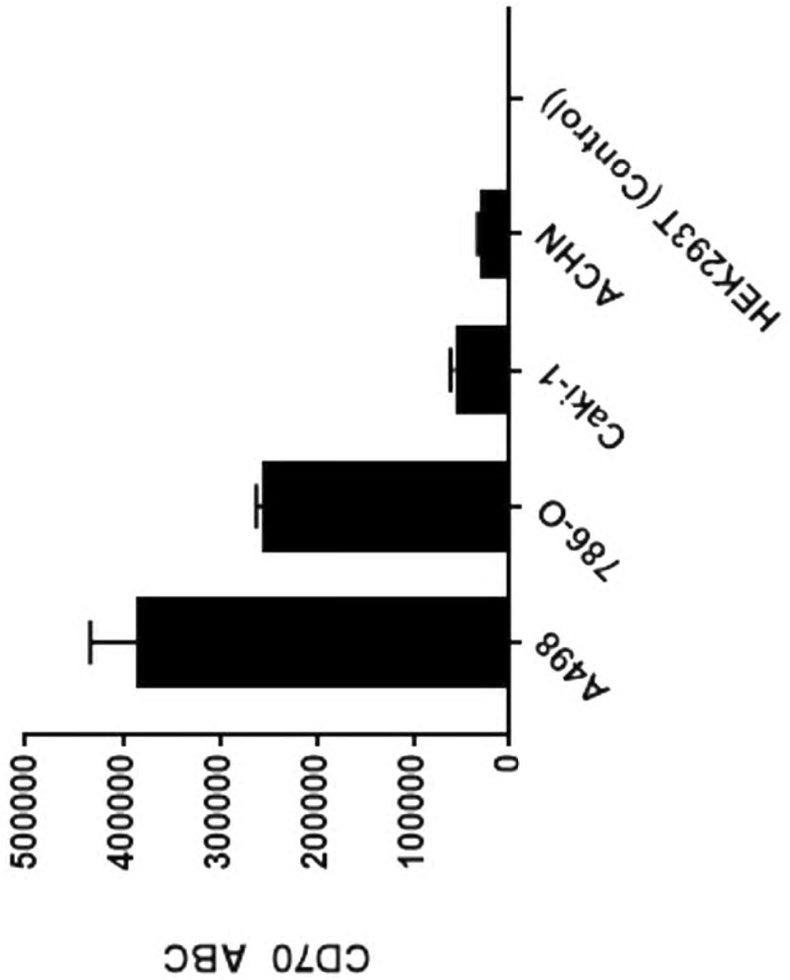
FIG. 12A



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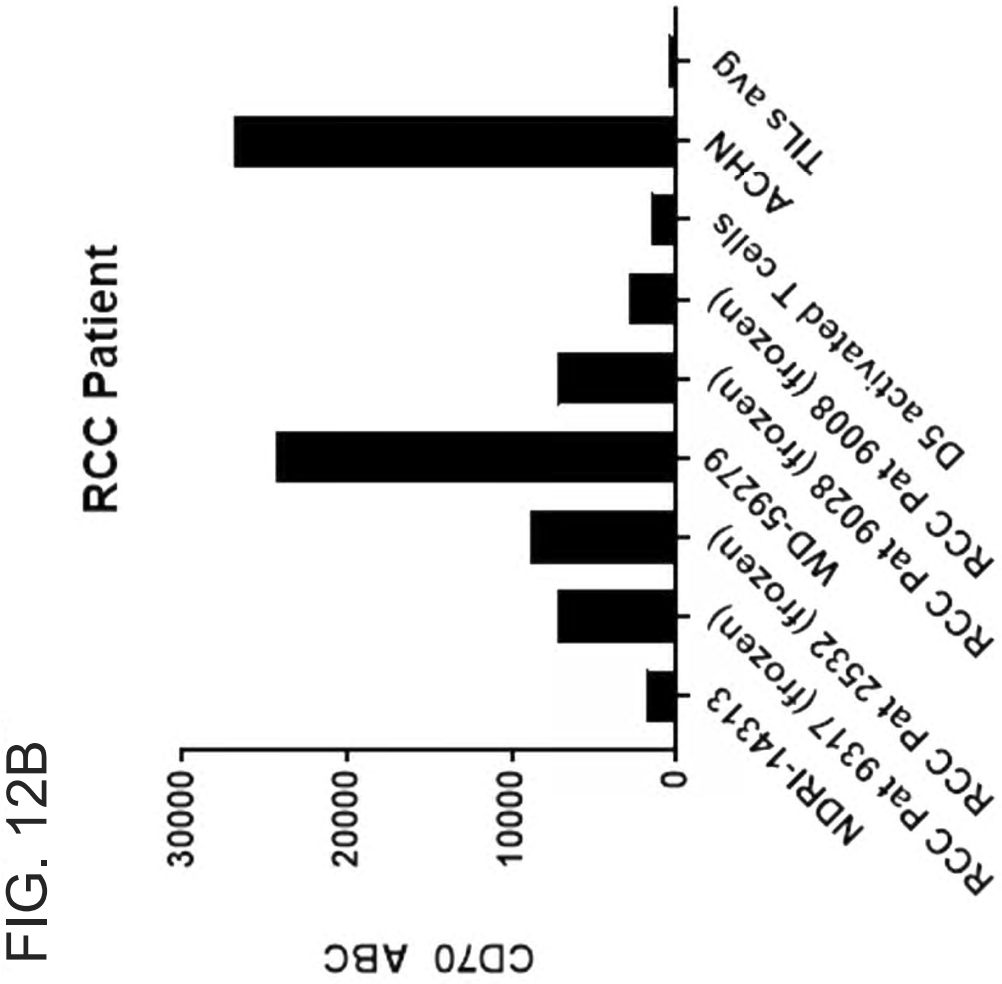

FIG. 12B

FIG. 12C

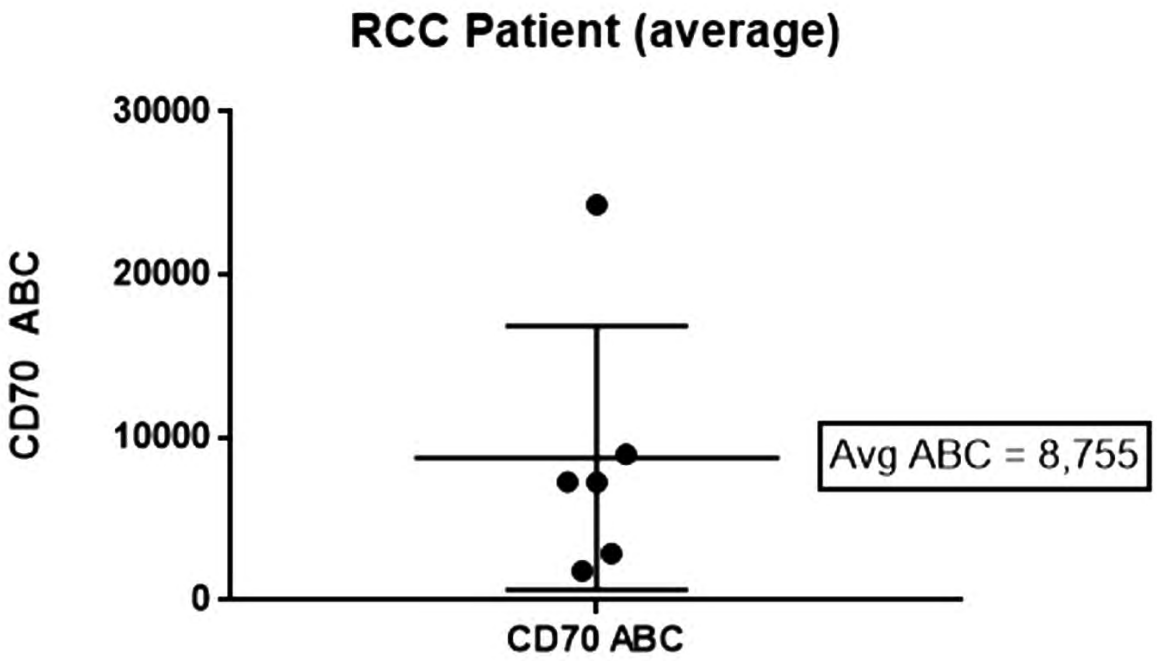
RCC Patient (average)
CD70 ABC
30000
20000
10000
0
CD70 ABC
Avg ABC = 8,755

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FIG. 13A

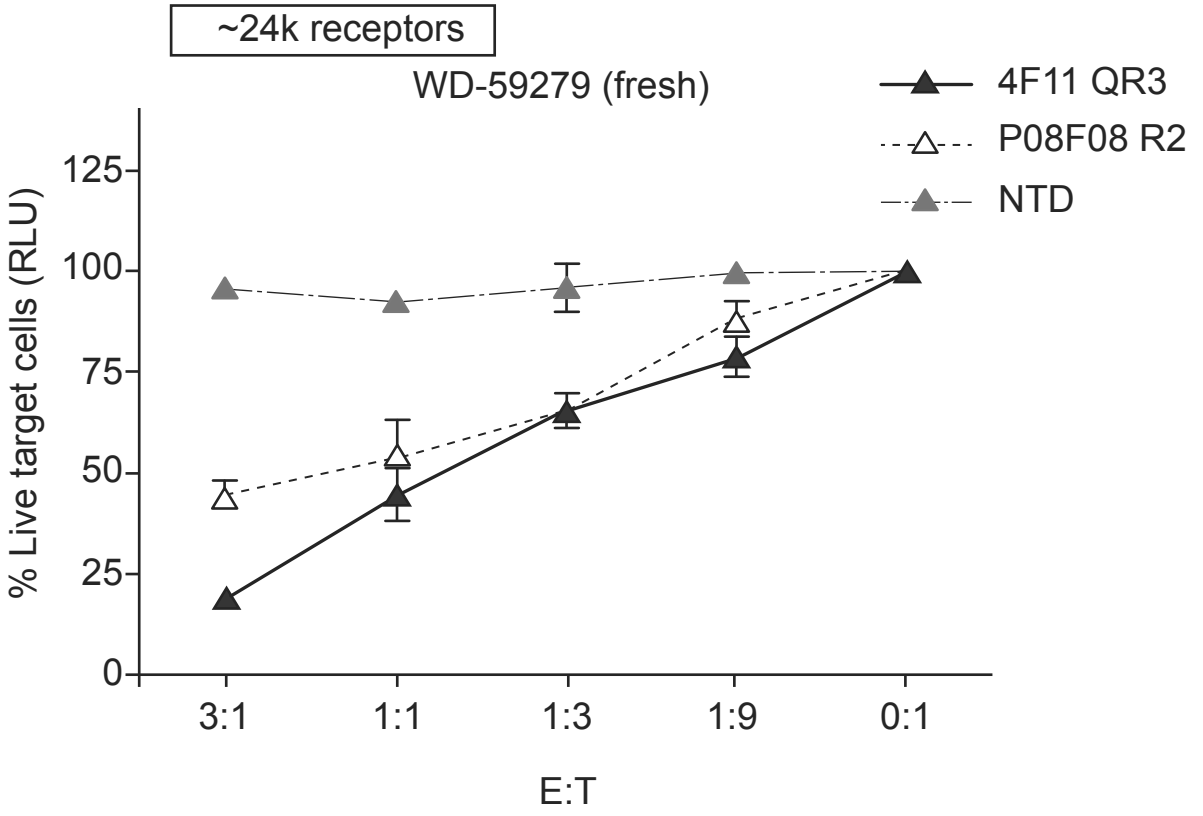

FIG. 13B

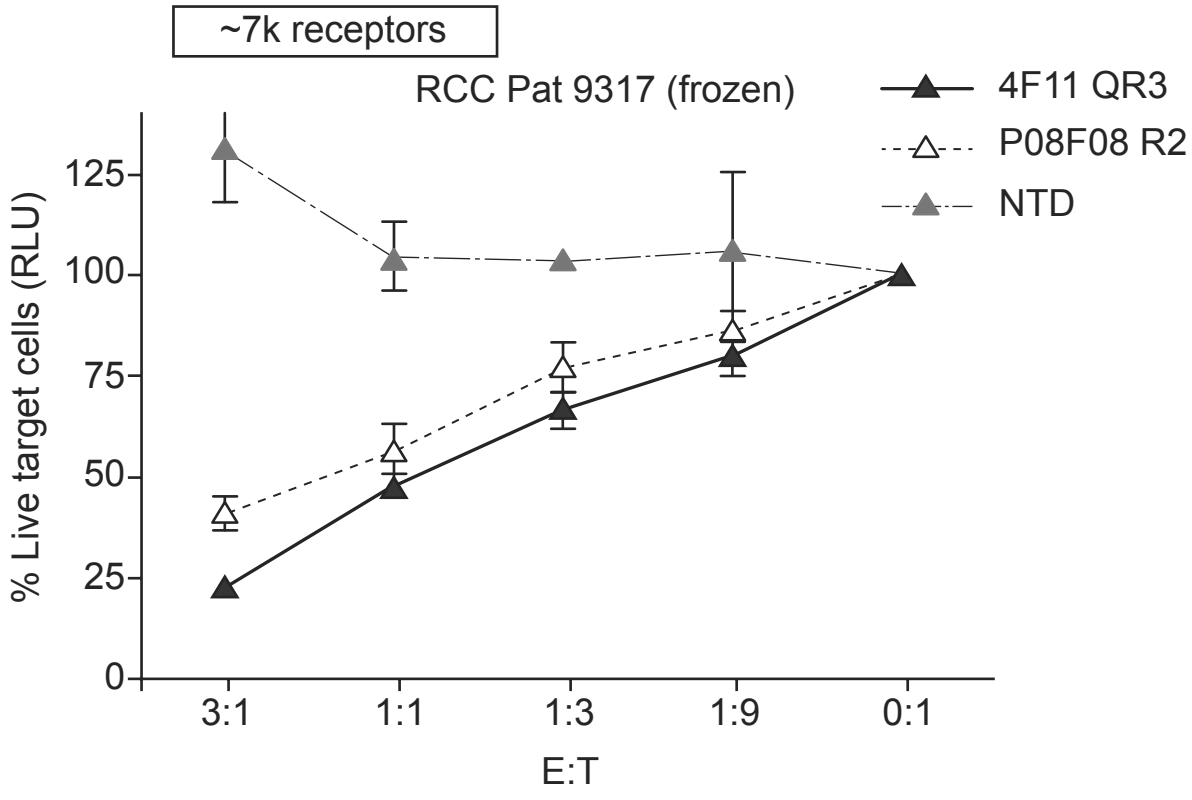

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FIG. 13C

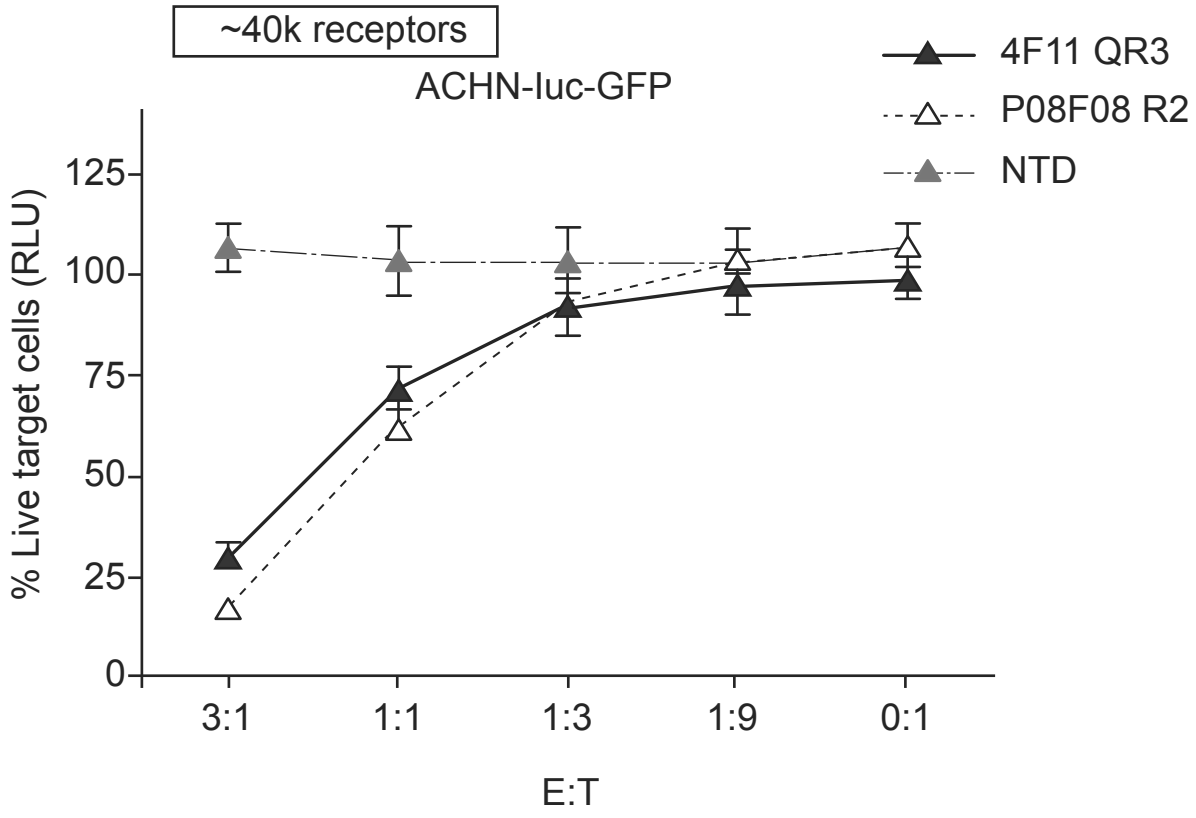

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FIG. 14A

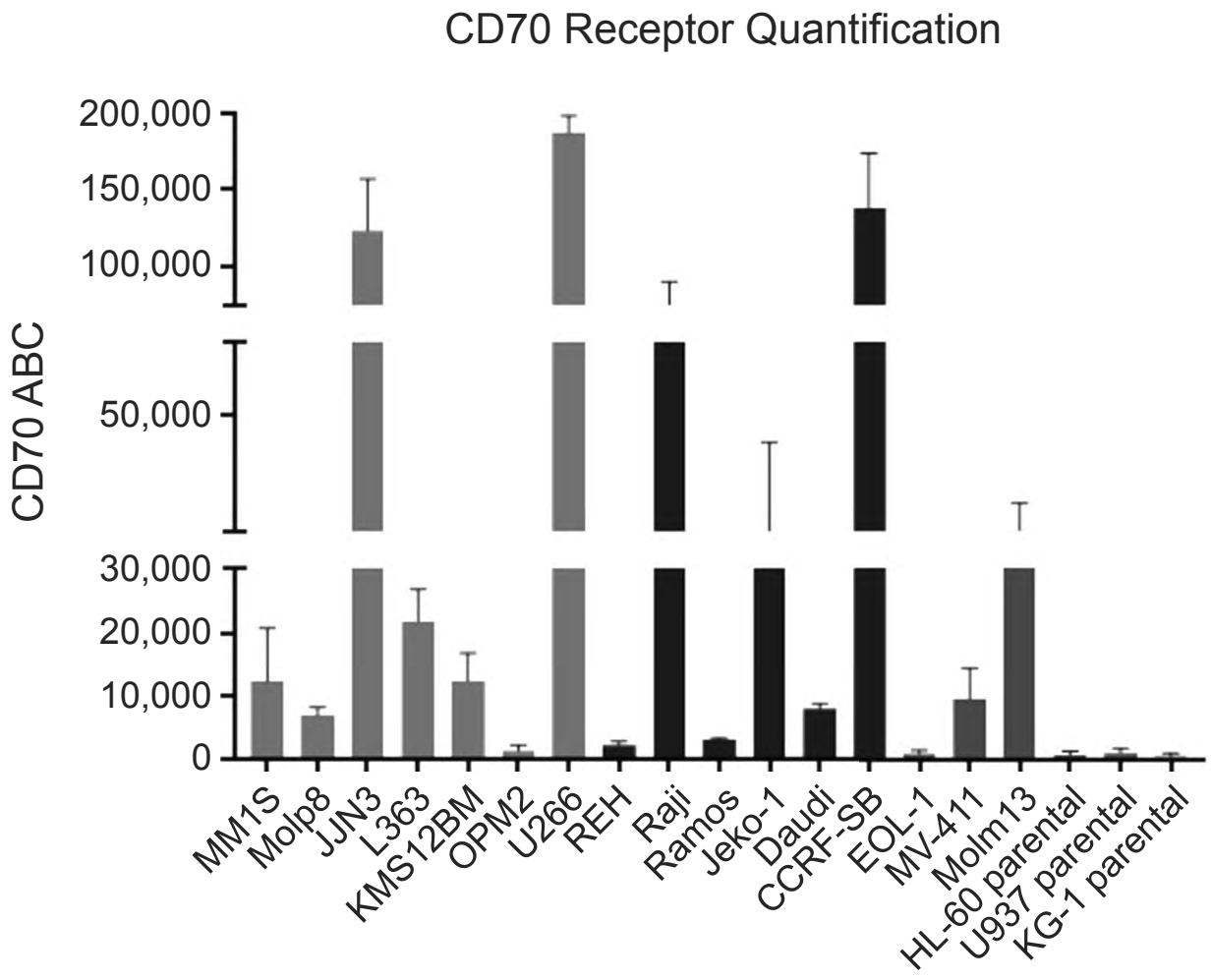

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FIG. 14B

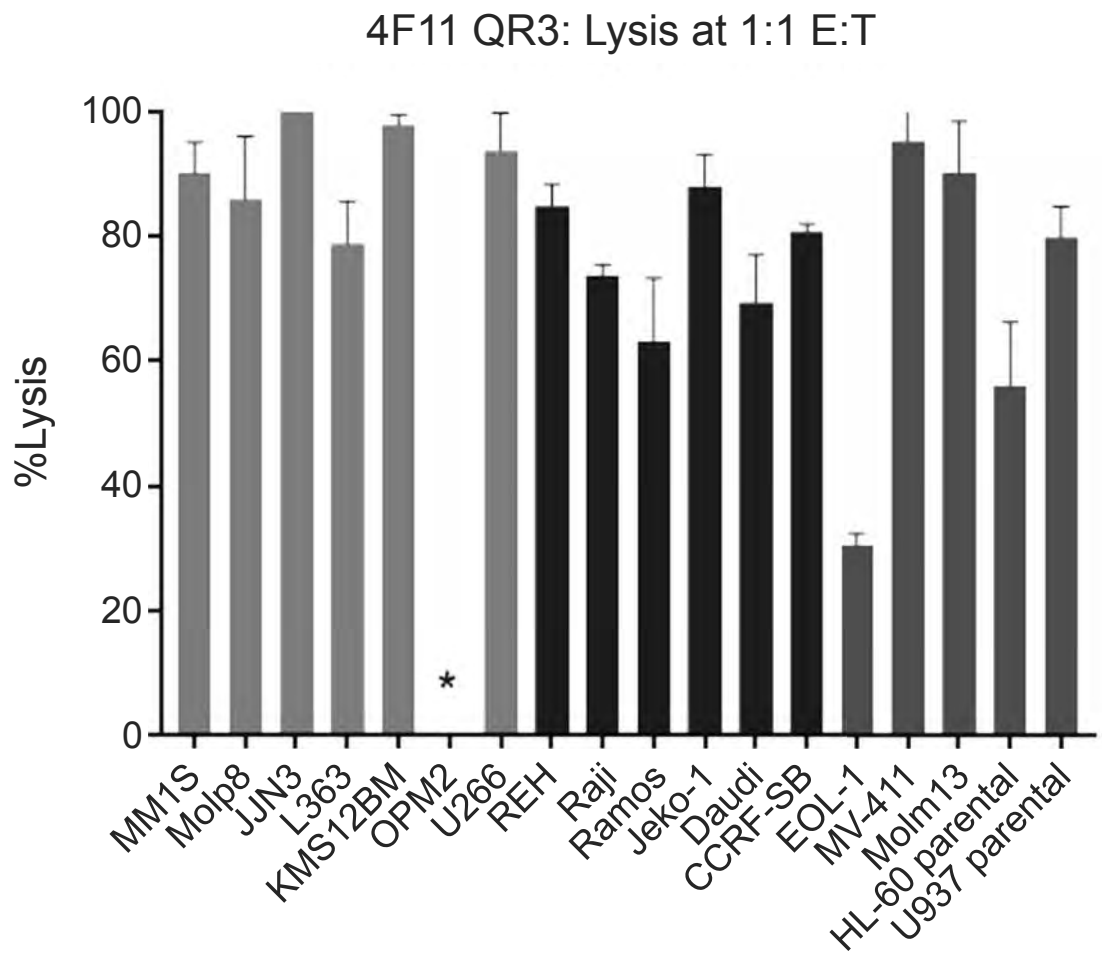


FIG. 15A

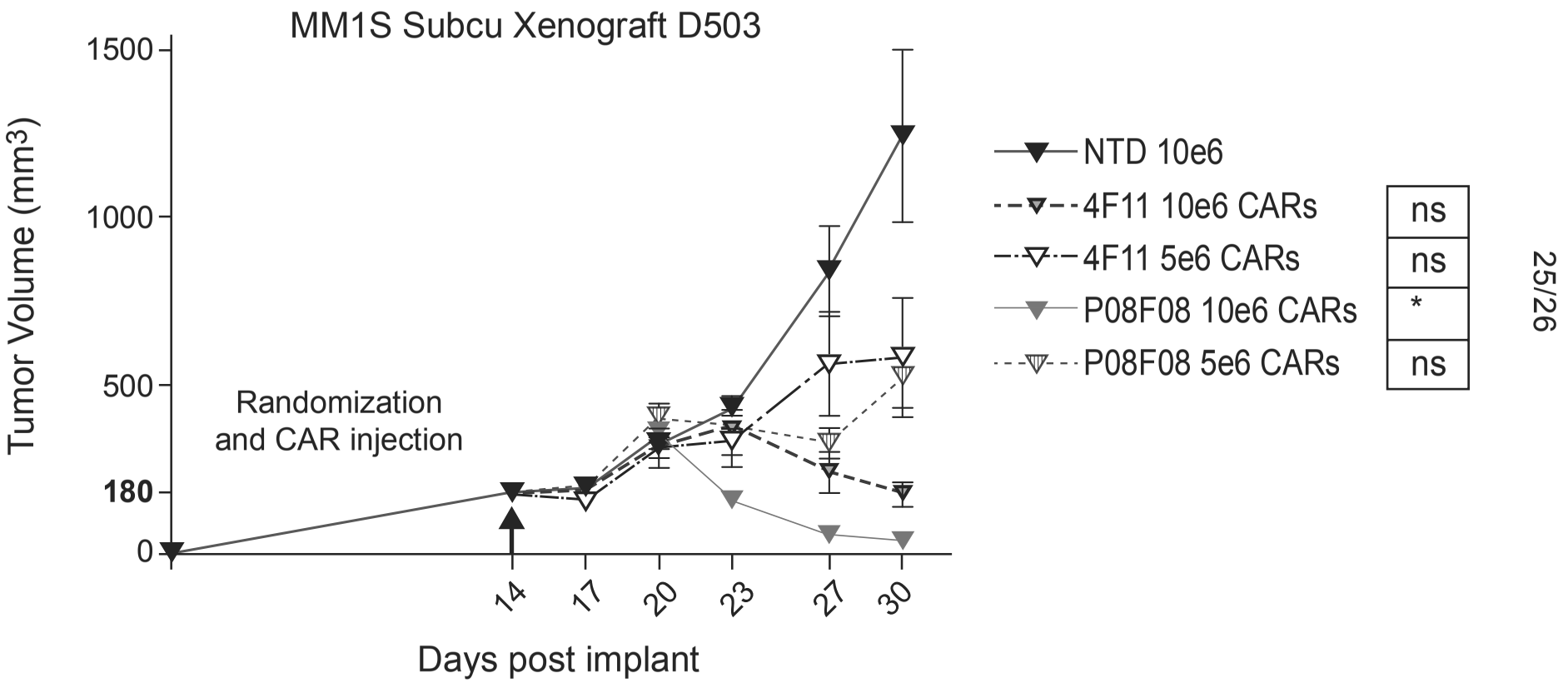
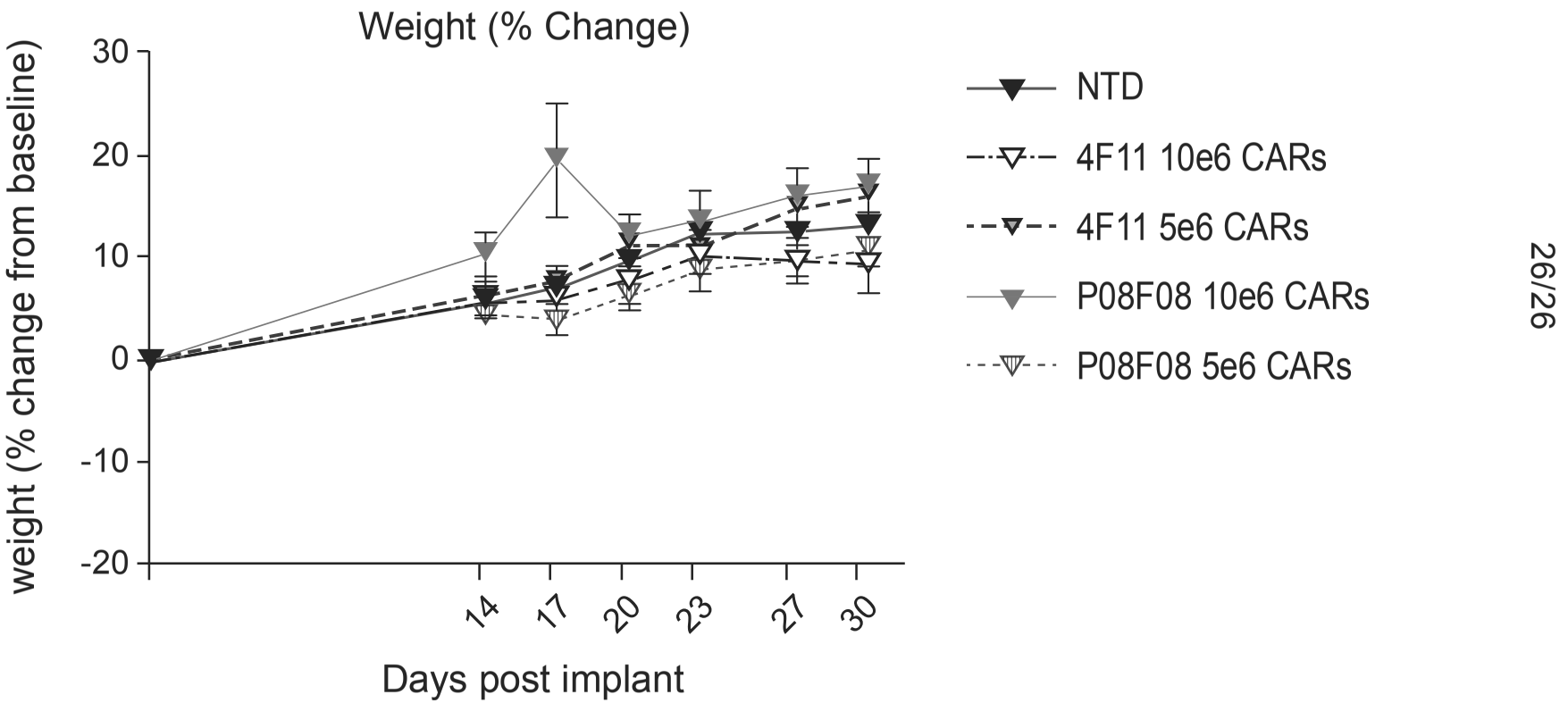

MM1S Subcu Xenograft D503
Tumor Volume (mm3)
1500
1000
500
180
0
Randomization
and CAR injection
14
17
20
23
27
30
Days post implant
NTD 10e6
4F11 10e6 CARs
4F11 5e6 CARs
P08F08 10e6 CARs
P08F08 5e6 CARs
ns
ns
*
ns

FIG. 15B


Weight (% Change)
weight (% change from baseline)
30
20
10
0
-10
-20
14
17
20
23
27
30
Days post implant
NTD
4F11 10e6 CARs
4F11 5e6 CARs
P08F08 10e6 CARs
P08F08 5e6 CARs

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Sequence Listing

1	**Sequence Listing Information**	
1-1	File Name	2024-10-17 Sequence_Listing_ST26 064422-511D02US.xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.3.0
1-5	Production Date	2024-10-17
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	US
2-2	Current application: Application number	18/919,327
2-3	Current application: Filing date	2024-10-17
2-4	Current application: Applicant file reference	064422-511D02US
2-5	Earliest priority application: IP Office	US
2-6	Earliest priority application: Application number	62/625,009
2-7	Earliest priority application: Filing date	2018-02-01
2-8en	Applicant name	PFIZER INC.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
2-10en	Invention title	CHIMERIC ANTIGEN RECEPTORS TARGETING CD70
2-11	Sequence Total Quantity	683

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3-1	**Sequences**	
3-1-1	Sequence Number [ID]	1
3-1-2	Molecule Type	AA
3-1-3	Length	112
3-1-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-1-5	Residues	DIVMTQNPLS SPVTLGQPAS ISCRSSQSLV HSDGNTYLSW LQQRPGQSPR LLIYKISNRF 60 SGVPDRFSGS GAGTDFTLKI SRVEAEDVGV YYCMQATQFP LTIGGGSKVE IK 112
3-2	**Sequences**	
3-2-1	Sequence Number [ID]	2
3-2-2	Molecule Type	AA
3-2-3	Length	118
3-2-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-2-5	Residues	QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYGFSWVRQA PGQGLEWMGG IIPIFGSANY 60 AQKFQGRVTI TADKSTSTVY MELISLRSED TAVYYCARGG SSSPFAYWGQ GTLVTVSS 118
3-3	**Sequences**	
3-3-1	Sequence Number [ID]	3
3-3-2	Molecule Type	AA
3-3-3	Length	112
3-3-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-3-5	Residues	DIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGNTYLSW LQQRPGQSPR LLIYKISNRF 60 SGVPDRFSGS GAGTDFTLKI SRVEAEDVGV YYCMQATQFP LTIGGGSKVE IK 112
3-4	**Sequences**	
3-4-1	Sequence Number [ID]	4
3-4-2	Molecule Type	AA
3-4-3	Length	118
3-4-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-4-5	Residues	QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYGFSWVRQA PGQGLEWMGG IIPIFGTANY 60 AQKFQGRVTI TADKSTSTVF MELISLRSEY TAVYYCARGG SSSPFAYWGQ GTLVTVSS 118
3-5	**Sequences**	
3-5-1	Sequence Number [ID]	5
3-5-2	Molecule Type	AA
3-5-3	Length	107
3-5-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-5-5	Residues	DIQMTQSPSS LSASVGDRVT ITCRASQGIS NYLAWFQQKP GKAPKSLIYA ASSLQSGVPS 60 KFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPLTFGG GTKVEIK 107
3-6	**Sequences**	
3-6-1	Sequence Number [ID]	6
3-6-2	Molecule Type	AA
3-6-3	Length	112
3-6-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct

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	NonEnglishQualifier Value	
3-6-5	Residues	QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWNWIRQP PGKGLEWIGY IYYSGSTNYN 60 PSLKSRVTIS VDTSKNQFSL KLRSVTAADT AVYYCARDIR TWGQGTLVTV SS 112
3-7	**Sequences**	
3-7-1	Sequence Number [ID]	7
3-7-2	Molecule Type	AA
3-7-3	Length	112
3-7-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..112** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-7-5	Residues	DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDENTYLNW FQQRPGQSLR RLIYQVSNRD 60 SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YFCMQGTYWP PTFGGGTKVE IK 112
3-8	**Sequences**	
3-8-1	Sequence Number [ID]	8
3-8-2	Molecule Type	AA
3-8-3	Length	117
3-8-4	Features	**REGION 1..117**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..117** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-8-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFTFR NSWMSWVRQA PGKGLEWVAN IKRDGSEKYY 60 VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDQ TGSFDYWGQG TLVTVSS 117
3-9	**Sequences**	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	AA
3-9-3	Length	106
3-9-4	Features	**REGION 1..106**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..106** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-9-5	Residues	EIVMTQSPAT LSMSLGERAT LSCRASQSVS SSLAWYQQKP GQAPRLLIYG ASTRATGIPA 60 RFGGSGSGTE FTLTISSLQS EDFAVYYCQQ YINWPHFGGG TKVEIK 106
3-10	**Sequences**	
3-10-1	Sequence Number [ID]	10
3-10-2	Molecule Type	AA
3-10-3	Length	115
3-10-4	Features	**REGION 1..115**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..115** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-10-5	Residues	QVQLRGSGPG LVKPSETLSL TCTVSDDSIS VYYWSWIRQP AGKGLEWIGR VYSSGNINYN 60 PSLESRVTMS VDTSKSRFSL NLSSVTAADT AVYYCARGLD AFDIWGQGTM VTVSS 115
3-11	**Sequences**	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	AA
3-11-3	Length	107
3-11-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..107** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-11-5	Residues	DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKILIYG ASNLETGVPS 60 RFSGSGSGTD FTFAISSLQP EDVATYYCQQ YDNFPITFGQ GTRLEIK 107
3-12	**Sequences**	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	AA
3-12-3	Length	115
3-12-4	Features	**REGION 1..115**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct

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		source 1..115
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-12-5	Residues	EVQLLESGGG LVQPGESLRL SCEVSGFTFT SYAMSWVRQV PGKGLEWVSI ISGVAFTTYY 60 ADSVKGRFTI SRDHSKNTLY LQMNGLRAED TAVYYCVKVD GEVYWGQGTL VTVSS 115
3-13	**Sequences**	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	AA
3-13-3	Length	108
3-13-4	Features	**REGION 1..108**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..108
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-13-5	Residues	EIVMTQSPDT LSVSPGERAI LSCRASQSVS SNLAWYQQKP GQAPRLLIYS ASTRASGIPA 60 RFSGSGSGTE FTLSISSLQS EDFAVYYCQQ YDNWPPLTFG GGTKVEIK 108
3-14	**Sequences**	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	AA
3-14-3	Length	117
3-14-4	Features	**REGION 1..117**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..117
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-14-5	Residues	QVQLVQSGAE VKKPGSSVKV SCEASGGTFI TYAISWVRQA PGQGLEWMGG IIPFFGTANY 60 AQKFQGRVTI TADKSTSTAS MELRSLRSED TAMYYCAQWE LFFFDFWGQG TPVTVSS 117
3-15	**Sequences**	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	AA
3-15-3	Length	108
3-15-4	Features	**REGION 1..108**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..108
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-15-5	Residues	EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQQ PGQAPRLLIY GASSRATGIP 60 DRFSGSGSGT DFTLTISRLE PEDFAIYYCQ QYGSSPLTFG GGTKVEIK 108
3-16	**Sequences**	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	AA
3-16-3	Length	120
3-16-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-16-5	Residues	AVQLVESGGG LVQPGGSLRL SCAASGFTFT YYSMNWVRQA PGKGLEWVSH ISIRSSTIYF 60 ADSAKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGS GWYGDYFDYW GQGTLVTVSS 120
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	AA
3-17-3	Length	107
3-17-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-17-5	Residues	DIQMTQSPSA MSASVGDRVT ITCRASQDIS NYLAWFQQKP GKVPKRLIYA ASSLQSGVPS 60 RFSGSGSGTE FTLTISSLLP EDFATYYCLQ LNSFPFTFGG GTKVEIN 107
3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	AA

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3-18-3	Length	123
3-18-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..123
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-18-5	Residues	QVTLKESGPV LVKPTETLTL TCTVSGFSLS NARMGVTWIR QPPGKALEWL AHIFSNDEKS 60 YSTSLKSRLT ISKDTSKTQV VLTMTNMDPV DTATYYCARI RDYYDISSYY DYWGQGTLVS 120 VSS 123
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	AA
3-19-3	Length	107
3-19-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-19-5	Residues	DIQMTQSPSS VSASVGDRVT ITCRASQGIS SWLAWYQQKP GKAPKVLIYA ASSLQSGVPS 60 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ AFSFPFTFGP GTKVDIK 107
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	AA
3-20-3	Length	119
3-20-4	Features	**REGION 1..119**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..119
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-20-5	Residues	EVQLVESGGG LVQPGGSLRL SCAVSGFTFS NHNIHWVRQA PGKGLEWISY ISRSSSTIYY 60 ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARDH AQWYGMDVWG QGTTVTVSS 119
3-21	**Sequences**	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	AA
3-21-3	Length	112
3-21-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-21-5	Residues	DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSYNNKNYVA WYQQKPGQPP NLLIFWASTR 60 ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQYYST LTFGGGTKVE IK 112
3-22	**Sequences**	
3-22-1	Sequence Number [ID]	22
3-22-2	Molecule Type	AA
3-22-3	Length	124
3-22-4	Features	**REGION 1..124**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..124
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-22-5	Residues	EVQLVESGGG LVQPGGSLRL SCVASGFTFS SYWMSWVRQA PGKGLEWVAS IKQDGSEKYY 60 VDSVKGRFTI SRDNAKNSVY LQMNSLRAED TGVYYCAREG VNWGWRLYWH FDLWGRGTLV 120 TVSS 124
3-23	**Sequences**	
3-23-1	Sequence Number [ID]	23
3-23-2	Molecule Type	AA
3-23-3	Length	108
3-23-4	Features	**REGION 1..108**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..108
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	

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3-23-5	Residues	EIVLTQSPGT LSLSPGERVT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY DASSRATGIP 60 DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLTFG GGTKVEIK 108
3-24	**Sequences**	
3-24-1	Sequence Number [ID]	24
3-24-2	Molecule Type	AA
3-24-3	Length	120
3-24-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-24-5	Residues	EVQVVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSH SSISRGNIYF 60 ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGS GWYGDYFDYW GQGTLVTVSS 120
3-25	**Sequences**	
3-25-1	Sequence Number [ID]	25
3-25-2	Molecule Type	AA
3-25-3	Length	112
3-25-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-25-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSSSN IGSNYVYWYQ QLPGTAPKLL IYRNNQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CAAWDDSLSG VVFGGGTKLT VL 112
3-26	**Sequences**	
3-26-1	Sequence Number [ID]	26
3-26-2	Molecule Type	AA
3-26-3	Length	120
3-26-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-26-5	Residues	EVQLLESGGG LVQPGGSLRL SCAASGFAFS NYAMSWVRQA PGKGLEWVSA IRGGGGSTYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDF ISGTWYPDYW GQGTLVTVSS 120
3-27	**Sequences**	
3-27-1	Sequence Number [ID]	27
3-27-2	Molecule Type	AA
3-27-3	Length	112
3-27-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-27-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSRSN IGSNYVYWYQ QLPGTAPKLL IYRNNQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CASWDGSLSA VVFGTGTKLT VL 112
3-28	**Sequences**	
3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	AA
3-28-3	Length	122
3-28-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-28-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYRFT SYWIGWVRQM PGKGLEWMGS IYPDDSDTRY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCASST VDYPGYSYFD YWGQGTLVTV 120 SS 122
3-29	**Sequences**	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	AA
3-29-3	Length	112
3-29-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct

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		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-29-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSSSN IGSNYVYWYQ QLPGTAPKLL IYRNNQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CATWDDSLGS PVFGTGTKLT VL 112
3-30	**Sequences**	
3-30-1	Sequence Number [ID]	30
3-30-2	Molecule Type	AA
3-30-3	Length	123
3-30-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..123
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-30-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYTFT NYWIAWVRQM PGKGLEWMGI IYPDGSDTRY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDI TSWYYGEPAF DIWGQGTLVT 120 VSS 123
3-31	**Sequences**	
3-31-1	Sequence Number [ID]	31
3-31-2	Molecule Type	AA
3-31-3	Length	110
3-31-4	Features	**REGION 1..110**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..110
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-31-5	Residues	ELDIQMTQSP SSLSASVGDR VTITCRASQS ISRYLNWYQQ KPGKAPKLLI YAASILQTGV 60 PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSYSTTMWT FGQGTKVEIK 110
3-32	**Sequences**	
3-32-1	Sequence Number [ID]	32
3-32-2	Molecule Type	AA
3-32-3	Length	122
3-32-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-32-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SSWIGWVRQM PGKGLEWMGI IYPGDSDTRY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCAKGL SQAMTGFGFD YWGQGTLVTV 120 SS 122
3-33	**Sequences**	
3-33-1	Sequence Number [ID]	33
3-33-2	Molecule Type	AA
3-33-3	Length	113
3-33-4	Features	**REGION 1..113**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..113
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-33-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSSSN IGSNYVNWYQ QLPGTAPKLL IYGDYQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CATRDDSLSG SVVFGTGTKL TVL 113
3-34	**Sequences**	
3-34-1	Sequence Number [ID]	34
3-34-2	Molecule Type	AA
3-34-3	Length	122
3-34-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-34-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYGFT SYWIGWVRQM PGKGLEWMGI IHPDDSDTKY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCASSY LRGLWGGYFD YWGQGTLVTV 120 SS 122

3-35	**Sequences**	
3-35-1	Sequence Number [ID]	35
3-35-2	Molecule Type	AA
3-35-3	Length	110
3-35-4	Features	**REGION 1..110**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..110
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-35-5	Residues	ELDIQMTQSP SSLSASVGDR VTITCRASQS IYDYLHWYQQ KPGKAPKLLI YDASNLQSGV 60 PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSYTTPLFT FGQGTKVEIK 110
3-36	**Sequences**	
3-36-1	Sequence Number [ID]	36
3-36-2	Molecule Type	AA
3-36-3	Length	126
3-36-4	Features	**REGION 1..126**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..126
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-36-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYTFP SSWIGWVRQM PGKGLEWMGI IYPDTSHTRY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARAS YFDRGTGYSS WWMDVWGQGT 120 LVTVSS 126
3-37	**Sequences**	
3-37-1	Sequence Number [ID]	37
3-37-2	Molecule Type	AA
3-37-3	Length	110
3-37-4	Features	**REGION 1..110**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..110
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-37-5	Residues	ELDIQMTQSP SSLSASVGDR VTITCRASQY IGRYLNWYQQ KRGKAPKLLI HGATSLASGV 60 PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSYSTTSPT FGQGTKVEIK 110
3-38	**Sequences**	
3-38-1	Sequence Number [ID]	38
3-38-2	Molecule Type	AA
3-38-3	Length	123
3-38-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..123
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-38-5	Residues	EVQLLESGGG LVQPGGSLRL SCAASGFTFS QYSMSWVRQA PGKGLEWVSA ISGGGVSTYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASDI SDSGGSHWYF DYWGQGTLVT 120 VSS 123
3-39	**Sequences**	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	AA
3-39-3	Length	112
3-39-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-39-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSTSN IGRNYVYWYQ QLPGTAPKLL IYRTNQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CAAWDDSLSG RVFGTGTKLT VL 112
3-40	**Sequences**	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	AA
3-40-3	Length	121
3-40-4	Features	**REGION 1..121**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..121

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-40-5	Residues	EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVST ISGTGGTTYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVR AGIDPTASDV WGQGTLVTVS 120 S 121
3-41	**Sequences**	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	AA
3-41-3	Length	112
3-41-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-41-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSSSN IGSNYVYWYQ QLPGTAPKPL IYMNNQRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CAAWDDSLSA VVFGTGTKLT VL 112
3-42	**Sequences**	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	AA
3-42-3	Length	124
3-42-4	Features	**REGION 1..124**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..124
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-42-5	Residues	EVQLLESGGG LVQPGGSLRL SCAASGFTFN NFAMSWVRQA PGKGLEWVSG ISGSGDNTYY 60 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR DIGLGWYSYY LDVWGQGTLV 120 TVSS 124
3-43	**Sequences**	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	AA
3-43-3	Length	113
3-43-4	Features	**REGION 1..113**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..113
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-43-5	Residues	ELQSVLTQPP SASGTPGQRV TISCSGSNSN IGTNYVSWYQ QLPGTAPKLL IYRSSRRPSG 60 VPDRFSGSKS GTSASLAISG LRSEDEADYY CAAWDGSLSG HWVFGTGTKL TVL 113
3-44	**Sequences**	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	AA
3-44-3	Length	119
3-44-4	Features	**REGION 1..119**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..119
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-44-5	Residues	QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGE IIPIFGTASY 60 AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARAG WDDSWFDYWG QGTLVTVSS 119
3-45	**Sequences**	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	AA
3-45-3	Length	110
3-45-4	Features	**REGION 1..110**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..110
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-45-5	Residues	ELDIQMTQSP SSLSASVGDR VTITCRASQS IDTYLNWYQQ KPGKAPKLLI YSASSLHSGV 60 PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSYSTTAWT FGQGTKVEIK 110
3-46	**Sequences**	
3-46-1	Sequence Number [ID]	46

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3-46-2	Molecule Type	AA
3-46-3	Length	122
3-46-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-46-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYSFA SYWIGWVRQM PGKGLEWMGV IYPGTSETRY 60 SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCAKGL SASASGYSFQ YWGQGTLVTV 120 SS 122
3-47	**Sequences**	
3-47-1	Sequence Number [ID]	47
3-47-2	Molecule Type	AA
3-47-3	Length	109
3-47-4	Features	**REGION 1..109**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..109
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-47-5	Residues	ELDIQMTQSP SSLSASVGDR VTITCRASQS IGQSLNWYQQ KPGKAPKLLI YGASSLQSGV 60 PSRFSGSGSG TDFTLTISSL QPEDFATYYC QQSYSTPITF GQGTKVEIK 109
3-48	**Sequences**	
3-48-1	Sequence Number [ID]	48
3-48-2	Molecule Type	AA
3-48-3	Length	124
3-48-4	Features	**REGION 1..124**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..124
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-48-5	Residues	EVQLVQSGAE VKKPGESLKI SCKGSGYSFT DYWIGWVRQM PGKGLEWMGM ISPGGSTTIY 60 RPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCAREM YTGGYGGSWY FDYWGQGTLV 120 TVSS 124
3-49	**Sequences**	
3-49-1	Sequence Number [ID]	49
3-49-2	Molecule Type	AA
3-49-3	Length	5
3-49-4	Features	**REGION 1..5**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..5
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-49-5	Residues	SYGFS 5
3-50	**Sequences**	
3-50-1	Sequence Number [ID]	50
3-50-2	Molecule Type	AA
3-50-3	Length	7
3-50-4	Features	**REGION 1..7**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-50-5	Residues	GGTFSSY 7
3-51	**Sequences**	
3-51-1	Sequence Number [ID]	51
3-51-2	Molecule Type	AA
3-51-3	Length	10
3-51-4	Features	**REGION 1..10**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..10
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-51-5	Residues	GGTFSSYGFS 10

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3-52	**Sequences**		
3-52-1	Sequence Number [ID]	52	
3-52-2	Molecule Type	AA	
3-52-3	Length	17	
3-52-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-52-5	Residues	GIIPIFGSAN YAQKFQG	17
3-53	**Sequences**		
3-53-1	Sequence Number [ID]	53	
3-53-2	Molecule Type	AA	
3-53-3	Length	6	
3-53-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-53-5	Residues	IPIFGS	6
3-54	**Sequences**		
3-54-1	Sequence Number [ID]	54	
3-54-2	Molecule Type	AA	
3-54-3	Length	9	
3-54-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-54-5	Residues	GGSSSPFAY	9
3-55	**Sequences**		
3-55-1	Sequence Number [ID]	55	
3-55-2	Molecule Type	AA	
3-55-3	Length	5	
3-55-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-55-5	Residues	SYGFS	5
3-56	**Sequences**		
3-56-1	Sequence Number [ID]	56	
3-56-2	Molecule Type	AA	
3-56-3	Length	7	
3-56-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-56-5	Residues	GGTFSSY	7
3-57	**Sequences**		
3-57-1	Sequence Number [ID]	57	
3-57-2	Molecule Type	AA	
3-57-3	Length	10	
3-57-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-57-5	Residues	GGTFSSYGFS	10
3-58	**Sequences**		
3-58-1	Sequence Number [ID]	58	

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3-58-2	Molecule Type	AA	
3-58-3	Length	17	
3-58-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-58-5	Residues	GIIPIFGTAN YAQKFQG	17
3-59	**Sequences**		
3-59-1	Sequence Number [ID]	59	
3-59-2	Molecule Type	AA	
3-59-3	Length	6	
3-59-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-59-5	Residues	IPIFGT	6
3-60	**Sequences**		
3-60-1	Sequence Number [ID]	60	
3-60-2	Molecule Type	AA	
3-60-3	Length	9	
3-60-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-60-5	Residues	GGSSSPFAY	9
3-61	**Sequences**		
3-61-1	Sequence Number [ID]	61	
3-61-2	Molecule Type	AA	
3-61-3	Length	5	
3-61-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-61-5	Residues	SYYWN	5
3-62	**Sequences**		
3-62-1	Sequence Number [ID]	62	
3-62-2	Molecule Type	AA	
3-62-3	Length	7	
3-62-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-62-5	Residues	GGSISSY	7
3-63	**Sequences**		
3-63-1	Sequence Number [ID]	63	
3-63-2	Molecule Type	AA	
3-63-3	Length	10	
3-63-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-63-5	Residues	GGSISSYYWN	10
3-64	**Sequences**		
3-64-1	Sequence Number [ID]	64	
3-64-2	Molecule Type	AA	
3-64-3	Length	16	

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3-64-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-64-5	Residues	YIYYSGSTNY NPSLKS	16
3-65	**Sequences**		
3-65-1	Sequence Number [ID]	65	
3-65-2	Molecule Type	AA	
3-65-3	Length	5	
3-65-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-65-5	Residues	YYSGS	5
3-66	**Sequences**		
3-66-1	Sequence Number [ID]	66	
3-66-2	Molecule Type	AA	
3-66-3	Length	5	
3-66-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-66-5	Residues	DIRTW	5
3-67	**Sequences**		
3-67-1	Sequence Number [ID]	67	
3-67-2	Molecule Type	AA	
3-67-3	Length	5	
3-67-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-67-5	Residues	NSWMS	5
3-68	**Sequences**		
3-68-1	Sequence Number [ID]	68	
3-68-2	Molecule Type	AA	
3-68-3	Length	7	
3-68-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-68-5	Residues	GFTFRNS	7
3-69	**Sequences**		
3-69-1	Sequence Number [ID]	69	
3-69-2	Molecule Type	AA	
3-69-3	Length	10	
3-69-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-69-5	Residues	GFTFRNSWMS	10
3-70	**Sequences**		
3-70-1	Sequence Number [ID]	70	
3-70-2	Molecule Type	AA	
3-70-3	Length	17	
3-70-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-70-5	Residues	NIKRDGSEKY YVDSVKG	17
3-71	**Sequences**		
3-71-1	Sequence Number [ID]	71	
3-71-2	Molecule Type	AA	
3-71-3	Length	6	
3-71-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-71-5	Residues	KRDGSE	6
3-72	**Sequences**		
3-72-1	Sequence Number [ID]	72	
3-72-2	Molecule Type	AA	
3-72-3	Length	8	
3-72-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-72-5	Residues	DQTGSFDY	8
3-73	**Sequences**		
3-73-1	Sequence Number [ID]	73	
3-73-2	Molecule Type	AA	
3-73-3	Length	5	
3-73-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-73-5	Residues	VYYWS	5
3-74	**Sequences**		
3-74-1	Sequence Number [ID]	74	
3-74-2	Molecule Type	AA	
3-74-3	Length	7	
3-74-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-74-5	Residues	DDSISVY	7
3-75	**Sequences**		
3-75-1	Sequence Number [ID]	75	
3-75-2	Molecule Type	AA	
3-75-3	Length	10	
3-75-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-75-5	Residues	DDSISVYYWS	10
3-76	**Sequences**		
3-76-1	Sequence Number [ID]	76	
3-76-2	Molecule Type	AA	
3-76-3	Length	15	
3-76-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..15	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-76-5	Residues	VYSSGNINYN PSLES	15
3-77	**Sequences**		
3-77-1	Sequence Number [ID]	77	
3-77-2	Molecule Type	AA	
3-77-3	Length	5	
3-77-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-77-5	Residues	YSSGN	5
3-78	**Sequences**		
3-78-1	Sequence Number [ID]	78	
3-78-2	Molecule Type	AA	
3-78-3	Length	7	
3-78-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-78-5	Residues	GLDAFDI	7
3-79	**Sequences**		
3-79-1	Sequence Number [ID]	79	
3-79-2	Molecule Type	AA	
3-79-3	Length	5	
3-79-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-79-5	Residues	SYAMS	5
3-80	**Sequences**		
3-80-1	Sequence Number [ID]	80	
3-80-2	Molecule Type	AA	
3-80-3	Length	7	
3-80-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-80-5	Residues	GFTFTSY	7
3-81	**Sequences**		
3-81-1	Sequence Number [ID]	81	
3-81-2	Molecule Type	AA	
3-81-3	Length	10	
3-81-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-81-5	Residues	GFTFTSYAMS	10
3-82	**Sequences**		
3-82-1	Sequence Number [ID]	82	
3-82-2	Molecule Type	AA	
3-82-3	Length	16	
3-82-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-82-5	Residues	RVYSSGNINY NPSLES	16
3-83	**Sequences**		
3-83-1	Sequence Number [ID]	83	
3-83-2	Molecule Type	AA	
3-83-3	Length	5	
3-83-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-83-5	Residues	YSSGN	5
3-84	**Sequences**		
3-84-1	Sequence Number [ID]	84	
3-84-2	Molecule Type	AA	
3-84-3	Length	7	
3-84-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-84-5	Residues	GLDAFDI	7
3-85	**Sequences**		
3-85-1	Sequence Number [ID]	85	
3-85-2	Molecule Type	AA	
3-85-3	Length	5	
3-85-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-85-5	Residues	TYAIS	5
3-86	**Sequences**		
3-86-1	Sequence Number [ID]	86	
3-86-2	Molecule Type	AA	
3-86-3	Length	7	
3-86-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-86-5	Residues	GGTFITY	7
3-87	**Sequences**		
3-87-1	Sequence Number [ID]	87	
3-87-2	Molecule Type	AA	
3-87-3	Length	10	
3-87-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-87-5	Residues	GGTFITYAIS	10
3-88	**Sequences**		
3-88-1	Sequence Number [ID]	88	
3-88-2	Molecule Type	AA	
3-88-3	Length	17	
3-88-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-88-5	Residues	GIIPFFGTAN YAQKFQG	17
3-89	**Sequences**		

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3-89-1	Sequence Number [ID]	89	
3-89-2	Molecule Type	AA	
3-89-3	Length	6	
3-89-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-89-5	Residues	IPFFGT	6
3-90	**Sequences**		
3-90-1	Sequence Number [ID]	90	
3-90-2	Molecule Type	AA	
3-90-3	Length	8	
3-90-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-90-5	Residues	WELFFFDF	8
3-91	**Sequences**		
3-91-1	Sequence Number [ID]	91	
3-91-2	Molecule Type	AA	
3-91-3	Length	5	
3-91-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-91-5	Residues	YYSMN	5
3-92	**Sequences**		
3-92-1	Sequence Number [ID]	92	
3-92-2	Molecule Type	AA	
3-92-3	Length	7	
3-92-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-92-5	Residues	GFTFTYY	7
3-93	**Sequences**		
3-93-1	Sequence Number [ID]	93	
3-93-2	Molecule Type	AA	
3-93-3	Length	10	
3-93-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-93-5	Residues	GFTFTYYSMN	10
3-94	**Sequences**		
3-94-1	Sequence Number [ID]	94	
3-94-2	Molecule Type	AA	
3-94-3	Length	17	
3-94-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-94-5	Residues	HISIRSSTIY FADSAKG	17
3-95	**Sequences**		
3-95-1	Sequence Number [ID]	95	
3-95-2	Molecule Type	AA	

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3-95-3	Length	6	
3-95-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-95-5	Residues	SIRSST	6
3-96	**Sequences**		
3-96-1	Sequence Number [ID]	96	
3-96-2	Molecule Type	AA	
3-96-3	Length	11	
3-96-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-96-5	Residues	GSGWYGDYFD Y	11
3-97	**Sequences**		
3-97-1	Sequence Number [ID]	97	
3-97-2	Molecule Type	AA	
3-97-3	Length	7	
3-97-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-97-5	Residues	NARMGVT	7
3-98	**Sequences**		
3-98-1	Sequence Number [ID]	98	
3-98-2	Molecule Type	AA	
3-98-3	Length	9	
3-98-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-98-5	Residues	GFSLSNARM	9
3-99	**Sequences**		
3-99-1	Sequence Number [ID]	99	
3-99-2	Molecule Type	AA	
3-99-3	Length	12	
3-99-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-99-5	Residues	GFSLSNARMG VT	12
3-100	**Sequences**		
3-100-1	Sequence Number [ID]	100	
3-100-2	Molecule Type	AA	
3-100-3	Length	16	
3-100-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-100-5	Residues	HIFSNDEKSY STSLKS	16
3-101	**Sequences**		
3-101-1	Sequence Number [ID]	101	
3-101-2	Molecule Type	AA	
3-101-3	Length	5	
3-101-4	Features	**REGION 1..5**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-101-5	Residues	FSNDE	5
3-102	**Sequences**		
3-102-1	Sequence Number [ID]	102	
3-102-2	Molecule Type	AA	
3-102-3	Length	13	
3-102-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-102-5	Residues	IRDYYDISSY YDY	13
3-103	**Sequences**		
3-103-1	Sequence Number [ID]	103	
3-103-2	Molecule Type	AA	
3-103-3	Length	5	
3-103-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-103-5	Residues	NHNIH	5
3-104	**Sequences**		
3-104-1	Sequence Number [ID]	104	
3-104-2	Molecule Type	AA	
3-104-3	Length	7	
3-104-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-104-5	Residues	GFTFSNH	7
3-105	**Sequences**		
3-105-1	Sequence Number [ID]	105	
3-105-2	Molecule Type	AA	
3-105-3	Length	10	
3-105-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-105-5	Residues	GFTFSNHNIH	10
3-106	**Sequences**		
3-106-1	Sequence Number [ID]	106	
3-106-2	Molecule Type	AA	
3-106-3	Length	17	
3-106-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-106-5	Residues	YISRSSSTIY YADSVKG	17
3-107	**Sequences**		
3-107-1	Sequence Number [ID]	107	
3-107-2	Molecule Type	AA	
3-107-3	Length	6	
3-107-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-107-5	Residues	SRSSST	6
3-108	**Sequences**		
3-108-1	Sequence Number [ID]	108	
3-108-2	Molecule Type	AA	
3-108-3	Length	10	
3-108-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-108-5	Residues	DHAQWYGMDV	10
3-109	**Sequences**		
3-109-1	Sequence Number [ID]	109	
3-109-2	Molecule Type	AA	
3-109-3	Length	5	
3-109-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-109-5	Residues	SYWMS	5
3-110	**Sequences**		
3-110-1	Sequence Number [ID]	110	
3-110-2	Molecule Type	AA	
3-110-3	Length	7	
3-110-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-110-5	Residues	GFTFSSY	7
3-111	**Sequences**		
3-111-1	Sequence Number [ID]	111	
3-111-2	Molecule Type	AA	
3-111-3	Length	10	
3-111-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-111-5	Residues	GFTFSSYWMS	10
3-112	**Sequences**		
3-112-1	Sequence Number [ID]	112	
3-112-2	Molecule Type	AA	
3-112-3	Length	17	
3-112-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-112-5	Residues	SIKQDGSEKY YVDSVKG	17
3-113	**Sequences**		
3-113-1	Sequence Number [ID]	113	
3-113-2	Molecule Type	AA	
3-113-3	Length	6	
3-113-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-113-5	Residues	KQDGSE	6
3-114	**Sequences**		
3-114-1	Sequence Number [ID]	114	
3-114-2	Molecule Type	AA	
3-114-3	Length	15	
3-114-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-114-5	Residues	EGVNWGWRLY WHFDL	15
3-115	**Sequences**		
3-115-1	Sequence Number [ID]	115	
3-115-2	Molecule Type	AA	
3-115-3	Length	5	
3-115-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-115-5	Residues	SYSMN	5
3-116	**Sequences**		
3-116-1	Sequence Number [ID]	116	
3-116-2	Molecule Type	AA	
3-116-3	Length	7	
3-116-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-116-5	Residues	GFTFSSY	7
3-117	**Sequences**		
3-117-1	Sequence Number [ID]	117	
3-117-2	Molecule Type	AA	
3-117-3	Length	10	
3-117-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-117-5	Residues	GFTFSSYSMN	10
3-118	**Sequences**		
3-118-1	Sequence Number [ID]	118	
3-118-2	Molecule Type	AA	
3-118-3	Length	17	
3-118-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-118-5	Residues	HSSISRGNIY FADSVKG	17
3-119	**Sequences**		
3-119-1	Sequence Number [ID]	119	
3-119-2	Molecule Type	AA	
3-119-3	Length	6	
3-119-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-119-5	Residues	SISRGN	6

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3-120	**Sequences**		
3-120-1	Sequence Number [ID]	120	
3-120-2	Molecule Type	AA	
3-120-3	Length	11	
3-120-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-120-5	Residues	GSGWYGDYFD Y	11
3-121	**Sequences**		
3-121-1	Sequence Number [ID]	121	
3-121-2	Molecule Type	AA	
3-121-3	Length	5	
3-121-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-121-5	Residues	NYAMS	5
3-122	**Sequences**		
3-122-1	Sequence Number [ID]	122	
3-122-2	Molecule Type	AA	
3-122-3	Length	7	
3-122-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-122-5	Residues	GFAFSNY	7
3-123	**Sequences**		
3-123-1	Sequence Number [ID]	123	
3-123-2	Molecule Type	AA	
3-123-3	Length	10	
3-123-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-123-5	Residues	GFAFSNYAMS	10
3-124	**Sequences**		
3-124-1	Sequence Number [ID]	124	
3-124-2	Molecule Type	AA	
3-124-3	Length	17	
3-124-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-124-5	Residues	AIRGGGGSTY YADSVKG	17
3-125	**Sequences**		
3-125-1	Sequence Number [ID]	125	
3-125-2	Molecule Type	AA	
3-125-3	Length	6	
3-125-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-125-5	Residues	RGGGGS	6
3-126	**Sequences**		
3-126-1	Sequence Number [ID]	126	

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3-126-2	Molecule Type	AA	
3-126-3	Length	11	
3-126-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-126-5	Residues	DFISGTWYPD Y	11
3-127	**Sequences**		
3-127-1	Sequence Number [ID]	127	
3-127-2	Molecule Type	AA	
3-127-3	Length	5	
3-127-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-127-5	Residues	SYWIG	5
3-128	**Sequences**		
3-128-1	Sequence Number [ID]	128	
3-128-2	Molecule Type	AA	
3-128-3	Length	7	
3-128-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-128-5	Residues	GYRFTSY	7
3-129	**Sequences**		
3-129-1	Sequence Number [ID]	129	
3-129-2	Molecule Type	AA	
3-129-3	Length	10	
3-129-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-129-5	Residues	GYRFTSYWIG	10
3-130	**Sequences**		
3-130-1	Sequence Number [ID]	130	
3-130-2	Molecule Type	AA	
3-130-3	Length	17	
3-130-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-130-5	Residues	SIYPDDSDTR YSPSFQG	17
3-131	**Sequences**		
3-131-1	Sequence Number [ID]	131	
3-131-2	Molecule Type	AA	
3-131-3	Length	6	
3-131-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-131-5	Residues	YPDDSD	6
3-132	**Sequences**		
3-132-1	Sequence Number [ID]	132	
3-132-2	Molecule Type	AA	
3-132-3	Length	13	

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3-132-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-132-5	Residues	STVDYPGYSY FDY	13
3-133	**Sequences**		
3-133-1	Sequence Number [ID]	133	
3-133-2	Molecule Type	AA	
3-133-3	Length	5	
3-133-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-133-5	Residues	NYWIA	5
3-134	**Sequences**		
3-134-1	Sequence Number [ID]	134	
3-134-2	Molecule Type	AA	
3-134-3	Length	7	
3-134-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-134-5	Residues	GYTFTNY	7
3-135	**Sequences**		
3-135-1	Sequence Number [ID]	135	
3-135-2	Molecule Type	AA	
3-135-3	Length	10	
3-135-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-135-5	Residues	GYTFTNYWIA	10
3-136	**Sequences**		
3-136-1	Sequence Number [ID]	136	
3-136-2	Molecule Type	AA	
3-136-3	Length	17	
3-136-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-136-5	Residues	IIYPDGSDTR YSPSFQG	17
3-137	**Sequences**		
3-137-1	Sequence Number [ID]	137	
3-137-2	Molecule Type	AA	
3-137-3	Length	6	
3-137-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-137-5	Residues	YPDGSD	6
3-138	**Sequences**		
3-138-1	Sequence Number [ID]	138	
3-138-2	Molecule Type	AA	
3-138-3	Length	14	
3-138-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-138-5	Residues	DITSWYYGEP AFDI	14
3-139	**Sequences**		
3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	AA	
3-139-3	Length	5	
3-139-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-139-5	Residues	SSWIG	5
3-140	**Sequences**		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	AA	
3-140-3	Length	7	
3-140-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-140-5	Residues	GYSFTSS	7
3-141	**Sequences**		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	AA	
3-141-3	Length	10	
3-141-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-141-5	Residues	GYSFTSSWIG	10
3-142	**Sequences**		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	AA	
3-142-3	Length	17	
3-142-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-142-5	Residues	IIYPGDSDTR YSPSFQG	17
3-143	**Sequences**		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	AA	
3-143-3	Length	6	
3-143-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-143-5	Residues	YPGDSD	6
3-144	**Sequences**		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	AA	
3-144-3	Length	13	
3-144-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-144-5	Residues	GLSQAMTGFG FDY	13
3-145	**Sequences**		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	AA	
3-145-3	Length	5	
3-145-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-145-5	Residues	SYWIG	5
3-146	**Sequences**		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	AA	
3-146-3	Length	7	
3-146-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-146-5	Residues	GYGFTSY	7
3-147	**Sequences**		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	AA	
3-147-3	Length	10	
3-147-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-147-5	Residues	GYGFTSYWIG	10
3-148	**Sequences**		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	AA	
3-148-3	Length	17	
3-148-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-148-5	Residues	IIHPDDSDTK YSPSFQG	17
3-149	**Sequences**		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	AA	
3-149-3	Length	6	
3-149-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-149-5	Residues	HPDDSD	6
3-150	**Sequences**		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	AA	
3-150-3	Length	13	
3-150-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-150-5	Residues	SYLRGLWGGY FDY	13
3-151	**Sequences**		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	AA	
3-151-3	Length	5	
3-151-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-151-5	Residues	SSWIG	5
3-152	**Sequences**		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	AA	
3-152-3	Length	7	
3-152-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-152-5	Residues	GYTFPSS	7
3-153	**Sequences**		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	AA	
3-153-3	Length	10	
3-153-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-153-5	Residues	GYTFPSSWIG	10
3-154	**Sequences**		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	AA	
3-154-3	Length	16	
3-154-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-154-5	Residues	IIYPDTSHTR YSPSFQ	16
3-155	**Sequences**		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	AA	
3-155-3	Length	6	
3-155-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-155-5	Residues	YPDTSH	6
3-156	**Sequences**		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	AA	
3-156-3	Length	17	
3-156-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-156-5	Residues	ASYFDRGTGY SSWWMDV	17
3-157	**Sequences**		

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3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	AA	
3-157-3	Length	5	
3-157-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-157-5	Residues	QYSMS	5
3-158	**Sequences**		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	AA	
3-158-3	Length	7	
3-158-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-158-5	Residues	GFTFSQY	7
3-159	**Sequences**		
3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	AA	
3-159-3	Length	10	
3-159-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-159-5	Residues	GFTFSQYSMS	10
3-160	**Sequences**		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	AA	
3-160-3	Length	17	
3-160-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-160-5	Residues	AISGGGVSTY YADSVKG	17
3-161	**Sequences**		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	AA	
3-161-3	Length	6	
3-161-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-161-5	Residues	SGGGVS	6
3-162	**Sequences**		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	AA	
3-162-3	Length	14	
3-162-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-162-5	Residues	DISDSGGSHW YFDY	14
3-163	**Sequences**		
3-163-1	Sequence Number [ID]	163	
3-163-2	Molecule Type	AA	

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3-163-3	Length	5	
3-163-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-163-5	Residues	SYAMS	5
3-164	**Sequences**		
3-164-1	Sequence Number [ID]	164	
3-164-2	Molecule Type	AA	
3-164-3	Length	7	
3-164-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-164-5	Residues	GFTFSSY	7
3-165	**Sequences**		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	AA	
3-165-3	Length	10	
3-165-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-165-5	Residues	GFTFSSYAMS	10
3-166	**Sequences**		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	AA	
3-166-3	Length	17	
3-166-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-166-5	Residues	TISGTGGTTY YADSVKG	17
3-167	**Sequences**		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	AA	
3-167-3	Length	6	
3-167-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-167-5	Residues	SGTGGT	6
3-168	**Sequences**		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	AA	
3-168-3	Length	12	
3-168-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-168-5	Residues	VRAGIDPTAS DV	12
3-169	**Sequences**		
3-169-1	Sequence Number [ID]	169	
3-169-2	Molecule Type	AA	
3-169-3	Length	5	
3-169-4	Features	**REGION 1..5**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-169-5	Residues	NFAMS	5
3-170	**Sequences**		
3-170-1	Sequence Number [ID]	170	
3-170-2	Molecule Type	AA	
3-170-3	Length	7	
3-170-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-170-5	Residues	GFTFNNF	7
3-171	**Sequences**		
3-171-1	Sequence Number [ID]	171	
3-171-2	Molecule Type	AA	
3-171-3	Length	10	
3-171-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-171-5	Residues	GFTFNNFAMS	10
3-172	**Sequences**		
3-172-1	Sequence Number [ID]	172	
3-172-2	Molecule Type	AA	
3-172-3	Length	17	
3-172-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-172-5	Residues	GISGSGDNTY YADSVKG	17
3-173	**Sequences**		
3-173-1	Sequence Number [ID]	173	
3-173-2	Molecule Type	AA	
3-173-3	Length	6	
3-173-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-173-5	Residues	SGSGDN	6
3-174	**Sequences**		
3-174-1	Sequence Number [ID]	174	
3-174-2	Molecule Type	AA	
3-174-3	Length	15	
3-174-4	Features	**REGION 1..15**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..15	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-174-5	Residues	DRDIGLGWYS YYLDV	15
3-175	**Sequences**		
3-175-1	Sequence Number [ID]	175	
3-175-2	Molecule Type	AA	
3-175-3	Length	5	
3-175-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-175-5	Residues	SYAIS	5
3-176	**Sequences**		
3-176-1	Sequence Number [ID]	176	
3-176-2	Molecule Type	AA	
3-176-3	Length	7	
3-176-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-176-5	Residues	GGTFSSY	7
3-177	**Sequences**		
3-177-1	Sequence Number [ID]	177	
3-177-2	Molecule Type	AA	
3-177-3	Length	10	
3-177-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-177-5	Residues	GGTFSSYAIS	10
3-178	**Sequences**		
3-178-1	Sequence Number [ID]	178	
3-178-2	Molecule Type	AA	
3-178-3	Length	17	
3-178-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-178-5	Residues	EIIPIFGTAS YAQKFQG	17
3-179	**Sequences**		
3-179-1	Sequence Number [ID]	179	
3-179-2	Molecule Type	AA	
3-179-3	Length	6	
3-179-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-179-5	Residues	IPIFGT	6
3-180	**Sequences**		
3-180-1	Sequence Number [ID]	180	
3-180-2	Molecule Type	AA	
3-180-3	Length	10	
3-180-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-180-5	Residues	AGWDDSWFDY	10
3-181	**Sequences**		
3-181-1	Sequence Number [ID]	181	
3-181-2	Molecule Type	AA	
3-181-3	Length	5	
3-181-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-181-5	Residues	SYWIG	5
3-182	**Sequences**		
3-182-1	Sequence Number [ID]	182	
3-182-2	Molecule Type	AA	
3-182-3	Length	7	
3-182-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-182-5	Residues	GYSFASY	7
3-183	**Sequences**		
3-183-1	Sequence Number [ID]	183	
3-183-2	Molecule Type	AA	
3-183-3	Length	10	
3-183-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-183-5	Residues	GYSFASYWIG	10
3-184	**Sequences**		
3-184-1	Sequence Number [ID]	184	
3-184-2	Molecule Type	AA	
3-184-3	Length	17	
3-184-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-184-5	Residues	VIYPGTSETR YSPSFQG	17
3-185	**Sequences**		
3-185-1	Sequence Number [ID]	185	
3-185-2	Molecule Type	AA	
3-185-3	Length	6	
3-185-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-185-5	Residues	YPGTSE	6
3-186	**Sequences**		
3-186-1	Sequence Number [ID]	186	
3-186-2	Molecule Type	AA	
3-186-3	Length	13	
3-186-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-186-5	Residues	GLSASASGYS FQY	13
3-187	**Sequences**		
3-187-1	Sequence Number [ID]	187	
3-187-2	Molecule Type	AA	
3-187-3	Length	5	
3-187-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-187-5	Residues	DYWIG	5

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3-188	**Sequences**		
3-188-1	Sequence Number [ID]	188	
3-188-2	Molecule Type	AA	
3-188-3	Length	7	
3-188-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-188-5	Residues	GYSFTDY	7
3-189	**Sequences**		
3-189-1	Sequence Number [ID]	189	
3-189-2	Molecule Type	AA	
3-189-3	Length	10	
3-189-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-189-5	Residues	GYSFTDYWIG	10
3-190	**Sequences**		
3-190-1	Sequence Number [ID]	190	
3-190-2	Molecule Type	AA	
3-190-3	Length	17	
3-190-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-190-5	Residues	MISPGGSTTI YRPSFQG	17
3-191	**Sequences**		
3-191-1	Sequence Number [ID]	191	
3-191-2	Molecule Type	AA	
3-191-3	Length	6	
3-191-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-191-5	Residues	SPGGST	6
3-192	**Sequences**		
3-192-1	Sequence Number [ID]	192	
3-192-2	Molecule Type	AA	
3-192-3	Length	14	
3-192-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-192-5	Residues	MYTGGYGGSW YFDY	14
3-193	**Sequences**		
3-193-1	Sequence Number [ID]	193	
3-193-2	Molecule Type	AA	
3-193-3	Length	16	
3-193-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-193-5	Residues	RSSQSLVHSD GNTYLS	16
3-194	**Sequences**		
3-194-1	Sequence Number [ID]	194	

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3-194-2	Molecule Type	AA	
3-194-3	Length	7	
3-194-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-194-5	Residues	KISNRFS	7
3-195	**Sequences**		
3-195-1	Sequence Number [ID]	195	
3-195-2	Molecule Type	AA	
3-195-3	Length	9	
3-195-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-195-5	Residues	MQATQFPLT	9
3-196	**Sequences**		
3-196-1	Sequence Number [ID]	196	
3-196-2	Molecule Type	AA	
3-196-3	Length	16	
3-196-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-196-5	Residues	RSSQSLVHSD GNTYLS	16
3-197	**Sequences**		
3-197-1	Sequence Number [ID]	197	
3-197-2	Molecule Type	AA	
3-197-3	Length	7	
3-197-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-197-5	Residues	KISNRFS	7
3-198	**Sequences**		
3-198-1	Sequence Number [ID]	198	
3-198-2	Molecule Type	AA	
3-198-3	Length	9	
3-198-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-198-5	Residues	MQATQFPLT	9
3-199	**Sequences**		
3-199-1	Sequence Number [ID]	199	
3-199-2	Molecule Type	AA	
3-199-3	Length	11	
3-199-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-199-5	Residues	RASQGISNYL A	11
3-200	**Sequences**		
3-200-1	Sequence Number [ID]	200	
3-200-2	Molecule Type	AA	
3-200-3	Length	7	

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3-200-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-200-5	Residues	AASSLQS	7
3-201	**Sequences**		
3-201-1	Sequence Number [ID]	201	
3-201-2	Molecule Type	AA	
3-201-3	Length	9	
3-201-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-201-5	Residues	QQYNSYPLT	9
3-202	**Sequences**		
3-202-1	Sequence Number [ID]	202	
3-202-2	Molecule Type	AA	
3-202-3	Length	16	
3-202-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-202-5	Residues	RSSQSLVYSD ENTYLN	16
3-203	**Sequences**		
3-203-1	Sequence Number [ID]	203	
3-203-2	Molecule Type	AA	
3-203-3	Length	7	
3-203-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-203-5	Residues	QVSNRDS	7
3-204	**Sequences**		
3-204-1	Sequence Number [ID]	204	
3-204-2	Molecule Type	AA	
3-204-3	Length	9	
3-204-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-204-5	Residues	MQGTYWPPT	9
3-205	**Sequences**		
3-205-1	Sequence Number [ID]	205	
3-205-2	Molecule Type	AA	
3-205-3	Length	11	
3-205-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-205-5	Residues	RASQSVSSSL A	11
3-206	**Sequences**		
3-206-1	Sequence Number [ID]	206	
3-206-2	Molecule Type	AA	
3-206-3	Length	7	
3-206-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-206-5	Residues	GASTRAT	7
3-207	**Sequences**		
3-207-1	Sequence Number [ID]	207	
3-207-2	Molecule Type	AA	
3-207-3	Length	8	
3-207-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-207-5	Residues	QQYINWPH	8
3-208	**Sequences**		
3-208-1	Sequence Number [ID]	208	
3-208-2	Molecule Type	AA	
3-208-3	Length	11	
3-208-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-208-5	Residues	QASQDISNYL N	11
3-209	**Sequences**		
3-209-1	Sequence Number [ID]	209	
3-209-2	Molecule Type	AA	
3-209-3	Length	7	
3-209-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-209-5	Residues	GASNLET	7
3-210	**Sequences**		
3-210-1	Sequence Number [ID]	210	
3-210-2	Molecule Type	AA	
3-210-3	Length	9	
3-210-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-210-5	Residues	QQYDNFPIT	9
3-211	**Sequences**		
3-211-1	Sequence Number [ID]	211	
3-211-2	Molecule Type	AA	
3-211-3	Length	11	
3-211-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-211-5	Residues	RASQSVSSNL A	11
3-212	**Sequences**		
3-212-1	Sequence Number [ID]	212	
3-212-2	Molecule Type	AA	
3-212-3	Length	7	
3-212-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-212-5	Residues	SASTRAS	7
3-213	**Sequences**		
3-213-1	Sequence Number [ID]	213	
3-213-2	Molecule Type	AA	
3-213-3	Length	10	
3-213-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-213-5	Residues	QQYDNWPPLT	10
3-214	**Sequences**		
3-214-1	Sequence Number [ID]	214	
3-214-2	Molecule Type	AA	
3-214-3	Length	12	
3-214-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-214-5	Residues	RASQSVSSSY LA	12
3-215	**Sequences**		
3-215-1	Sequence Number [ID]	215	
3-215-2	Molecule Type	AA	
3-215-3	Length	7	
3-215-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-215-5	Residues	GASSRAT	7
3-216	**Sequences**		
3-216-1	Sequence Number [ID]	216	
3-216-2	Molecule Type	AA	
3-216-3	Length	9	
3-216-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-216-5	Residues	QQYGSSPLT	9
3-217	**Sequences**		
3-217-1	Sequence Number [ID]	217	
3-217-2	Molecule Type	AA	
3-217-3	Length	11	
3-217-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-217-5	Residues	RASQDISNYL A	11
3-218	**Sequences**		
3-218-1	Sequence Number [ID]	218	
3-218-2	Molecule Type	AA	
3-218-3	Length	7	
3-218-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-218-5	Residues	AASSLQS	7
3-219	**Sequences**		
3-219-1	Sequence Number [ID]	219	
3-219-2	Molecule Type	AA	
3-219-3	Length	9	
3-219-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-219-5	Residues	LQLNSFPFT	9
3-220	**Sequences**		
3-220-1	Sequence Number [ID]	220	
3-220-2	Molecule Type	AA	
3-220-3	Length	11	
3-220-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-220-5	Residues	RASQGISSWL A	11
3-221	**Sequences**		
3-221-1	Sequence Number [ID]	221	
3-221-2	Molecule Type	AA	
3-221-3	Length	7	
3-221-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-221-5	Residues	AASSLQS	7
3-222	**Sequences**		
3-222-1	Sequence Number [ID]	222	
3-222-2	Molecule Type	AA	
3-222-3	Length	9	
3-222-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-222-5	Residues	QQAFSFPFT	9
3-223	**Sequences**		
3-223-1	Sequence Number [ID]	223	
3-223-2	Molecule Type	AA	
3-223-3	Length	17	
3-223-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-223-5	Residues	KSSQSVLYSY NNKNYVA	17
3-224	**Sequences**		
3-224-1	Sequence Number [ID]	224	
3-224-2	Molecule Type	AA	
3-224-3	Length	7	
3-224-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-224-5	Residues	WASTRES	7
3-225	**Sequences**		

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3-225-1	Sequence Number [ID]	225	
3-225-2	Molecule Type	AA	
3-225-3	Length	8	
3-225-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-225-5	Residues	QQYYSTLT	8
3-226	**Sequences**		
3-226-1	Sequence Number [ID]	226	
3-226-2	Molecule Type	AA	
3-226-3	Length	12	
3-226-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-226-5	Residues	RASQSVSSSY LA	12
3-227	**Sequences**		
3-227-1	Sequence Number [ID]	227	
3-227-2	Molecule Type	AA	
3-227-3	Length	7	
3-227-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-227-5	Residues	DASSRAT	7
3-228	**Sequences**		
3-228-1	Sequence Number [ID]	228	
3-228-2	Molecule Type	AA	
3-228-3	Length	9	
3-228-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-228-5	Residues	QQYGSSPLT	9
3-229	**Sequences**		
3-229-1	Sequence Number [ID]	229	
3-229-2	Molecule Type	AA	
3-229-3	Length	13	
3-229-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-229-5	Residues	SGSSSNIGSN YVY	13
3-230	**Sequences**		
3-230-1	Sequence Number [ID]	230	
3-230-2	Molecule Type	AA	
3-230-3	Length	7	
3-230-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-230-5	Residues	RNNQRPS	7
3-231	**Sequences**		
3-231-1	Sequence Number [ID]	231	
3-231-2	Molecule Type	AA	

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3-231-3	Length	11	
3-231-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-231-5	Residues	AAWDDSLSGV V	11
3-232	**Sequences**		
3-232-1	Sequence Number [ID]	232	
3-232-2	Molecule Type	AA	
3-232-3	Length	13	
3-232-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-232-5	Residues	SGSRSNIGSN YVY	13
3-233	**Sequences**		
3-233-1	Sequence Number [ID]	233	
3-233-2	Molecule Type	AA	
3-233-3	Length	7	
3-233-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-233-5	Residues	RNNQRPS	7
3-234	**Sequences**		
3-234-1	Sequence Number [ID]	234	
3-234-2	Molecule Type	AA	
3-234-3	Length	11	
3-234-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-234-5	Residues	ASWDGSLSAV V	11
3-235	**Sequences**		
3-235-1	Sequence Number [ID]	235	
3-235-2	Molecule Type	AA	
3-235-3	Length	13	
3-235-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-235-5	Residues	SGSSSNIGSN YVY	13
3-236	**Sequences**		
3-236-1	Sequence Number [ID]	236	
3-236-2	Molecule Type	AA	
3-236-3	Length	7	
3-236-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-236-5	Residues	RNNQRPS	7
3-237	**Sequences**		
3-237-1	Sequence Number [ID]	237	
3-237-2	Molecule Type	AA	
3-237-3	Length	11	
3-237-4	Features	**REGION 1..11**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-237-5	Residues	ATWDDSLGSP V	11
3-238	**Sequences**		
3-238-1	Sequence Number [ID]	238	
3-238-2	Molecule Type	AA	
3-238-3	Length	11	
3-238-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-238-5	Residues	RASQSISRYL N	11
3-239	**Sequences**		
3-239-1	Sequence Number [ID]	239	
3-239-2	Molecule Type	AA	
3-239-3	Length	7	
3-239-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-239-5	Residues	AASILQT	7
3-240	**Sequences**		
3-240-1	Sequence Number [ID]	240	
3-240-2	Molecule Type	AA	
3-240-3	Length	10	
3-240-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-240-5	Residues	QQSYSTTMWT	10
3-241	**Sequences**		
3-241-1	Sequence Number [ID]	241	
3-241-2	Molecule Type	AA	
3-241-3	Length	13	
3-241-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-241-5	Residues	SGSSSNIGSN YVN	13
3-242	**Sequences**		
3-242-1	Sequence Number [ID]	242	
3-242-2	Molecule Type	AA	
3-242-3	Length	7	
3-242-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-242-5	Residues	GDYQRPS	7
3-243	**Sequences**		
3-243-1	Sequence Number [ID]	243	
3-243-2	Molecule Type	AA	
3-243-3	Length	12	
3-243-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-243-5	Residues	ATRDDSLSGS VV	12
3-244	**Sequences**		
3-244-1	Sequence Number [ID]	244	
3-244-2	Molecule Type	AA	
3-244-3	Length	11	
3-244-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-244-5	Residues	RASQSIYDYL H	11
3-245	**Sequences**		
3-245-1	Sequence Number [ID]	245	
3-245-2	Molecule Type	AA	
3-245-3	Length	7	
3-245-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-245-5	Residues	DASNLQS	7
3-246	**Sequences**		
3-246-1	Sequence Number [ID]	246	
3-246-2	Molecule Type	AA	
3-246-3	Length	10	
3-246-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-246-5	Residues	QQSYTTPLFT	10
3-247	**Sequences**		
3-247-1	Sequence Number [ID]	247	
3-247-2	Molecule Type	AA	
3-247-3	Length	11	
3-247-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-247-5	Residues	RASQYIGRYL N	11
3-248	**Sequences**		
3-248-1	Sequence Number [ID]	248	
3-248-2	Molecule Type	AA	
3-248-3	Length	7	
3-248-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-248-5	Residues	GATSLAS	7
3-249	**Sequences**		
3-249-1	Sequence Number [ID]	249	
3-249-2	Molecule Type	AA	
3-249-3	Length	10	
3-249-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-249-5	Residues	QQSYSTTSPT	10
3-250	**Sequences**		
3-250-1	Sequence Number [ID]	250	
3-250-2	Molecule Type	AA	
3-250-3	Length	13	
3-250-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-250-5	Residues	SGSTSNIGRN YVY	13
3-251	**Sequences**		
3-251-1	Sequence Number [ID]	251	
3-251-2	Molecule Type	AA	
3-251-3	Length	7	
3-251-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-251-5	Residues	RTNQRPS	7
3-252	**Sequences**		
3-252-1	Sequence Number [ID]	252	
3-252-2	Molecule Type	AA	
3-252-3	Length	11	
3-252-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-252-5	Residues	AAWDDSLSGR V	11
3-253	**Sequences**		
3-253-1	Sequence Number [ID]	253	
3-253-2	Molecule Type	AA	
3-253-3	Length	13	
3-253-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-253-5	Residues	SGSSSNIGSN YVY	13
3-254	**Sequences**		
3-254-1	Sequence Number [ID]	254	
3-254-2	Molecule Type	AA	
3-254-3	Length	7	
3-254-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-254-5	Residues	MNNQRPS	7
3-255	**Sequences**		
3-255-1	Sequence Number [ID]	255	
3-255-2	Molecule Type	AA	
3-255-3	Length	11	
3-255-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-255-5	Residues	AAWDDSLSAV V	11

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3-256	**Sequences**		
3-256-1	Sequence Number [ID]	256	
3-256-2	Molecule Type	AA	
3-256-3	Length	13	
3-256-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-256-5	Residues	SGSNSNIGTN YVS	13
3-257	**Sequences**		
3-257-1	Sequence Number [ID]	257	
3-257-2	Molecule Type	AA	
3-257-3	Length	7	
3-257-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-257-5	Residues	RSSRRPS	7
3-258	**Sequences**		
3-258-1	Sequence Number [ID]	258	
3-258-2	Molecule Type	AA	
3-258-3	Length	12	
3-258-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-258-5	Residues	AAWDGSLSGH WV	12
3-259	**Sequences**		
3-259-1	Sequence Number [ID]	259	
3-259-2	Molecule Type	AA	
3-259-3	Length	11	
3-259-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-259-5	Residues	RASQSIDTYL N	11
3-260	**Sequences**		
3-260-1	Sequence Number [ID]	260	
3-260-2	Molecule Type	AA	
3-260-3	Length	7	
3-260-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-260-5	Residues	SASSLHS	7
3-261	**Sequences**		
3-261-1	Sequence Number [ID]	261	
3-261-2	Molecule Type	AA	
3-261-3	Length	10	
3-261-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-261-5	Residues	QQSYSTTAWT	10
3-262	**Sequences**		
3-262-1	Sequence Number [ID]	262	

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3-262-2	Molecule Type	AA	
3-262-3	Length	11	
3-262-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-262-5	Residues	RASQSIGQSL N	11
3-263	**Sequences**		
3-263-1	Sequence Number [ID]	263	
3-263-2	Molecule Type	AA	
3-263-3	Length	7	
3-263-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-263-5	Residues	GASSLQS	7
3-264	**Sequences**		
3-264-1	Sequence Number [ID]	264	
3-264-2	Molecule Type	AA	
3-264-3	Length	9	
3-264-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-264-5	Residues	QQSYSTPIT	9
3-265	**Sequences**		
3-265-1	Sequence Number [ID]	265	
3-265-2	Molecule Type		
3-265-3	Length		
3-265-4	Features		
	Location/Qualifiers		
	NonEnglishQualifier Value		
3-265-5	Residues	000	3
3-266	**Sequences**		
3-266-1	Sequence Number [ID]	266	
3-266-2	Molecule Type	AA	
3-266-3	Length	21	
3-266-4	Features	**source 1..21**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-266-5	Residues	MALPVTALLL PLALLLHAAR P	21
3-267	**Sequences**		
3-267-1	Sequence Number [ID]	267	
3-267-2	Molecule Type	AA	
3-267-3	Length	16	
3-267-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-267-5	Residues	GLAVSTISSF FPPGYQ	16
3-268	**Sequences**		
3-268-1	Sequence Number [ID]	268	
3-268-2	Molecule Type	AA	
3-268-3	Length	45	
3-268-4	Features	**source 1..45**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-268-5	Residues	TTTPAPRPPT PAPTIASQPL SLRPEACRPA AGGAVHTRGL DFACD	45
3-269	**Sequences**		
3-269-1	Sequence Number [ID]	269	

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3-269-2	Molecule Type	AA
3-269-3	Length	231
3-269-4	Features	**source 1..231**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-269-5	Residues	EPKSPDKTHT CPPCPAPPVA GPSVFLFPPK PKDTLMIART PEVTCVVVDV SHEDPEVKFN 60 WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI 120 SKAKGQPREP QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 180 VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K 231
3-270	**Sequences**	
3-270-1	Sequence Number [ID]	270
3-270-2	Molecule Type	AA
3-270-3	Length	24
3-270-4	Features	**source 1..24**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-270-5	Residues	IYIWAPLAGT CGVLLLSLVI TLYC 24
3-271	**Sequences**	
3-271-1	Sequence Number [ID]	271
3-271-2	Molecule Type	AA
3-271-3	Length	42
3-271-4	Features	**source 1..42**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-271-5	Residues	KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC EL 42
3-272	**Sequences**	
3-272-1	Sequence Number [ID]	272
3-272-2	Molecule Type	AA
3-272-3	Length	112
3-272-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-272-5	Residues	RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112
3-273	**Sequences**	
3-273-1	Sequence Number [ID]	273
3-273-2	Molecule Type	AA
3-273-3	Length	52
3-273-4	Features	**source 1..52**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-273-5	Residues	FFIPLLVVIL FAVDTGLFIS TQQQVTFLLK IKRTRKGFRL LNPHPKPNPK NN 52
3-274	**Sequences**	
3-274-1	Sequence Number [ID]	274
3-274-2	Molecule Type	AA
3-274-3	Length	215
3-274-4	Features	**source 1..215**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-274-5	Residues	MDTESNRRAN LALPQEPSSV PAFEVLEISP QEVSSGRLLK SASSPPLHTW LTVLKKEQEF 60 LGVTQILTAM ICLCFGTVVC SVLDISHIEG DIFSSFKAGY PFWGAIFFSI SGMLSIISER 120 RNATYLVRGS LGANTASSIA GGTGITILII NLKKSLAYIH IHSCQKFFET KCFMASFSTE 180 IVVMMLFLTI LGLGSAVSLT ICGAGEELKG NKVPE 215
3-275	**Sequences**	
3-275-1	Sequence Number [ID]	275
3-275-2	Molecule Type	AA
3-275-3	Length	42
3-275-4	Features	**source 1..42**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-275-5	Residues	KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC EL 42
3-276	**Sequences**	

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3-276-1	Sequence Number [ID]	276	
3-276-2	Molecule Type	AA	
3-276-3	Length	41	
3-276-4	Features	**source 1..41**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-276-5	Residues	RSKRSRGGHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR S	41
3-277	**Sequences**		
3-277-1	Sequence Number [ID]	277	
3-277-2	Molecule Type	AA	
3-277-3	Length	18	
3-277-4	Features	**source 1..18**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-277-5	Residues	MIPAVVLLLL LLVEQAAA	18
3-278	**Sequences**		
3-278-1	Sequence Number [ID]	278	
3-278-2	Molecule Type	AA	
3-278-3	Length	43	
3-278-4	Features	**source 1..43**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-278-5	Residues	LGEPQLCYIL DAILFLYGIV LTLLYCRLKI QVRKAAITSY EKS	43
3-279	**Sequences**		
3-279-1	Sequence Number [ID]	279	
3-279-2	Molecule Type	AA	
3-279-3	Length	22	
3-279-4	Features	**source 1..22**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-279-5	Residues	GSGATNFSLL KQAGDVEENP GP	22
3-280	**Sequences**		
3-280-1	Sequence Number [ID]	280	
3-280-2	Molecule Type	AA	
3-280-3	Length	21	
3-280-4	Features	**source 1..21**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-280-5	Residues	GSGEGRGSLL TCGDVEENPG P	21
3-281	**Sequences**		
3-281-1	Sequence Number [ID]	281	
3-281-2	Molecule Type	AA	
3-281-3	Length	530	
3-281-4	Features	**REGION 1..530**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..530	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-281-5	Residues	LTPQQVVAIA SNGGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL	60
		PVLCQAHGLT PQQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA	120
		LETVQRLLPV LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA	180
		SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASNIGGK QALETVQALL PVLCQAHGLT	240
		PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA LETVQALLPV	300
		LCQAHGLTPQ QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNIGGKQALE	360
		TVQALLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT PEQVVAIASN	420
		IGGKQALETV QALLPVLCQA HGLTPQQVVA IASNGGGKQA LETVQRLLPV LCQAHGLTPE	480
		QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE	530
3-282	**Sequences**		
3-282-1	Sequence Number [ID]	282	
3-282-2	Molecule Type	AA	
3-282-3	Length	530	
3-282-4	Features	**REGION 1..530**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-282-5	Residues	LTPEQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL 60 PVLCQAHGLT PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA 120 LETVQALLPV LCQAHGLTPQ QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 180 SHDGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PQQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNNGGKQA LETVQRLLPV 300 LCQAHGLTPQ QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPEQVVAIA SNIGGKQALE 360 TVQALLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL PVLCQAHGLT PEQVVAIASN 420 IGGKQALETV QALLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV LCQAHGLTPQ 480 QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-283	**Sequences**	
3-283-1	Sequence Number [ID]	283
3-283-2	Molecule Type	AA
3-283-3	Length	530
3-283-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-283-5	Residues	LTPQQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL 60 PVLCQAHGLT PQQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA 120 LETVQRLLPV LCQAHGLTPQ QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPQQVVAIA 180 SNGGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL PVLCQAHGLT 240 PEQVVAIASN IGGKQALETV QALLPVLCQA HGLTPQQVVA IASNNGGKQA LETVQRLLPV 300 LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA SHDGGKQALE 360 TVQRLLPVLC QAHGLTPEQV VAIASNIGGK QALETVQALL PVLCQAHGLT PQQVVAIASN 420 GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV LCQAHGLTPE 480 QVVAIASNIG GKQALETVQA LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-284	**Sequences**	
3-284-1	Sequence Number [ID]	284
3-284-2	Molecule Type	AA
3-284-3	Length	539
3-284-4	Features	**REGION 1..539**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..539
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-284-5	Residues	NPQRSTVWYL TPQQVVAIAS NNGGKQALET VQRLLPVLCQ AHGLTPQQVV AIASNGGGKQ 60 ALETVQRLLP VLCQAHGLTP QQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPQQVVAI 120 ASNNGGKQAL ETVQRLLPVL CQAHGLTPEQ VVAIASHDGG KQALETVQRL LPVLCQAHGL 180 TPEQVVAIAS HDGGKQALET VQRLLPVLCQ AHGLTPQQVV AIASNGGGKQ ALETVQRLLP 240 VLCQAHGLTP QQVVAIASNG GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNGGGKQAL 300 ETVQRLLPVL CQAHGLTPQQ VVAIASNGGG KQALETVQRL LPVLCQAHGL TPQQVVAIAS 360 NNGGKQALET VQRLLPVLCQ AHGLTPQQVV AIASNNGGKQ ALETVQRLLP VLCQAHGLTP 420 QQVVAIASNN GGKQALETVQ RLLPVLCQAH GLTPQQVVAI ASNGGGKQAL ETVQRLLPVL 480 CQAHGLTPQQ VVAIASNNGG KQALETVQRL LPVLCQAHGL TPQQVVAIAS NGGGRPALE 539
3-285	**Sequences**	
3-285-1	Sequence Number [ID]	285
3-285-2	Molecule Type	AA
3-285-3	Length	530
3-285-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-285-5	Residues	LTPEQVVAIA SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL 60 PVLCQAHGLT PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA 120 LETVQALLPV LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 180 SHDGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL PVLCQAHGLT 240 PQQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA LETVQALLPV 300 LCQAHGLTPQ QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNNGGKQALE 360 TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT PEQVVAIASH 420 DGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPE 480 QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-286	**Sequences**	
3-286-1	Sequence Number [ID]	286

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3-286-2	Molecule Type	AA
3-286-3	Length	530
3-286-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-286-5	Residues	LTPQQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL 60 PVLCQAHGLT PQQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA 120 LETVQALLPV LCQAHGLTPQ QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 180 SNIGGKQALE TVQALLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA LETVQRLLPV 300 LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGKQALE 360 TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL PVLCQAHGLT PEQVVAIASH 420 DGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA LETVQRLLPV LCQAHGLTPQ 480 QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-287	**Sequences**	
3-287-1	Sequence Number [ID]	287
3-287-2	Molecule Type	AA
3-287-3	Length	530
3-287-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-287-5	Residues	LTPQQVVAIA SNGGGKQALE TVQRLLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL 60 PVLCQAHGLT PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA 120 LETVQRLLPV LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 180 SHDGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PEQVVAIASN IGGKQALETV QALLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV 300 LCQAHGLTPQ QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPEQVVAIA SHDGGKQALE 360 TVQRLLPVLC QAHGLTPEQV VAIASNIGGK QALETVQALL PVLCQAHGLT PEQVVAIASH 420 DGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV LCQAHGLTPE 480 QVVAIASNIG GKQALETVQA LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-288	**Sequences**	
3-288-1	Sequence Number [ID]	288
3-288-2	Molecule Type	AA
3-288-3	Length	530
3-288-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-288-5	Residues	LTPQQVVAIA SNGGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL 60 PVLCQAHGLT PEQVVAIASH DGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA 120 LETVQRLLPV LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA 180 SNGGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PEQVVAIASN IGGKQALETV QALLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV 300 LCQAHGLTPE QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGKQALE 360 TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL PVLCQAHGLT PQQVVAIASN 420 GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA LETVQALLPV LCQAHGLTPE 480 QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-289	**Sequences**	
3-289-1	Sequence Number [ID]	289
3-289-2	Molecule Type	AA
3-289-3	Length	530
3-289-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-289-5	Residues	LTPQQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNNGGK QALETVQRLL 60 PVLCQAHGLT PQQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA 120 LETVQRLLPV LCQAHGLTPQ QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPQQVVAIA 180 SNGGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PQQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV 300 LCQAHGLTPQ QVVAIASNGG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGKQALE 360

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		TVQRLLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL PVLCQAHGLT PEQVVAIASH 420 DGGKQALETV QRLLPVLCQA HGLTPEQVVA IASNIGGKQA LETVQALLPV LCQAHGLTPQ 480 QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-290	**Sequences**	
3-290-1	Sequence Number [ID]	290
3-290-2	Molecule Type	AA
3-290-3	Length	530
3-290-4	Features	**REGION 1..530**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..530
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-290-5	Residues	LTPQQVVAIA SNNGGKQALE TVQRLLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL 60 PVLCQAHGLT PQQVVAIASN NGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNGGGKQA 120 LETVQRLLPV LCQAHGLTPQ QVVAIASNNG GKQALETVQR LLPVLCQAHG LTPEQVVAIA 180 SNIGGKQALE TVQALLPVLC QAHGLTPQQV VAIASNGGGK QALETVQRLL PVLCQAHGLT 240 PQQVVAIASN GGGKQALETV QRLLPVLCQA HGLTPEQVVA IASHDGGKQA LETVQRLLPV 300 LCQAHGLTPE QVVAIASNIG GKQALETVQA LLPVLCQAHG LTPQQVVAIA SNNGGKQALE 360 TVQRLLPVLC QAHGLTPEQV VAIASHDGGK QALETVQRLL PVLCQAHGLT PQQVVAIASN 420 GGGKQALETV QRLLPVLCQA HGLTPQQVVA IASNNGGKQA LETVQRLLPV LCQAHGLTPE 480 QVVAIASHDG GKQALETVQR LLPVLCQAHG LTPQQVVAIA SNGGGRPALE 530
3-291	**Sequences**	
3-291-1	Sequence Number [ID]	291
3-291-2	Molecule Type	AA
3-291-3	Length	136
3-291-4	Features	**REGION 1..136**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..136
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-291-5	Residues	CPYSNPSLCS GGGGSELPTQ GTFSNVSTNV SPAKPTTTAC PYSNPSLCSG GGGSPAPRPP 60 TPAPTIASQP LSLRPEACRP AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC 120 NHRNRRRVCK CPRPVV 136
3-292	**Sequences**	
3-292-1	Sequence Number [ID]	292
3-292-2	Molecule Type	AA
3-292-3	Length	157
3-292-4	Features	**REGION 1..157**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..157
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-292-5	Residues	MGTSLLCWMA LCLLGADHAD ACPYSNPSLC SGGGGSELPT QGTFSNVSTN VSPAKPTTTA 60 CPYSNPSLCS GGGGSPAPRP PTPAPTIASQ PLSLRPEACR PAAGGAVHTR GLDFACDIYI 120 WAPLAGTCGV LLLSLVITLY CNHRNRRRVC KCPRPVV 157
3-293	**Sequences**	
3-293-1	Sequence Number [ID]	293
3-293-2	Molecule Type	AA
3-293-3	Length	9
3-293-4	Features	**REGION 1..9**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..9
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-293-5	Residues	CPYSNPSLC 9
3-294	**Sequences**	
3-294-1	Sequence Number [ID]	294
3-294-2	Molecule Type	AA
3-294-3	Length	37
3-294-4	Features	**REGION 1..37**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..37
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-294-5	Residues	GSGGGGSCPY SNPSLCSGGG GSCPYSNPSL CSGGGGS 37

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3-295	**Sequences**	
3-295-1	Sequence Number [ID]	295
3-295-2	Molecule Type	AA
3-295-3	Length	24
3-295-4	Features	**REGION 1..24**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..24
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-295-5	Residues	ELPTQGTFSN VSTNVSPAKP TTTA 24
3-296	**Sequences**	
3-296-1	Sequence Number [ID]	296
3-296-2	Molecule Type	AA
3-296-3	Length	15
3-296-4	Features	**REGION 1..15**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..15
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-296-5	Residues	GGGGSGGGGS GGGGS 15
3-297	**Sequences**	
3-297-1	Sequence Number [ID]	297
3-297-2	Molecule Type	DNA
3-297-3	Length	369
3-297-4	Features	**misc_feature 1..369**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..369
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-297-5	Residues	caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60 acctgcaccg tctctgggtt ctcactcagt aatgctagaa tgggtgtgac ctggatccgt 120 cagcccccag ggaaggccct ggagtggctt gcacacattt tttcgaatga cgaaaaatcc 180 tacagtacat ctctgaagag caggctcacc atctccaagg acacttccaa aacccaggtg 240 gtccttacca tgaccaacat ggaccctgtg gacacagcca catattactg tgcacggata 300 cgagattact atgacattag tagttattat gactactggg gccagggaac cctggtcagc 360 gtctcctca 369
3-298	**Sequences**	
3-298-1	Sequence Number [ID]	298
3-298-2	Molecule Type	DNA
3-298-3	Length	321
3-298-4	Features	**misc_feature 1..321**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..321
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-298-5	Residues	gacatccaga tgacccagtc tccatctgcc atgtctgcat ctgtaggaga cagagtcacc 60 atcacttgtc gggcgagtca ggacattagc aattatttag cctggtttca gcagaaacca 120 gggaaagtcc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180 aggttcagcg gcagtggatc ggggacagaa ttcactctca caatcagcag cctgctgcct 240 gaagattttg caacttatta ctgtctacag cttaatagtt tcccgttcac ttttggcgga 300 gggaccaagg tggagatcaa c 321
3-299	**Sequences**	
3-299-1	Sequence Number [ID]	299
3-299-2	Molecule Type	DNA
3-299-3	Length	372
3-299-4	Features	**misc_feature 1..372**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..372
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-299-5	Residues	gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60 tcctgtgtag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120 ccagggaagg ggctggagtg ggtggccagc ataaagcaag atggaagtga gaaatactat 180 gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcagtgtat 240 ctgcaaatga acagcctgag agccgaggac acgggtgtgt attactgtgc gagagaagga 300

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		gtcaactggg gatggagact ctactggcac ttcgatctct ggggccgtgg aaccctggtc 360 actgtctcct ca 372
3-300	**Sequences**	
3-300-1	Sequence Number [ID]	300
3-300-2	Molecule Type	DNA
3-300-3	Length	336
3-300-4	Features	**misc_feature 1..336**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..336
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-300-5	Residues	gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60 atcaactgca agtccagcca gagtgtttta tacagctaca acaataagaa ctacgtagct 120 tggtaccagc agaaaccagg acaacctcct aacctactca ttttctgggc atctacccgg 180 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240 atcagcagcc tgcaggctga agatgtggca gtttactact gtcagcaata ttatagtacg 300 ctcactttcg gcggagggac caaggtggag atcaaa 336
3-301	**Sequences**	
3-301-1	Sequence Number [ID]	301
3-301-2	Molecule Type	DNA
3-301-3	Length	357
3-301-4	Features	**misc_feature 1..357**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..357
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-301-5	Residues	gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60 tcctgtgcag tctctggatt caccttcagt aaccataaca tacactgggt ccgccaggct 120 ccagggaagg ggctggagtg gatttcatac attagtcgaa gtagtagtac catatattac 180 gcagactctg tgaagggccg attcacaatc tccagagaca atgccaagaa ctcactgtat 240 ctgcaaatga acagcctgag agacgaagac acggctgtgt attactgtgc gagagatcac 300 gctcagtggt acggtatgga cgtttggggc caagggacca cggtcaccgt ctcctca 357
3-302	**Sequences**	
3-302-1	Sequence Number [ID]	302
3-302-2	Molecule Type	DNA
3-302-3	Length	321
3-302-4	Features	**misc_feature 1..321**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..321
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-302-5	Residues	gacatccaga tgacccagtc tccatcttcc gtgtctgcat cggtaggaga cagagtcacc 60 atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120 gggaaagccc ctaaggtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240 gaagattttg caacttacta ttgtcaacag gctttcagtt tcccattcac tttcggccct 300 gggaccaaag tggatatcaa a 321
3-303	**Sequences**	
3-303-1	Sequence Number [ID]	303
3-303-2	Molecule Type	DNA
3-303-3	Length	366
3-303-4	Features	**misc_feature 1..366**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..366
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-303-5	Residues	gaagtgcagc ttgtccagag cggagccgaa gtgaagaagc ctggcgagag cctgaagatc 60 agctgcaagg gctccggata tcgcttcaca agttactgga tagggtgggt gcgccagatg 120 cctggtaagg gactggaatg gatgggctct atatatcctg atgattccga cacacgttat 180 agcccaagct ttcagggcca ggtcacaatc agcgctgaca agagcatcag caccgcctac 240 cttcagtggt cgtctctgaa ggccagcgac accgcaatgt actactgcgc ctctagcaca 300 gttgactacc cgggatacag ttacttcgac tactggggcc aaggtacact ggtcaccgtc 360 agcagc 366
3-304	**Sequences**	
3-304-1	Sequence Number [ID]	304
3-304-2	Molecule Type	DNA
3-304-3	Length	336

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3-304-4	Features	**misc_feature 1..336**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..336
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-304-5	Residues	gagctccaga gcgtgctgac ccagcctcct agcgcaagcg gcacccctgg acagcgtgtg 60 acaattagct gtagcggaag tcgtagcaat atcggatcaa actatgtgta ttggtatcag 120 caattgcccg gtacagcacc caaattgctc atatatagaa ataatcagag acctagcgga 180 gtgcctgatc gttttagcgg tagcaaaagc ggcaccagcg catcactggc aatttcaggc 240 ctgcgtagcg aagatgaggc ggattattac tgtgcgagtt gggatggttc gctgagtgct 300 gttgtgttcg gcaccggtac aaaactgacc gttctg 336
3-305	**Sequences**	
3-305-1	Sequence Number [ID]	305
3-305-2	Molecule Type	DNA
3-305-3	Length	378
3-305-4	Features	**misc_feature 1..378**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..378
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-305-5	Residues	gaagtgcagc ttgtccagag cggagccgaa gtgaagaagc ctggcgagag cctgaagatc 60 agctgcaagg gctccggata cacctttcct tcatcatgga taggttgggt gcgccagatg 120 cctggtaagg gactggaatg gatgggcatc atataccctg atactagcca tacccgttac 180 agcccaagct ttcagggcca ggtcacaatc agcgctgaca agagcatcag caccgcctac 240 cttcagtggt cgtctctgaa ggccagcgac accgcaatgt actactgtgc ccgtgcgagc 300 tatttcgatc gtggaacagg gtatagttct tggtggatgg atgtgtgggg ccaaggtaca 360 ctggtcaccg tcagcagc 378
3-306	**Sequences**	
3-306-1	Sequence Number [ID]	306
3-306-2	Molecule Type	DNA
3-306-3	Length	330
3-306-4	Features	**misc_feature 1..330**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..330
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-306-5	Residues	gagctcgata ttcagatgac ccagagccct agcagcctga gcgcaagcgt gggcgataga 60 gtgaccatta cctgtagggc ctcacaatcc atatacgact atttgcactg gtatcagcag 120 aaacccggga aagcacccaa actgctgatt tacgatgctt ccaacctaca gagtggcgtt 180 ccttcacgtt ttagcggtag cggttcaggc accgatttca ccctgaccat tagcagcctt 240 cagcccgaag atttcgctac gtattattgc cagcaatcat acaccacgcc gttgtttaca 300 ttcggccagg gtaccaaagt ggaaatcaaa 330
3-307	**Sequences**	
3-307-1	Sequence Number [ID]	307
3-307-2	Molecule Type	DNA
3-307-3	Length	366
3-307-4	Features	**misc_feature 1..366**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..366
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-307-5	Residues	gaagtgcagc ttgtccagag cggagccgaa gtgaagaagc ctggcgagag cctgaagatc 60 agctgcaagg gctccggata cggattcaca agttattgga taggttgggt gcgccagatg 120 cctggtaagg gactggaatg gatgggtatc attcatcccg atgatagcga caccaaatac 180 agcccaagct ttcagggcca ggtcacaatc agcgctgaca agagcatcag caccgcctac 240 cttcagtggt cgtctctgaa ggccagcgac accgcaatgt actactgtgc ctctagctat 300 ttgcgtggct tgtggggagg ctattttgac tattggggcc aaggtacact ggtcaccgtc 360 agcagc 366
3-308	**Sequences**	
3-308-1	Sequence Number [ID]	308
3-308-2	Molecule Type	DNA
3-308-3	Length	339
3-308-4	Features	**misc_feature 1..339**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..339
		mol_type=other DNA
		organism=synthetic construct

	NonEnglishQualifier Value	
3-308-5	Residues	gagctccaga gcgtgctgac ccagcctcct agcgcaagcg gcacccctgg acagcgtgtg 60 acaattagct gtagcggatc aagctcaaac attggctcaa attatgtgaa ttggtatcag 120 caattgcccg gtacagcacc caaactgctc atttatggag attatcaacg acctagcgga 180 gtgcctgatc gttttagcgg tagcaaaagc ggcaccagcg catcactggc aatttcaggc 240 ctgcgtagcg aagatgaggc ggattattac tgtgctaccc gcgacgattc gttatctggg 300 tctgtcgttt ttggcaccgg tacaaaactg accgtgctg 339
3-309	**Sequences**	
3-309-1	Sequence Number [ID]	309
3-309-2	Molecule Type	DNA
3-309-3	Length	366
3-309-4	Features	**misc_feature 1..366**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..366
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-309-5	Residues	gaagtgcagc ttgtccagag cggagccgaa gtgaagaagc ctggcgagag cctgaagatc 60 agctgcaagg gctccggata cagttttgcc tcatactgga tcggttgggt gcgccagatg 120 cctggtaagg gactggaatg gatgggcgta atttaccccg gaactagcga gacacgttac 180 agcccaagct ttcagggcca ggtcacaatc agcgctgaca agagcatcag caccgcctac 240 cttcagtggt cgtctctgaa ggccagcgac accgcaatgt actactgcgc taaagggttg 300 agtgcgagtg caagtggata ttctttccaa tattggggcc aaggtacact ggtcaccgtc 360 agcagc 366
3-310	**Sequences**	
3-310-1	Sequence Number [ID]	310
3-310-2	Molecule Type	DNA
3-310-3	Length	330
3-310-4	Features	**misc_feature 1..330**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..330
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-310-5	Residues	gagctcgata ttcagatgac ccagagccct agcagcctga gcgcaagcgt gggcgataga 60 gtgaccatta cctgtagggc ctcacaaagc atcgacacat atttaaactg gtatcagcag 120 aaacccggga aagcacccaa actgctgatt tattcagcta gtagcctaca cagtggcgtt 180 ccttcacgtt ttagcggtag cggttcaggc accgatttca ccctgaccat tagcagcctt 240 cagcccgaag atttcgctac gtattattgc caacaatcat acagcacaac tgcttggaca 300 ttcggccagg gtaccaaagt ggaaatcaaa 330
3-311	**Sequences**	
3-311-1	Sequence Number [ID]	311
3-311-2	Molecule Type	AA
3-311-3	Length	494
3-311-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-311-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTF SSYGFSWVRQ 60 APGQGLEWMG GIIPIFGSAN YAQKFQGRVT ITADKSTSTV YMELISLRSE DTAVYYCARG 120 GSSSPFAYWG QGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IVMTQNPLSS PVTLGQPASI 180 SCRSSQSLVH SDGNTYLSWL QQRPGQSPRL LIYKISNRFS GVPDRFSGSG AGTDFTLKIS 240 RVEAEDVGVY YCMQATQFPL TIGGGSKVEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-312	**Sequences**	
3-312-1	Sequence Number [ID]	312
3-312-2	Molecule Type	AA
3-312-3	Length	494
3-312-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-312-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTF SSYGFSWVRQ 60 APGQGLEWMG GIIPIFGTAN YAQKFQGRVT ITADKSTSTV FMELISLRSE YTAVYYCARG 120

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		GSSSPFAYWG QGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IVMTQTPLSS PVTLGQPASI 180 SCRSSQSLVH SDGNTYLSWL QQRPGQSPRL LIYKISNRFS GVPDRFSGSG AGTDFTLKIS 240 RVEAEDVGVY YCMQATQFPL TIGGGSKVEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-313	**Sequences**	
3-313-1	Sequence Number [ID]	313
3-313-2	Molecule Type	AA
3-313-3	Length	483
3-313-4	Features	**REGION 1..483**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..483** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-313-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SSYYWNWIRQ 60 PPGKGLEWIG YIYYSGSTNY NPSLKSRVTI SVDTSKNQFS LKLRSVTAAD TAVYYCARDI 120 RTWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSDIQMTQS PSSLSASVGD RVTITCRASQ 180 GISNYLAWFQ QKPGKAPKSL IYAASSLQSG VPSKFSGSGS GTDFTLTISS LQPEDFATYY 240 CQQYNSYPLT FGGGTKVEIK TTTPAPRPPT PAPTIASQPL SLRPEACRPA AGGAVHTRGL 300 DFACDIYIWA PLAGTCGVLL LSLVITLYCK RGRKKLLYIF KQPFMRPVQT TQEEDGCSCR 360 FPEEEEGGCE LRVKFSRSAD APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP 420 RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL 480 PPR 483
3-314	**Sequences**	
3-314-1	Sequence Number [ID]	314
3-314-2	Molecule Type	AA
3-314-3	Length	493
3-314-4	Features	**REGION 1..493**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..493** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-314-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAASGFTF RNSWMSWVRQ 60 APGKGLEWVA NIKRDGSEKY YVDSVKGRFT ISRDNAKNSL YLQMNSLRAE DTAVYYCARD 120 QTGSFDYWGQ GTLVTVSSGG GGSGGGGSGG GGSGGGGSDV VMTQSPLSLP VTLGQPASIS 180 CRSSQSLVYS DENTYLNWFQ QRPGQSLRRL IYQVSNRDSG VPDRFSGSGS GTDFTLKISR 240 VEAEDVGVYF CMQGTYWPPT FGGGTKVEIK TTTPAPRPPT PAPTIASQPL SLRPEACRPA 300 AGGAVHTRGL DFACDIYIWA PLAGTCGVLL LSLVITLYCK RGRKKLLYIF KQPFMRPVQT 360 TQEEDGCSCR FPEEEEGGCE LRVKFSRSAD APAYQQGQNQ LYNELNLGRR EEYDVLDKRR 420 GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD 480 TYDALHMQAL PPR 493
3-315	**Sequences**	
3-315-1	Sequence Number [ID]	315
3-315-2	Molecule Type	AA
3-315-3	Length	485
3-315-4	Features	**REGION 1..485**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..485** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-315-5	Residues	MALPVTALLL PLALLLHAAR PQVQLRGSGP GLVKPSETLS LTCTVSDDSI SVYYWSWIRQ 60 PAGKGLEWIG RVYSSGNINY NPSLESRVTM SVDTSKSRFS LNLSSVTAAD TAVYYCARGL 120 DAFDIWGQGT MVTVSSGGGG SGGGGSGGGG SGGGGSEIVM TQSPATLSMS LGERATLSCR 180 ASQSVSSSLA WYQQKPGQAP RLLIYGASTR ATGIPARFGG SGSGTEFTLT ISSLQSEDFA 240 VYYCQQYINW PHFGGGTKVE IKTTTPAPRP PTPAPTIASQ PLSLRPEACR PAAGGAVHTR 300 GLDFACDIYI WAPLAGTCGV LLLSLVITLY CKRGRKKLLY IFKQPFMRPV QTTQEEDGCS 360 CRFPEEEEGG CELRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK RRGRDPEMGG 420 KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD GLYQGLSTAT KDTYDALHMQ 480 ALPPR 485
3-316	**Sequences**	
3-316-1	Sequence Number [ID]	316
3-316-2	Molecule Type	AA
3-316-3	Length	486
3-316-4	Features	**REGION 1..486**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..486**

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-316-5	Residues	MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGESLR LSCEVSGFTF TSYAMSWVRQ 60 VPGKGLEWVS IISGVAFTTY YADSVKGRFT ISRDHSKNTL YLQMNGLRAE DTAVYYCVKV 120 DGEVYWGQGT LVTVSSGGGG SGGGGSGGGG SGGGGSDIQM TQSPSSLSAS VGDRVTITCQ 180 ASQDISNYLN WYQQKPGKAP KILIYGASNL ETGVPSRFSG SGSGTDFTFA ISSLQPEDVA 240 TYYCQQYDNF PITFGQGTRL EIKTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT 300 RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC 360 SCRFPEEEEG GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG 420 GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM 480 QALPPR 486
3-317	**Sequences**	
3-317-1	Sequence Number [ID]	317
3-317-2	Molecule Type	AA
3-317-3	Length	489
3-317-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-317-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCEASGGTF ITYAISWVRQ 60 APGQGLEWMG GIIPFFGTAN YAQKFQGRVT ITADKSTSTA SMELRSLRSE DTAMYYCAQW 120 ELFFFDFWGQ GTPVTVSSGG GGSGGGGSGG GGSGGGGSEI VMTQSPDTLS VSPGERAILS 180 CRASQSVSSN LAWYQQKPGQ APRLLIYSAS TRASGIPARF SGSGSGTEFT LSISSLQSED 240 FAVYYCQQYD NWPPLTFGGG TKVEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-318	**Sequences**	
3-318-1	Sequence Number [ID]	318
3-318-2	Molecule Type	AA
3-318-3	Length	492
3-318-4	Features	**REGION 1..492**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..492
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-318-5	Residues	MALPVTALLL PLALLLHAAR PAVQLVESGG GLVQPGGSLR LSCAASGFTF TYYSMNWVRQ 60 APGKGLEWVS HISIRSSTIY FADSAKGRFT ISRDNAKNSL YLQMNSLRDE DTAVYYCARG 120 SGWYGDYFDY WGQGTLVTVS SGGGGSGGGG SGGGGSGGGG SEIVLTQSPG TLSLSPGERA 180 TLSCRASQSV SSSYLAWYQQ QPGQAPRLLI YGASSRATGI PDRFSGSGSG TDFTLTISRL 240 EPEDFAIYYC QQYGSSPLTF GGGTKVEIKT TTPAPRPPTP APTIASQPLS LRPEACRPAA 300 GGAVHTRGLD FACDIYIWAP LAGTCGVLLL SLVITLYCKR GRKKLLYIFK QPFMRPVQTT 360 QEEDGCSCRF PEEEEGGCEL RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG 420 RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT 480 YDALHMQALP PR 492
3-319	**Sequences**	
3-319-1	Sequence Number [ID]	319
3-319-2	Molecule Type	AA
3-319-3	Length	494
3-319-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-319-5	Residues	MALPVTALLL PLALLLHAAR PQVTLKESGP VLVKPTETLT LTCTVSGFSL SNARMGVTWI 60 RQPPGKALEW LAHIFSNDEK SYSTSLKSRL TISKDTSKTQ VVLTMTNMDP VDTATYYCAR 120 IRDYYDISSY YDYWGQGTLV SVSSGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSAMSASVG 180 DRVTITCRAS QDISNYLAWF QQKPGKVPKR LIYAASSLQS GVPSRFSGSG SGTEFTLTIS 240 SLLPEDFATY YCLQLNSFPF TFGGGTKVEI NTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-320	**Sequences**	
3-320-1	Sequence Number [ID]	320
3-320-2	Molecule Type	AA

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3-320-3	Length	490
3-320-4	Features	**REGION 1..490**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..490
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-320-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAVSGFTF SNHNIHWVRQ 60 APGKGLEWIS YISRSSSTIY YADSVKGRFT ISRDNAKNSL YLQMNSLRDE DTAVYYCARD 120 HAQWYGMDVW GQGTTVTVSS GGGGSGGGGS GGGGSGGGGS DIQMTQSPSS VSASVGDRVT 180 ITCRASQGIS SWLAWYQQKP GKAPKVLIYA ASSLQSGVPS RFSGSGSGTD FTLTISSLQP 240 EDFATYYCQQ AFSFPFTFGP GTKVDIKTTT PAPRPPTPAP TIASQPLSLR PEACRPAAGG 300 AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCKRGR KKLLYIFKQP FMRPVQTTQE 360 EDGCSCRFPE EEEGGCELRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY DVLDKRRGRD 420 PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGHDGLYQG LSTATKDTYD 480 ALHMQALPPR 490
3-321	**Sequences**	
3-321-1	Sequence Number [ID]	321
3-321-2	Molecule Type	AA
3-321-3	Length	500
3-321-4	Features	**REGION 1..500**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..500
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-321-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCVASGFTF SSYWMSWVRQ 60 APGKGLEWVA SIKQDGSEKY YVDSVKGRFT ISRDNAKNSV YLQMNSLRAE DTGVYYCARE 120 GVNWGWRLYW HFDLWGRGTL VTVSSGGGGS GGGGSGGGGS GGGGSDIVMT QSPDSLAVSL 180 GERATINCKS SQSVLYSYNN KNYVAWYQQK PGQPPNLLIF WASTRESGVP DRFSGSGSGT 240 DFTLTISSLQ AEDVAVYYCQ QYYSTLTFGG GTKVEIKTTT PAPRPPTPAP TIASQPLSLR 300 PEACRPAAGG AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCKRGR KKLLYIFKQP 360 FMRPVQTTQE EDGCSCRFPE EEEGGCELRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY 420 DVLDKRRGRD PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGHDGLYQG 480 LSTATKDTYD ALHMQALPPR 500
3-322	**Sequences**	
3-322-1	Sequence Number [ID]	322
3-322-2	Molecule Type	AA
3-322-3	Length	492
3-322-4	Features	**REGION 1..492**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..492
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-322-5	Residues	MALPVTALLL PLALLLHAAR PEVQVVESGG GLVQPGGSLR LSCAASGFTF SSYSMNWVRQ 60 APGKGLEWVS HSSISRGNIY FADSVKGRFT ISRDNAKNSL YLQMNSLRDE DTAVYYCARG 120 SGWYGDYFDY WGQGTLVTVS SGGGGSGGGG SGGGGSGGGG SEIVLTQSPG TLSLSPGERV 180 TLSCRASQSV SSSYLAWYQQ KPGQAPRLLI YDASSRATGI PDRFSGSGSG TDFTLTISRL 240 EPEDFAVYYC QQYGSSPLTF GGGTKVEIKT TTPAPRPPTP APTIASQPLS LRPEACRPAA 300 GGAVHTRGLD FACDIYIWAP LAGTCGVLLL SLVITLYCKR GRKKLLYIFK QPFMRPVQTT 360 QEEDGCSCRF PEEEEGGCEL RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG 420 RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT 480 YDALHMQALP PR 492
3-323	**Sequences**	
3-323-1	Sequence Number [ID]	323
3-323-2	Molecule Type	AA
3-323-3	Length	496
3-323-4	Features	**REGION 1..496**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..496
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-323-5	Residues	MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFAF SNYAMSWVRQ 60 APGKGLEWVS AIRGGGGSTY YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARD 120 FISGTWYPDY WGQGTLVTVS SGGGGSGGGG SGGGGSGGGG SELQSVLTQP PSASGTPGQR 180 VTISCSGSSS NIGSNYVYWY QQLPGTAPKL LIYRNNQRPS GVPDRFSGSK SGTSASLAIS 240 GLRSEDEADY YCAAWDDSLS GVVFGGGTKL TVLTTTPAPR PPTPAPTIAS QPLSLRPEAC 300 RPAAGGAVHT RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP 360 VQTTQEEDGC SCRFPEEEEG GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD 420

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		KRRGRDPEMG GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA 480 TKDTYDALHM QALPPR 496
3-324	**Sequences**	
3-324-1	Sequence Number [ID]	324
3-324-2	Molecule Type	AA
3-324-3	Length	498
3-324-4	Features	**REGION 1..498**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..498** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-324-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYRF TSYWIGWVRQ 60 MPGKGLEWMG SIYPDDSDTR YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCASS 120 TVDYPGYSYF DYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSELQSVLT QPPSASGTPG 180 QRVTISCSGS RSNIGSNYVY WYQQLPGTAP KLLIYRNNQR PSGVPDRFSG SKSGTSASLA 240 ISGLRSEDEA DYYCASWDGS LSAVVFGTGT KLTVLTTTPA PRPPTPAPTI ASQPLSLRPE 300 ACRPAAGGAV HTRGLDFACD IYIWAPLAGT CGVLLLSLVI TLYCKRGRKK LLYIFKQPFM 360 RPVQTTQEED GCSCRFPEEE EGGCELRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV 420 LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS 480 TATKDTYDAL HMQALPPR 498
3-325	**Sequences**	
3-325-1	Sequence Number [ID]	325
3-325-2	Molecule Type	AA
3-325-3	Length	499
3-325-4	Features	**REGION 1..499**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..499** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-325-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYTF TNYWIAWVRQ 60 MPGKGLEWMG IIYPDGSDTR YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCARD 120 ITSWYYGEPA FDIWGQGTLV TVSSGGGGSG GGGSGGGGSG GGGSELQSVL TQPPSASGTP 180 GQRVTISCSG SSSNIGSNYV YWYQQLPGTA PKLLIYRNNQ RPSGVPDRFS GSKSGTSASL 240 AISGLRSEDE ADYYCATWDD SLGSPVFGTG TKLTVLTTTP APRPPTPAPT IASQPLSLRP 300 EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF 360 MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD 420 VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL 480 STATKDTYDA LHMQALPPR 499
3-326	**Sequences**	
3-326-1	Sequence Number [ID]	326
3-326-2	Molecule Type	AA
3-326-3	Length	496
3-326-4	Features	**REGION 1..496**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..496** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-326-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYSF TSSWIGWVRQ 60 MPGKGLEWMG IIYPGDSDTR YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCAKG 120 LSQAMTGFGF DYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSELDIQMT QSPSSLSASV 180 GDRVTITCRA SQSISRYLNW YQQKPGKAPK LLIYAASILQ TGVPSRFSGS GSGTDFTLTI 240 SSLQPEDFAT YYCQQSYSTT MWTFGQGTKV EIKTTTPAPR PPTPAPTIAS QPLSLRPEAC 300 RPAAGGAVHT RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP 360 VQTTQEEDGC SCRFPEEEEG GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD 420 KRRGRDPEMG GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA 480 TKDTYDALHM QALPPR 496
3-327	**Sequences**	
3-327-1	Sequence Number [ID]	327
3-327-2	Molecule Type	AA
3-327-3	Length	499
3-327-4	Features	**REGION 1..499**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..499** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-327-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYGF TSYWIGWVRQ 60 MPGKGLEWMG IIHPDDSDTK YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCASS 120

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		YLRGLWGGYF DYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSELQSVLT QPPSASGTPG 180 QRVTISCSGS SSNIGSNYVN WYQQLPGTAP KLLIYGDYQR PSGVPDRFSG SKSGTSASLA 240 ISGLRSEDEA DYYCATRDDS LSGSVVFGTG TKLTVLTTTP APRPPTPAPT IASQPLSLRP 300 EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF 360 MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD 420 VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL 480 STATKDTYDA LHMQALPPR 499
3-328	**Sequences**	
3-328-1	Sequence Number [ID]	328
3-328-2	Molecule Type	AA
3-328-3	Length	500
3-328-4	Features	**REGION 1..500**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..500
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-328-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYTF PSSWIGWVRQ 60 MPGKGLEWMG IIYPDTSHTR YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCARA 120 SYFDRGTGYS SWWMDVWGQG TLVTVSSGGG GSGGGGSGGG GSGGGGSELD IQMTQSPSSL 180 SASVGDRVTI TCRASQSIYD YLHWYQQKPG KAPKLLIYDA SNLQSGVPSR FSGSGSGTDF 240 TLTISSLQPE DFATYYCQQS YTTPLFTFGQ GTKVEIKTTT PAPRPPTPAP TIASQPLSLR 300 PEACRPAAGG AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCKRGR KKLLYIFKQP 360 FMRPVQTTQE EDGCSCRFPE EEEGGCELRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY 420 DVLDKRRGRD PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGHDGLYQG 480 LSTATKDTYD ALHMQALPPR 500
3-329	**Sequences**	
3-329-1	Sequence Number [ID]	329
3-329-2	Molecule Type	AA
3-329-3	Length	497
3-329-4	Features	**REGION 1..497**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..497
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-329-5	Residues	MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF SQYSMSWVRQ 60 APGKGLEWVS AISGGGVSTY YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCASD 120 ISDSGGSHWY FDYWGQGTLV TVSSGGGGSG GGGSGGGGSG GGGSELDIQM TQSPSSLSAS 180 VGDRVTITCR ASQYIGRYLN WYQQKRGKAP KLLIHGATSL ASGVPSRFSG SGSGTDFTLT 240 ISSLQPEDFA TYYCQQSYST TSPTFGQGTK VEIKTTTPAP RPPTPAPTIA SQPLSLRPEA 300 CRPAAGGAVH TRGLDFACDI YIWAPLAGTC GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR 360 PVQTTQEEDG CSCRFPEEEE GGCELRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL 420 DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST 480 ATKDTYDALH MQALPPR 497
3-330	**Sequences**	
3-330-1	Sequence Number [ID]	330
3-330-2	Molecule Type	AA
3-330-3	Length	497
3-330-4	Features	**REGION 1..497**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..497
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-330-5	Residues	MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF SSYAMSWVRQ 60 APGKGLEWVS TISGTGGTTY YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCAKV 120 RAGIDPTASD VWGQGTLVTV SSGGGGSGGG GSGGGGSGGG GSELQSVLTQ PPSASGTPGQ 180 RVTISCSGST SNIGRNYVYW YQQLPGTAPK LLIYRTNQRP SGVPDRFSGS KSGTSASLAI 240 SGLRSEDEAD YYCAAWDDSL SGRVFGTGTK LTVLTTTPAP RPPTPAPTIA SQPLSLRPEA 300 CRPAAGGAVH TRGLDFACDI YIWAPLAGTC GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR 360 PVQTTQEEDG CSCRFPEEEE GGCELRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL 420 DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST 480 ATKDTYDALH MQALPPR 497
3-331	**Sequences**	
3-331-1	Sequence Number [ID]	331
3-331-2	Molecule Type	AA
3-331-3	Length	500
3-331-4	Features	**REGION 1..500**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..500

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-331-5	Residues	MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF NNFAMSWVRQ 60 APGKGLEWVS GISGSGDNTY YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCAKD 120 RDIGLGWYSY YLDVWGQGTL VTVSSGGGGS GGGGSGGGGS GGGGSELQSV LTQPPSASGT 180 PGQRVTISCS GSSSNIGSNY VYWYQQLPGT APKPLIYMNN QRPSGVPDRF SGSKSGTSAS 240 LAISGLRSED EADYYCAAWD DSLSAVVFGT GTKLTVLTTT PAPRPPTPAP TIASQPLSLR 300 PEACRPAAGG AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCKRGR KKLLYIFKQP 360 FMRPVQTTQE EDGCSCRFPE EEEGGCELRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY 420 DVLDKRRGRD PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGHDGLYQG 480 LSTATKDTYD ALHMQALPPR 500
3-332	**Sequences**	
3-332-1	Sequence Number [ID]	332
3-332-2	Molecule Type	AA
3-332-3	Length	496
3-332-4	Features	**REGION 1..496**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..496
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-332-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTF SSYAISWVRQ 60 APGQGLEWMG EIIPIFGTAS YAQKFQGRVT ITADESTSTA YMELSSLRSE DTAVYYCARA 120 GWDDSWFDYW GQGTLVTVSS GGGGSGGGGS GGGGSGGGGS ELQSVLTQPP SASGTPGQRV 180 TISCSGSNSN IGTNYVSWYQ QLPGTAPKLL IYRSSRRPSG VPDRFSGSKS GTSASLAISG 240 LRSEDEADYY CAAWDGSLSG HWVFGTGTKL TVLTTTPAPR PPTPAPTIAS QPLSLRPEAC 300 RPAAGGAVHT RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP 360 VQTTQEEDGC SCRFPEEEEG GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD 420 KRRGRDPEMG GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA 480 TKDTYDALHM QALPPR 496
3-333	**Sequences**	
3-333-1	Sequence Number [ID]	333
3-333-2	Molecule Type	AA
3-333-3	Length	496
3-333-4	Features	**REGION 1..496**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..496
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-333-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYSF ASYWIGWVRQ 60 MPGKGLEWMG VIYPGTSETR YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCAKG 120 LSASASGYSF QYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSELDIQMT QSPSSLSASV 180 GDRVTITCRA SQSIDTYLNW YQQKPGKAPK LLIYSASSLH SGVPSRFSGS GSGTDFTLTI 240 SSLQPEDFAT YYCQQSYSTT AWTFGQGTKV EIKTTTPAPR PPTPAPTIAS QPLSLRPEAC 300 RPAAGGAVHT RGLDFACDIY IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP 360 VQTTQEEDGC SCRFPEEEEG GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD 420 KRRGRDPEMG GKPRRKNPQE GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA 480 TKDTYDALHM QALPPR 496
3-334	**Sequences**	
3-334-1	Sequence Number [ID]	334
3-334-2	Molecule Type	AA
3-334-3	Length	497
3-334-4	Features	**REGION 1..497**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..497
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-334-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYSF TDYWIGWVRQ 60 MPGKGLEWMG MISPGGSTTI YRPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCARE 120 MYTGGYGGSW YFDYWGQGTL VTVSSGGGGS GGGGSGGGGS GGGGSELDIQ MTQSPSSLSA 180 SVGDRVTITC RASQSIGQSL NWYQQKPGKA PKLLIYGASS LQSGVPSRFS GSGSGTDFTL 240 TISSLQPEDF ATYYCQQSYS TPITFGQGTK VEIKTTTPAP RPPTPAPTIA SQPLSLRPEA 300 CRPAAGGAVH TRGLDFACDI YIWAPLAGTC GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR 360 PVQTTQEEDG CSCRFPEEEE GGCELRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL 420 DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST 480 ATKDTYDALH MQALPPR 497
3-335	**Sequences**	
3-335-1	Sequence Number [ID]	335
3-335-2	Molecule Type	AA

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3-335-3	Length	193
3-335-4	Features	**source 1..193**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-335-5	Residues	MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60 QLNHTGPQQD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMVHIQV TLAICSSTTA 120 SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN 180 TDETFFGVQW VRP 193
3-336	**Sequences**	
3-336-1	Sequence Number [ID]	336
3-336-2	Molecule Type	DNA
3-336-3	Length	933
3-336-4	Features	**misc_feature 1..933**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..933
		mol_type=other DNA
		organism=synthetic construct
		misc_difference 793
		note=a, c, t, or g
		misc_difference 797
		note=a, c, t, or g
	NonEnglishQualifier Value	
3-336-5	Residues	atggctctcc cggtcacggc cctgctgctg cctctggcgc tgctcctgca cgcggcgcgc 60 ccgcaggtca ccttgaagga gtctggtcct gtgctggtga aacccacaga gaccctcacg 120 ctgacctgca ccgtctctgg gttctcactc agtaatgcta gaatgggtgt gacctggatc 180 cgtcagcccc cagggaaggc cctggagtgg cttgcacaca ttttttcgaa tgacgaaaaa 240 tcctacagta catctctgaa gagcaggctc accatctcca aggacacttc caaaacccag 300 gtggtcctta ccatgaccaa catggaccct gtggacacag ccacatatta ctgtgcacgg 360 atacgagatt actatgacat tagtagttat tatgactact ggggccaggg aaccctggtc 420 agcgtctcct caggcggagg cggttctggc ggaggtggca gcggtggtgg cggaagtggg 480 ggtggcggct ccgacatcca gatgacccag tctccatctg ccatgtctgc atctgtagga 540 gacagagtca ccatcacttg tcgggcgagt caggacatta gcaattattt agcctggttt 600 cagcagaaac cagggaaagt ccctaagcgc ctgatctatg ctgcatccag tttgcaaagt 660 ggggtcccat caaggttcag cggcagtgga tcggggacag aattcactct cacaatcagc 720 agcctgctgc ctgaagattt tgcaacttat tactgtctac agcttaatag tttcccgttc 780 acttttggcg ganggancaa ggtggagatc aacactacca caccagcacc tcgaccacca 840 actccagcac caaccattgc atcacagcca ctgagcctgc gaccagaggc ctgtagacct 900 gctgcaggag gagctgtgca tacccgagga ctg 933
3-337	**Sequences**	
3-337-1	Sequence Number [ID]	337
3-337-2	Molecule Type	DNA
3-337-3	Length	948
3-337-4	Features	**misc_feature 1..948**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..948
		mol_type=other DNA
		organism=synthetic construct
	NonEnglishQualifier Value	
3-337-5	Residues	atggctctcc cggtcacggc cctgctgctg cctctggcgc tgctcctgca cgcggcgcgc 60 ccggaagtgc agcttgtcca gagcggagcc gaagtgaaga agcctggcga gagcctgaag 120 atcagctgca agggctccgg atacggattc acaagttatt ggataggttg ggtgcgccag 180 atgcctggta agggactgga atggatgggt atcattcatc ccgatgatag cgacaccaaa 240 tacagcccaa gctttcaggg ccaggtcaca atcagcgctg acaagagcat cagcaccgcc 300 taccttcagt ggtcgtctct gaaggccagc gacaccgcaa tgtactactg tgcctctagc 360 tatttgcgtg gcttgtgggg aggctatttt gactattggg gccaaggtac actggtcacc 420 gtcagcagcg gcggaggcgg ttctggcgga ggtggcagcg gtggtggcgg aagtgggggt 480 ggcggctccg agctccagag cgtgctgacc cagcctccta gcgcaagcgg caccctgga 540 cagcgtgtga caattagctg tagcggatca agctcaaaca ttggctcaaa ttatgtgaat 600 tggtatcagc aattgcccgg tacagcaccc aaactgctca tttatggaga ttatcaacga 660 cctagcggag tgcctgatcg ttttagcggt agcaaaagcg gcaccagcgc atcactggca 720 atttcaggcc tgcgtagcga agatgaggcg gattattact gtgctacccg cgacgattcg 780 ttatctgggt ctgtcgtttt tggcaccggt acaaaactga ccgtgctgac taccacacca 840 gcacctcgac caccaactcc agcaccaacc attgcatcac agccactgag cctgcgacca 900 gaggcctgta gacctgctgc aggaggagct gtgcataccc gaggactg 948
3-338	**Sequences**	
3-338-1	Sequence Number [ID]	338
3-338-2	Molecule Type	AA
3-338-3	Length	107
3-338-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-338-5	Residues	DIQMTQSPST LSASVGDRVT ITCRASQSIS TWLAWYQQKP GKAPKVLIYK ASSLESGVPS 60 RFSGSGSGTE FILTINSLQP DDFASYYCQQ YKSYSHTFGQ GTKLEIK 107
3-339	**Sequences**	
3-339-1	Sequence Number [ID]	339
3-339-2	Molecule Type	AA
3-339-3	Length	118
3-339-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-339-5	Residues	QVQLQESGPG LVKPSETLSL TCTVSGGSIS YYYWTWIRQP PGKGLEWIGH IYYSGSTNYN 60 PSLKSRVTIS IDTSKNLFSL KLSSVTAADT AVYYCARAEG SLDAFDFWGQ GTMVTVSS 118
3-340	**Sequences**	
3-340-1	Sequence Number [ID]	340
3-340-2	Molecule Type	AA
3-340-3	Length	107
3-340-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-340-5	Residues	DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKVLIYK ASSLESGVPS 60 RFSGSGSGTE FTLTINSLQP DDFATYYCQQ YKSFSLTFGQ GTKLEIK 107
3-341	**Sequences**	
3-341-1	Sequence Number [ID]	341
3-341-2	Molecule Type	AA
3-341-3	Length	113
3-341-4	Features	**REGION 1..113**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..113
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-341-5	Residues	EVQLVESGGG LIQPGGSLRL SCAASGFTVS SNYMTWVRQA PGKGLEWVSV IYSGGSTYYA 60 DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARNWG DYWGQGTLVT VSS 113
3-342	**Sequences**	
3-342-1	Sequence Number [ID]	342
3-342-2	Molecule Type	AA
3-342-3	Length	107
3-342-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-342-5	Residues	DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKVLIYK ASTLESGVPS 60 RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YNSYSYTFGH GTKLEIK 107
3-343	**Sequences**	
3-343-1	Sequence Number [ID]	343
3-343-2	Molecule Type	AA
3-343-3	Length	118
3-343-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-343-5	Residues	QVQLQESGPG LVKPSGTLSL TCTVSGGSID YYFWNWFRQS PVKGLEWIGH VYDIGNTKYN 60 PSLKSRVTIS IDTSENQFSL KLNSVTAADT AVYYCARGEG ALDAFDIWGQ GTMVTVSS 118
3-344	**Sequences**	
3-344-1	Sequence Number [ID]	344
3-344-2	Molecule Type	AA
3-344-3	Length	107

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3-344-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-344-5	Residues	DIQMTQSPSI LSASVGDRVT ITCRASQSVS SWLAWYQQKP GKAPKVLIYK ASSLESGVPS 60 RFSGTGSGTE FTLTISSLQS DDFATYYCQQ YNTYSHTFGQ GTKLEIK 107
3-345	**Sequences**	
3-345-1	Sequence Number [ID]	345
3-345-2	Molecule Type	AA
3-345-3	Length	118
3-345-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-345-5	Residues	QVQLQESGPG LVKPSETLSL NCTVSGGSIS YYYWTWIRQP PGKGLEWIGH VIYSGTTNYN 60 PSLKSRVTIS VDTSKNQFSL KLNSVTAADT AVYYCVRAEG SLDAFDLWGQ GTMVTVSS 118
3-346	**Sequences**	
3-346-1	Sequence Number [ID]	346
3-346-2	Molecule Type	AA
3-346-3	Length	107
3-346-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-346-5	Residues	AIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKLLIYA ASSLQSGVPS 60 RFSGSGSGTD FTLTISSLQP EDFATYYCLQ DYNYPFTFGP GTKVDIK 107
3-347	**Sequences**	
3-347-1	Sequence Number [ID]	347
3-347-2	Molecule Type	AA
3-347-3	Length	120
3-347-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-347-5	Residues	QVQLVESGGG VVQPGRSLRL SCVASGFTFS DYGIHWVRQA PGMGQEWVAV IWYDGSIKKY 60 SDSVKGRFII SRDNSENTVY LQMNSLRGED TAIYYCARDE VGTFGAFDFW GQGTKVTVSS 120
3-348	**Sequences**	
3-348-1	Sequence Number [ID]	348
3-348-2	Molecule Type	AA
3-348-3	Length	107
3-348-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-348-5	Residues	DIQMTQSPSS LSASVGDSIT ITCRASQDID NYLAWYQQKT GKVPKVLIYA ASALQSGVPS 60 RFSGSGSGTD FTLTISSLQP EDVATYYCQN YNSGPRTFGQ GTKVEIK 107
3-349	**Sequences**	
3-349-1	Sequence Number [ID]	349
3-349-2	Molecule Type	AA
3-349-3	Length	118
3-349-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-349-5	Residues	QVQLQESGPG LVKPLQTLSL TCTVSGGSIS SDGYYWSWIR QNPGKGLEWI GYMYYSGSTY 60 YNPSLKSRVT ISVDTSKNQF SLKLRSVTAA DTAVYYCTRD FGWYFDLWGR GTLVTVSS 118
3-350	**Sequences**	

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3-350-1	Sequence Number [ID]	350
3-350-2	Molecule Type	AA
3-350-3	Length	107
3-350-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-350-5	Residues	DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLTWYQQKP GRVPEVLIYA ASALQSGVPS 60 RFSGSGSGTD FTLTISSLQP EDVATYYCQN YNSAPRTFGQ GTKVEIK 107
3-351	**Sequences**	
3-351-1	Sequence Number [ID]	351
3-351-2	Molecule Type	AA
3-351-3	Length	118
3-351-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-351-5	Residues	QVQLQESGPG LVKPSQSLSL TCSVSGGSVS SDGYYWSWIR QHPGKGLEWI GYIYYRRITD 60 YNPSLKSRVN ISLDTSKNQF SLKLSSVTAA DTAVYYCARD FGWYFDLWGR GTLVAVSS 118
3-352	**Sequences**	
3-352-1	Sequence Number [ID]	352
3-352-2	Molecule Type	AA
3-352-3	Length	112
3-352-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-352-5	Residues	DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ VLILLGSNRA 60 SGVPDRVSAS GSGTDFTLKI SRMQAEDVGI YYCMQTLQTP FTFGQGTKLE IK 112
3-353	**Sequences**	
3-353-1	Sequence Number [ID]	353
3-353-2	Molecule Type	AA
3-353-3	Length	122
3-353-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-353-5	Residues	QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYLHWVRQA PGQGLEWMGW INPNSGGTNY 60 AQKFQGRVTM TRDTSITTAY MELSRLRIDD TAVYYCARDR GVTMIVDGMD DWGQGTTVTV 120 SS 122
3-354	**Sequences**	
3-354-1	Sequence Number [ID]	354
3-354-2	Molecule Type	AA
3-354-3	Length	107
3-354-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-354-5	Residues	DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 60 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLDIN 107
3-355	**Sequences**	
3-355-1	Sequence Number [ID]	355
3-355-2	Molecule Type	AA
3-355-3	Length	120
3-355-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..120
		mol_type=protein
		organism=synthetic construct

	NonEnglishQualifier Value	
3-355-5	Residues	EVELVESGGG MVQPGRSLRL SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY 60 ADSVKGRFTI SRDNSKNTVF LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS 120
3-356	**Sequences**	
3-356-1	Sequence Number [ID]	356
3-356-2	Molecule Type	AA
3-356-3	Length	107
3-356-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-356-5	Residues	DIQMTQSPSS LSASVGDRVT ITCRASQGIS NYLAWYQQKP GKVPKLLIYA ASTLHSGVPS 60 RFSGSGSGTD FTLTISSLQP EDVATYYCQK YNSAPRTFGQ GTKVEIK 107
3-357	**Sequences**	
3-357-1	Sequence Number [ID]	357
3-357-2	Molecule Type	AA
3-357-3	Length	118
3-357-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-357-5	Residues	QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SDGYYWSWIR QHPGKGLEWI GYMYYSGITY 60 HNPSLKSRVT ISVDTSKNQF SLRLSSVTAA DTAVYYCARD FGWYFDLWGR GTLVTVSS 118
3-358	**Sequences**	
3-358-1	Sequence Number [ID]	358
3-358-2	Molecule Type	AA
3-358-3	Length	107
3-358-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-358-5	Residues	DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLAWYQQKP GKVPKLLIYA ASTLHSGVPS 60 RFSGSGSGTD FTLTISSLQP DDFAAYYCQK YNSAPRTFGQ GTKVEIK 107
3-359	**Sequences**	
3-359-1	Sequence Number [ID]	359
3-359-2	Molecule Type	AA
3-359-3	Length	118
3-359-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-359-5	Residues	QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SDAYYWSWIR QHPGKGLEWI GYMYYSGITY 60 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARD FGWYFDLWGR GTLVTVSS 118
3-360	**Sequences**	
3-360-1	Sequence Number [ID]	360
3-360-2	Molecule Type	AA
3-360-3	Length	107
3-360-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-360-5	Residues	DIQLTQSPSF LSASVGDRVS ITCRASQDIS SFLAWYQQKP GKAPVLLIYV ASTLQSGVPS 60 RFSGSGSGTE FTLTVSSLQP EDFATYYCQQ LHVYPITFGQ GTRLEIR 107
3-361	**Sequences**	
3-361-1	Sequence Number [ID]	361
3-361-2	Molecule Type	AA
3-361-3	Length	120
3-361-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct

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		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-361-5	Residues	QVQLVESGGG VVQPGRSLRL SCVASGFTFS DYGIHWVRQA PGMGQEWVAV IWYDGSIKKY 60 SDSVKGRFII SRDNSENTVY LQMNSLRGED TAIYYCARDE VGTFGAFDFW GQGTKVTVSS 120
3-362	**Sequences**	
3-362-1	Sequence Number [ID]	362
3-362-2	Molecule Type	AA
3-362-3	Length	113
3-362-4	Features	**REGION 1..113**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..113
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-362-5	Residues	DIVMTQTPLS LPVTPGEPAS ISCRSSQSLL DSDDGNTYLD WYLQKPGQSP QLLIYTLSYR 60 ASGVPDRFSG SGSGTDFTLK ISRVEAEDVG VYYCMQRIEF PFTFGPGTKV DIK 113
3-363	**Sequences**	
3-363-1	Sequence Number [ID]	363
3-363-2	Molecule Type	AA
3-363-3	Length	122
3-363-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-363-5	Residues	EVQLVESGGG LVKPGGSLRL SCAASGFTFS NAWMSWVRQA PGKGLEWVGR IKSKTGGGTT 60 DYAAPVKGRF TISRDDSKNT LYLQMNSLKT EDTAVYYCTS LIVGAISLFD YWGQGTLVTV 120 SS 122
3-364	**Sequences**	
3-364-1	Sequence Number [ID]	364
3-364-2	Molecule Type	AA
3-364-3	Length	107
3-364-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-364-5	Residues	DIQMTQSPSA LSASVGDRVA ITCRASQTIS TWLAWYQQKP GKAPKVLIYK ASNLESGVPS 60 RFSGSGSGTE FTLTINSLQP DDFATYYCQQ YQTFSHTFGQ GTKLEIK 107
3-365	**Sequences**	
3-365-1	Sequence Number [ID]	365
3-365-2	Molecule Type	AA
3-365-3	Length	118
3-365-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-365-5	Residues	QVQLRESGPG LVKPSETLSL TCTISGGSIS YYFWTWIRQP PGRGLEWIGQ IYYSGNTNSN 60 PSLKSRVTIS IDTSKNQFSL KLTSVTVADT AVYYCVRAEG SLDAFDIWGQ GTMVAVSS 118
3-366	**Sequences**	
3-366-1	Sequence Number [ID]	366
3-366-2	Molecule Type	AA
3-366-3	Length	107
3-366-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-366-5	Residues	DMQMTQSPSS LSASVGDRVT LTCRASQGIS NYLAWFQLKP GKVPKLLIYA ASTLQSGVPS 60 RFSGSGSGTD FALTISSLQP EDVATYYCQK YNSAPLTFGG GTKVEIK 107
3-367	**Sequences**	
3-367-1	Sequence Number [ID]	367

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3-367-2	Molecule Type	AA
3-367-3	Length	122
3-367-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-367-5	Residues	EVQLVESGGG LVKPGGSLRL SCVASGFTFS SYSMNWVRQF PGKGLEWVSS ISTSSNYIHY 60 ADSLQGRFTI SRDNAKNSLY LQMSSLRVED TAVYYCVRDK GTTLTNWYFD LWGRGTLVTV 120 SS 122
3-368	**Sequences**	
3-368-1	Sequence Number [ID]	368
3-368-2	Molecule Type	AA
3-368-3	Length	112
3-368-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-368-5	Residues	DIVMTQSPLS LPVTPGEPAS ISCRSSQTLV HSNGYNYLNW YLQKPGQSPQ LLIYLGSNRA 60 SGVPDRFSGS GSGSDFTLKI SRMEAEDVGV YYCMQAIQTP YTFGQGTNVE IK 112
3-369	**Sequences**	
3-369-1	Sequence Number [ID]	369
3-369-2	Molecule Type	AA
3-369-3	Length	121
3-369-4	Features	**REGION 1..121**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..121
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-369-5	Residues	QVQLVESGGG VVQPGRSLRL SCGASGFTFS SYGMHWVRQA PGKGLEWVAV IWYDGSNKYY 60 ADSLKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDG YSGSSDAFDI WGQGTMVTVS 120 S 121
3-370	**Sequences**	
3-370-1	Sequence Number [ID]	370
3-370-2	Molecule Type	AA
3-370-3	Length	107
3-370-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-370-5	Residues	DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKVLIYK ASNLESGVPS 60 RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YNSYSCTFGQ GTKLEIK 107
3-371	**Sequences**	
3-371-1	Sequence Number [ID]	371
3-371-2	Molecule Type	AA
3-371-3	Length	118
3-371-4	Features	**REGION 1..118**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..118
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-371-5	Residues	QVQLQESGPG LVQPSETLSL TCTVSGGSIS YYYWSWIRQP PGKGLEWIGN INYMGNTIYN 60 PSLKSRVTIS VDTSKDQFSL KLTSVSAADT AVYYCVRAEG SLDAFDFWGQ GTLVAVSL 118
3-372	**Sequences**	
3-372-1	Sequence Number [ID]	372
3-372-2	Molecule Type	AA
3-372-3	Length	107
3-372-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct

	NonEnglishQualifier Value	
3-372-5	Residues	DIQMTQSPSS LSASVGDRII FTCQASQDIN NYLHWYQQKP GKAPKLLIYD ASDWETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YDHLPITFGQ GTRVEIK 107
3-373	**Sequences**	
3-373-1	Sequence Number [ID]	373
3-373-2	Molecule Type	AA
3-373-3	Length	123
3-373-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..123** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-373-5	Residues	QVQLVQSGAE VTKPGASVKV SCKASGYIFT GYYIYWVRQA PGQGLEWMGW INPSSGGTNY 60 AQKFQGRVTM ARDTSISTAY MELSSLRSDD TAVYYCARDR KREYYYNFGM DVWGQGTTVT 120 VST 123
3-374	**Sequences**	
3-374-1	Sequence Number [ID]	374
3-374-2	Molecule Type	AA
3-374-3	Length	107
3-374-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..107** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-374-5	Residues	DIQMTQSPSS LSASVGDRVI LTCQASQDIS NYLHWYQQKP GKAPKLLIYD ASDLETGVPS 60 RFSGSGSGAD FTFTISNLQP EDFATYYCQQ YDHLPITFGQ GTRLEIK 107
3-375	**Sequences**	
3-375-1	Sequence Number [ID]	375
3-375-2	Molecule Type	AA
3-375-3	Length	123
3-375-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..123** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-375-5	Residues	QVQLVQSGAE VTKPGASVKV SCKASGYTFT SHYIYWVRQA PGQGLEWMGW INPNSGGTNY 60 AQKFQDRVTM ARDTSISTAY MELSRLRSDD TAVYYCAKDR KREYYYNFGM DVWGQGTTVT 120 VSA 123
3-376	**Sequences**	
3-376-1	Sequence Number [ID]	376
3-376-2	Molecule Type	AA
3-376-3	Length	107
3-376-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..107** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-376-5	Residues	DIQMTQSPSS LSASVGDRVI LTCQASQDIS NYLHWYQQKP GKAPKLLIYD ASDLETGVPS 60 RFSGSGSGAD FTFTISNLQP EDFATYYCQQ YDHLPITFGQ GTRLEIK 107
3-377	**Sequences**	
3-377-1	Sequence Number [ID]	377
3-377-2	Molecule Type	AA
3-377-3	Length	123
3-377-4	Features	**REGION 1..123**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct **source 1..123** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-377-5	Residues	QVQLVQFGVE VRKPGASVKV SCKVSGFTFT SHYIYWVRQA PGQGLEWMGW INPNSGGTKY 60 AQKFQDRVTM ARDTSISTAY MELSRLRSDD TSVYYCVKDR KREYYYNFGM DVWGQGTTVT 120 VSS 123
3-378	**Sequences**	
3-378-1	Sequence Number [ID]	378
3-378-2	Molecule Type	AA

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3-378-3	Length	107
3-378-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-378-5	Residues	DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYD ASNLETGVPS 60 RFSGSGSGTD FTFTISSLQP EDIATYYCQQ YDNLPYTFGQ GTKLEIK 107
3-379	**Sequences**	
3-379-1	Sequence Number [ID]	379
3-379-2	Molecule Type	AA
3-379-3	Length	119
3-379-4	Features	**REGION 1..119**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..119
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-379-5	Residues	EVQMLESGGG LIQPGGSLRL SCKTSGFTLS IYAIHWVRQA PGRGLEWVSS FGGRGSSTYF 60 ADSVKGRFTI SRDASENSLY LHMNSLRAED TAVYYCAKEK DWGRGFDYWG QGTLVTVSS 119
3-380	**Sequences**	
3-380-1	Sequence Number [ID]	380
3-380-2	Molecule Type	AA
3-380-3	Length	112
3-380-4	Features	**REGION 1..112**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..112
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-380-5	Residues	DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL YSNGYNYLDW YLQKPGQSPQ LLIFLNSNRA 60 SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YFCMQALQTP LTFGGGTKVE IK 112
3-381	**Sequences**	
3-381-1	Sequence Number [ID]	381
3-381-2	Molecule Type	AA
3-381-3	Length	122
3-381-4	Features	**REGION 1..122**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..122
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-381-5	Residues	EVQLVESGGG LVKPGGSLRL SCAASGFTFS NYSMNWVRQA PGKGLEWVSS ISSSTIYIYY 60 ADSVKGRFTI SRDNAKKSLY LQMNSLRAED TAVYYCARDI GWEVFTLGFD YWGQGTQVTV 120 SS 122
3-382	**Sequences**	
3-382-1	Sequence Number [ID]	382
3-382-2	Molecule Type	AA
3-382-3	Length	5
3-382-4	Features	**REGION 1..5**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..5
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-382-5	Residues	YYYWT 5
3-383	**Sequences**	
3-383-1	Sequence Number [ID]	383
3-383-2	Molecule Type	AA
3-383-3	Length	7
3-383-4	Features	**REGION 1..7**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-383-5	Residues	GGSISYY 7
3-384	**Sequences**	

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3-384-1	Sequence Number [ID]	384	
3-384-2	Molecule Type	AA	
3-384-3	Length	10	
3-384-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-384-5	Residues	GGSISYYYWT	10
3-385	**Sequences**		
3-385-1	Sequence Number [ID]	385	
3-385-2	Molecule Type	AA	
3-385-3	Length	16	
3-385-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-385-5	Residues	HIYYSGSTNY NPSLKS	16
3-386	**Sequences**		
3-386-1	Sequence Number [ID]	386	
3-386-2	Molecule Type	AA	
3-386-3	Length	5	
3-386-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-386-5	Residues	YYSGS	5
3-387	**Sequences**		
3-387-1	Sequence Number [ID]	387	
3-387-2	Molecule Type	AA	
3-387-3	Length	10	
3-387-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-387-5	Residues	AEGSLDAFDF	10
3-388	**Sequences**		
3-388-1	Sequence Number [ID]	388	
3-388-2	Molecule Type	AA	
3-388-3	Length	5	
3-388-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-388-5	Residues	SNYMT	5
3-389	**Sequences**		
3-389-1	Sequence Number [ID]	389	
3-389-2	Molecule Type	AA	
3-389-3	Length	7	
3-389-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-389-5	Residues	GFTVSSN	7
3-390	**Sequences**		
3-390-1	Sequence Number [ID]	390	
3-390-2	Molecule Type	AA	

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3-390-3	Length	10	
3-390-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-390-5	Residues	GFTVSSNYMT	10
3-391	**Sequences**		
3-391-1	Sequence Number [ID]	391	
3-391-2	Molecule Type	AA	
3-391-3	Length	16	
3-391-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-391-5	Residues	VIYSGGSTYY ADSVKG	16
3-392	**Sequences**		
3-392-1	Sequence Number [ID]	392	
3-392-2	Molecule Type	AA	
3-392-3	Length	5	
3-392-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-392-5	Residues	YSGGS	5
3-393	**Sequences**		
3-393-1	Sequence Number [ID]	393	
3-393-2	Molecule Type	AA	
3-393-3	Length	6	
3-393-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-393-5	Residues	NWGDYW	6
3-394	**Sequences**		
3-394-1	Sequence Number [ID]	394	
3-394-2	Molecule Type	AA	
3-394-3	Length	5	
3-394-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-394-5	Residues	YYFWN	5
3-395	**Sequences**		
3-395-1	Sequence Number [ID]	395	
3-395-2	Molecule Type	AA	
3-395-3	Length	7	
3-395-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-395-5	Residues	GGSIDYY	7
3-396	**Sequences**		
3-396-1	Sequence Number [ID]	396	
3-396-2	Molecule Type	AA	
3-396-3	Length	10	
3-396-4	Features	**REGION 1..10**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-396-5	Residues	GGSIDYYFWN	10
3-397	**Sequences**		
3-397-1	Sequence Number [ID]	397	
3-397-2	Molecule Type	AA	
3-397-3	Length	16	
3-397-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-397-5	Residues	HVYDIGNTKY NPSLKS	16
3-398	**Sequences**		
3-398-1	Sequence Number [ID]	398	
3-398-2	Molecule Type	AA	
3-398-3	Length	5	
3-398-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-398-5	Residues	YDIGN	5
3-399	**Sequences**		
3-399-1	Sequence Number [ID]	399	
3-399-2	Molecule Type	AA	
3-399-3	Length	10	
3-399-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-399-5	Residues	GEGALDAFDI	10
3-400	**Sequences**		
3-400-1	Sequence Number [ID]	400	
3-400-2	Molecule Type	AA	
3-400-3	Length	5	
3-400-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-400-5	Residues	YYYWT	5
3-401	**Sequences**		
3-401-1	Sequence Number [ID]	401	
3-401-2	Molecule Type	AA	
3-401-3	Length	7	
3-401-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-401-5	Residues	GGSISYY	7
3-402	**Sequences**		
3-402-1	Sequence Number [ID]	402	
3-402-2	Molecule Type	AA	
3-402-3	Length	10	
3-402-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-402-5	Residues	GGSISYYYWT	10
3-403	**Sequences**		
3-403-1	Sequence Number [ID]	403	
3-403-2	Molecule Type	AA	
3-403-3	Length	16	
3-403-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-403-5	Residues	HVIYSGTTNY NPSLKS	16
3-404	**Sequences**		
3-404-1	Sequence Number [ID]	404	
3-404-2	Molecule Type	AA	
3-404-3	Length	5	
3-404-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-404-5	Residues	IYSGT	5
3-405	**Sequences**		
3-405-1	Sequence Number [ID]	405	
3-405-2	Molecule Type	AA	
3-405-3	Length	10	
3-405-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-405-5	Residues	AEGSLDAFDL	10
3-406	**Sequences**		
3-406-1	Sequence Number [ID]	406	
3-406-2	Molecule Type	AA	
3-406-3	Length	5	
3-406-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-406-5	Residues	DYGIH	5
3-407	**Sequences**		
3-407-1	Sequence Number [ID]	407	
3-407-2	Molecule Type	AA	
3-407-3	Length	7	
3-407-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-407-5	Residues	GFTFSDY	7
3-408	**Sequences**		
3-408-1	Sequence Number [ID]	408	
3-408-2	Molecule Type	AA	
3-408-3	Length	10	
3-408-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-408-5	Residues	GFTFSDYGIH	10
3-409	**Sequences**		
3-409-1	Sequence Number [ID]	409	
3-409-2	Molecule Type	AA	
3-409-3	Length	17	
3-409-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-409-5	Residues	VIWYDGSIKK YSDSVKG	17
3-410	**Sequences**		
3-410-1	Sequence Number [ID]	410	
3-410-2	Molecule Type	AA	
3-410-3	Length	6	
3-410-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-410-5	Residues	WYDGSI	6
3-411	**Sequences**		
3-411-1	Sequence Number [ID]	411	
3-411-2	Molecule Type	AA	
3-411-3	Length	11	
3-411-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-411-5	Residues	DEVGTFGAFD F	11
3-412	**Sequences**		
3-412-1	Sequence Number [ID]	412	
3-412-2	Molecule Type	AA	
3-412-3	Length	7	
3-412-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-412-5	Residues	SDGYYWS	7
3-413	**Sequences**		
3-413-1	Sequence Number [ID]	413	
3-413-2	Molecule Type	AA	
3-413-3	Length	9	
3-413-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-413-5	Residues	GGSISSDGY	9
3-414	**Sequences**		
3-414-1	Sequence Number [ID]	414	
3-414-2	Molecule Type	AA	
3-414-3	Length	12	
3-414-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-414-5	Residues	GGSISSDGYY WS	12

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3-415	**Sequences**		
3-415-1	Sequence Number [ID]	415	
3-415-2	Molecule Type	AA	
3-415-3	Length	16	
3-415-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-415-5	Residues	YMYYSGSTYY NPSLKS	16
3-416	**Sequences**		
3-416-1	Sequence Number [ID]	416	
3-416-2	Molecule Type	AA	
3-416-3	Length	5	
3-416-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-416-5	Residues	YYSGS	5
3-417	**Sequences**		
3-417-1	Sequence Number [ID]	417	
3-417-2	Molecule Type	AA	
3-417-3	Length	8	
3-417-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-417-5	Residues	DFGWYFDL	8
3-418	**Sequences**		
3-418-1	Sequence Number [ID]	418	
3-418-2	Molecule Type	AA	
3-418-3	Length	7	
3-418-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-418-5	Residues	SDGYYWS	7
3-419	**Sequences**		
3-419-1	Sequence Number [ID]	419	
3-419-2	Molecule Type	AA	
3-419-3	Length	9	
3-419-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-419-5	Residues	GGSVSSDGY	9
3-420	**Sequences**		
3-420-1	Sequence Number [ID]	420	
3-420-2	Molecule Type	AA	
3-420-3	Length	12	
3-420-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-420-5	Residues	GGSVSSDGYY WS	12
3-421	**Sequences**		
3-421-1	Sequence Number [ID]	421	

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3-421-2	Molecule Type	AA	
3-421-3	Length	16	
3-421-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-421-5	Residues	YIYYRRITDY NPSLKS	16
3-422	**Sequences**		
3-422-1	Sequence Number [ID]	422	
3-422-2	Molecule Type	AA	
3-422-3	Length	5	
3-422-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-422-5	Residues	YYRRI	5
3-423	**Sequences**		
3-423-1	Sequence Number [ID]	423	
3-423-2	Molecule Type	AA	
3-423-3	Length	8	
3-423-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-423-5	Residues	DFGWYFDL	8
3-424	**Sequences**		
3-424-1	Sequence Number [ID]	424	
3-424-2	Molecule Type	AA	
3-424-3	Length	5	
3-424-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-424-5	Residues	GYYLH	5
3-425	**Sequences**		
3-425-1	Sequence Number [ID]	425	
3-425-2	Molecule Type	AA	
3-425-3	Length	7	
3-425-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-425-5	Residues	GYTFTGY	7
3-426	**Sequences**		
3-426-1	Sequence Number [ID]	426	
3-426-2	Molecule Type	AA	
3-426-3	Length	10	
3-426-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-426-5	Residues	GYTFTGYYLH	10
3-427	**Sequences**		
3-427-1	Sequence Number [ID]	427	
3-427-2	Molecule Type	AA	
3-427-3	Length	17	

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3-427-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-427-5	Residues	WINPNSGGTN YAQKFQG	17
3-428	**Sequences**		
3-428-1	Sequence Number [ID]	428	
3-428-2	Molecule Type	AA	
3-428-3	Length	6	
3-428-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-428-5	Residues	NPNSGG	6
3-429	**Sequences**		
3-429-1	Sequence Number [ID]	429	
3-429-2	Molecule Type	AA	
3-429-3	Length	13	
3-429-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-429-5	Residues	DRGVTMIVDG MDD	13
3-430	**Sequences**		
3-430-1	Sequence Number [ID]	430	
3-430-2	Molecule Type	AA	
3-430-3	Length	5	
3-430-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-430-5	Residues	DYGMH	5
3-431	**Sequences**		
3-431-1	Sequence Number [ID]	431	
3-431-2	Molecule Type	AA	
3-431-3	Length	7	
3-431-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-431-5	Residues	GFTFSDY	7
3-432	**Sequences**		
3-432-1	Sequence Number [ID]	432	
3-432-2	Molecule Type	AA	
3-432-3	Length	10	
3-432-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-432-5	Residues	GFTFSDYGMH	10
3-433	**Sequences**		
3-433-1	Sequence Number [ID]	433	
3-433-2	Molecule Type	AA	
3-433-3	Length	17	
3-433-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-433-5	Residues	VIWYDGSNKY YADSVKG	17
3-434	**Sequences**		
3-434-1	Sequence Number [ID]	434	
3-434-2	Molecule Type	AA	
3-434-3	Length	6	
3-434-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-434-5	Residues	WYDGSN	6
3-435	**Sequences**		
3-435-1	Sequence Number [ID]	435	
3-435-2	Molecule Type	AA	
3-435-3	Length	11	
3-435-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-435-5	Residues	DEVGFVGAFD I	11
3-436	**Sequences**		
3-436-1	Sequence Number [ID]	436	
3-436-2	Molecule Type	AA	
3-436-3	Length	7	
3-436-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-436-5	Residues	SDGYYWS	7
3-437	**Sequences**		
3-437-1	Sequence Number [ID]	437	
3-437-2	Molecule Type	AA	
3-437-3	Length	9	
3-437-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-437-5	Residues	GGSISSDGY	9
3-438	**Sequences**		
3-438-1	Sequence Number [ID]	438	
3-438-2	Molecule Type	AA	
3-438-3	Length	12	
3-438-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-438-5	Residues	GGSISSDGYY WS	12
3-439	**Sequences**		
3-439-1	Sequence Number [ID]	439	
3-439-2	Molecule Type	AA	
3-439-3	Length	16	
3-439-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-439-5	Residues	YMYYSGITYH NPSLKS	16
3-440	**Sequences**		
3-440-1	Sequence Number [ID]	440	
3-440-2	Molecule Type	AA	
3-440-3	Length	5	
3-440-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-440-5	Residues	YYSGI	5
3-441	**Sequences**		
3-441-1	Sequence Number [ID]	441	
3-441-2	Molecule Type	AA	
3-441-3	Length	8	
3-441-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-441-5	Residues	DFGWYFDL	8
3-442	**Sequences**		
3-442-1	Sequence Number [ID]	442	
3-442-2	Molecule Type	AA	
3-442-3	Length	7	
3-442-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-442-5	Residues	SDAYYWS	7
3-443	**Sequences**		
3-443-1	Sequence Number [ID]	443	
3-443-2	Molecule Type	AA	
3-443-3	Length	9	
3-443-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-443-5	Residues	GGSISSDAY	9
3-444	**Sequences**		
3-444-1	Sequence Number [ID]	444	
3-444-2	Molecule Type	AA	
3-444-3	Length	12	
3-444-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-444-5	Residues	GGSISSDAYY WS	12
3-445	**Sequences**		
3-445-1	Sequence Number [ID]	445	
3-445-2	Molecule Type	AA	
3-445-3	Length	16	
3-445-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-445-5	Residues	YMYYSGITYY NPSLKS	16
3-446	**Sequences**		
3-446-1	Sequence Number [ID]	446	
3-446-2	Molecule Type	AA	
3-446-3	Length	5	
3-446-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-446-5	Residues	YYSGI	5
3-447	**Sequences**		
3-447-1	Sequence Number [ID]	447	
3-447-2	Molecule Type	AA	
3-447-3	Length	8	
3-447-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-447-5	Residues	DFGWYFDL	8
3-448	**Sequences**		
3-448-1	Sequence Number [ID]	448	
3-448-2	Molecule Type	AA	
3-448-3	Length	5	
3-448-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-448-5	Residues	DYGIH	5
3-449	**Sequences**		
3-449-1	Sequence Number [ID]	449	
3-449-2	Molecule Type	AA	
3-449-3	Length	7	
3-449-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-449-5	Residues	GFTFSDY	7
3-450	**Sequences**		
3-450-1	Sequence Number [ID]	450	
3-450-2	Molecule Type	AA	
3-450-3	Length	10	
3-450-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-450-5	Residues	GFTFSDYGIH	10
3-451	**Sequences**		
3-451-1	Sequence Number [ID]	451	
3-451-2	Molecule Type	AA	
3-451-3	Length	17	
3-451-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-451-5	Residues	VIWYDGSIKK YSDSVKG	17
3-452	**Sequences**		

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3-452-1	Sequence Number [ID]	452	
3-452-2	Molecule Type	AA	
3-452-3	Length	6	
3-452-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-452-5	Residues	WYDGSI	6
3-453	**Sequences**		
3-453-1	Sequence Number [ID]	453	
3-453-2	Molecule Type	AA	
3-453-3	Length	11	
3-453-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-453-5	Residues	DEVGTFGAFD F	11
3-454	**Sequences**		
3-454-1	Sequence Number [ID]	454	
3-454-2	Molecule Type	AA	
3-454-3	Length	5	
3-454-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-454-5	Residues	NAWMS	5
3-455	**Sequences**		
3-455-1	Sequence Number [ID]	455	
3-455-2	Molecule Type	AA	
3-455-3	Length	7	
3-455-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-455-5	Residues	GFTFSNA	7
3-456	**Sequences**		
3-456-1	Sequence Number [ID]	456	
3-456-2	Molecule Type	AA	
3-456-3	Length	10	
3-456-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-456-5	Residues	GFTFSNAWMS	10
3-457	**Sequences**		
3-457-1	Sequence Number [ID]	457	
3-457-2	Molecule Type	AA	
3-457-3	Length	19	
3-457-4	Features	**REGION 1..19**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..19	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-457-5	Residues	RIKSKTGGGT TDYAAPVKG	19
3-458	**Sequences**		
3-458-1	Sequence Number [ID]	458	
3-458-2	Molecule Type	AA	

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3-458-3	Length	8	
3-458-4	Features	**REGION 1..8**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..8	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-458-5	Residues	KSKTGGGT	8
3-459	**Sequences**		
3-459-1	Sequence Number [ID]	459	
3-459-2	Molecule Type	AA	
3-459-3	Length	11	
3-459-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-459-5	Residues	LIVGAISLFD Y	11
3-460	**Sequences**		
3-460-1	Sequence Number [ID]	460	
3-460-2	Molecule Type	AA	
3-460-3	Length	5	
3-460-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-460-5	Residues	YYFWT	5
3-461	**Sequences**		
3-461-1	Sequence Number [ID]	461	
3-461-2	Molecule Type	AA	
3-461-3	Length	7	
3-461-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-461-5	Residues	GGSISYY	7
3-462	**Sequences**		
3-462-1	Sequence Number [ID]	462	
3-462-2	Molecule Type	AA	
3-462-3	Length	10	
3-462-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-462-5	Residues	GGSISYYFWT	10
3-463	**Sequences**		
3-463-1	Sequence Number [ID]	463	
3-463-2	Molecule Type	AA	
3-463-3	Length	16	
3-463-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-463-5	Residues	QIYYSGNTNS NPSLKS	16
3-464	**Sequences**		
3-464-1	Sequence Number [ID]	464	
3-464-2	Molecule Type	AA	
3-464-3	Length	5	
3-464-4	Features	**REGION 1..5**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-464-5	Residues	YYSGN	5
3-465	**Sequences**		
3-465-1	Sequence Number [ID]	465	
3-465-2	Molecule Type	AA	
3-465-3	Length	10	
3-465-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-465-5	Residues	AEGSLDAFDI	10
3-466	**Sequences**		
3-466-1	Sequence Number [ID]	466	
3-466-2	Molecule Type	AA	
3-466-3	Length	5	
3-466-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-466-5	Residues	SYSMN	5
3-467	**Sequences**		
3-467-1	Sequence Number [ID]	467	
3-467-2	Molecule Type	AA	
3-467-3	Length	7	
3-467-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-467-5	Residues	GFTFSSY	7
3-468	**Sequences**		
3-468-1	Sequence Number [ID]	468	
3-468-2	Molecule Type	AA	
3-468-3	Length	10	
3-468-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-468-5	Residues	GFTFSSYSMN	10
3-469	**Sequences**		
3-469-1	Sequence Number [ID]	469	
3-469-2	Molecule Type	AA	
3-469-3	Length	17	
3-469-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-469-5	Residues	SISTSSNYIH YADSLQG	17
3-470	**Sequences**		
3-470-1	Sequence Number [ID]	470	
3-470-2	Molecule Type	AA	
3-470-3	Length	6	
3-470-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-470-5	Residues	STSSNY	6
3-471	**Sequences**		
3-471-1	Sequence Number [ID]	471	
3-471-2	Molecule Type	AA	
3-471-3	Length	13	
3-471-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-471-5	Residues	DKGTTLTNWY FDL	13
3-472	**Sequences**		
3-472-1	Sequence Number [ID]	472	
3-472-2	Molecule Type	AA	
3-472-3	Length	5	
3-472-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-472-5	Residues	SYGMH	5
3-473	**Sequences**		
3-473-1	Sequence Number [ID]	473	
3-473-2	Molecule Type	AA	
3-473-3	Length	7	
3-473-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-473-5	Residues	GFTFSSY	7
3-474	**Sequences**		
3-474-1	Sequence Number [ID]	474	
3-474-2	Molecule Type	AA	
3-474-3	Length	10	
3-474-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-474-5	Residues	GFTFSSYGMH	10
3-475	**Sequences**		
3-475-1	Sequence Number [ID]	475	
3-475-2	Molecule Type	AA	
3-475-3	Length	17	
3-475-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-475-5	Residues	VIWYDGSNKY YADSLKG	17
3-476	**Sequences**		
3-476-1	Sequence Number [ID]	476	
3-476-2	Molecule Type	AA	
3-476-3	Length	6	
3-476-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-476-5	Residues	WYDGSN	6
3-477	**Sequences**		
3-477-1	Sequence Number [ID]	477	
3-477-2	Molecule Type	AA	
3-477-3	Length	12	
3-477-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-477-5	Residues	DGYSGSSDAF DI	12
3-478	**Sequences**		
3-478-1	Sequence Number [ID]	478	
3-478-2	Molecule Type	AA	
3-478-3	Length	5	
3-478-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-478-5	Residues	YYYWS	5
3-479	**Sequences**		
3-479-1	Sequence Number [ID]	479	
3-479-2	Molecule Type	AA	
3-479-3	Length	7	
3-479-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-479-5	Residues	GGSISYY	7
3-480	**Sequences**		
3-480-1	Sequence Number [ID]	480	
3-480-2	Molecule Type	AA	
3-480-3	Length	10	
3-480-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-480-5	Residues	GGSISYYYWS	10
3-481	**Sequences**		
3-481-1	Sequence Number [ID]	481	
3-481-2	Molecule Type	AA	
3-481-3	Length	16	
3-481-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-481-5	Residues	NINYMGNTIY NPSLKS	16
3-482	**Sequences**		
3-482-1	Sequence Number [ID]	482	
3-482-2	Molecule Type	AA	
3-482-3	Length	5	
3-482-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-482-5	Residues	NYMGN	5

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3-483	**Sequences**		
3-483-1	Sequence Number [ID]	483	
3-483-2	Molecule Type	AA	
3-483-3	Length	10	
3-483-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-483-5	Residues	AEGSLDAFDF	10
3-484	**Sequences**		
3-484-1	Sequence Number [ID]	484	
3-484-2	Molecule Type	AA	
3-484-3	Length	5	
3-484-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-484-5	Residues	GYYIY	5
3-485	**Sequences**		
3-485-1	Sequence Number [ID]	485	
3-485-2	Molecule Type	AA	
3-485-3	Length	7	
3-485-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-485-5	Residues	GYIFTGY	7
3-486	**Sequences**		
3-486-1	Sequence Number [ID]	486	
3-486-2	Molecule Type	AA	
3-486-3	Length	10	
3-486-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-486-5	Residues	GYIFTGYYIY	10
3-487	**Sequences**		
3-487-1	Sequence Number [ID]	487	
3-487-2	Molecule Type	AA	
3-487-3	Length	17	
3-487-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-487-5	Residues	WINPSSGGTN YAQKFQG	17
3-488	**Sequences**		
3-488-1	Sequence Number [ID]	488	
3-488-2	Molecule Type	AA	
3-488-3	Length	6	
3-488-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-488-5	Residues	NPSSGG	6
3-489	**Sequences**		
3-489-1	Sequence Number [ID]	489	

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3-489-2	Molecule Type	AA	
3-489-3	Length	14	
3-489-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-489-5	Residues	DRKREYYYNF GMDV	14
3-490	**Sequences**		
3-490-1	Sequence Number [ID]	490	
3-490-2	Molecule Type	AA	
3-490-3	Length	5	
3-490-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-490-5	Residues	SHYIY	5
3-491	**Sequences**		
3-491-1	Sequence Number [ID]	491	
3-491-2	Molecule Type	AA	
3-491-3	Length	7	
3-491-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-491-5	Residues	GYTFTSH	7
3-492	**Sequences**		
3-492-1	Sequence Number [ID]	492	
3-492-2	Molecule Type	AA	
3-492-3	Length	10	
3-492-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-492-5	Residues	GYTFTSHYIY	10
3-493	**Sequences**		
3-493-1	Sequence Number [ID]	493	
3-493-2	Molecule Type	AA	
3-493-3	Length	17	
3-493-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-493-5	Residues	WINPNSGGTN YAQKFQD	17
3-494	**Sequences**		
3-494-1	Sequence Number [ID]	494	
3-494-2	Molecule Type	AA	
3-494-3	Length	6	
3-494-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-494-5	Residues	NPNSGG	6
3-495	**Sequences**		
3-495-1	Sequence Number [ID]	495	
3-495-2	Molecule Type	AA	
3-495-3	Length	14	

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3-495-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-495-5	Residues	DRKREYYYNF GMDV	14
3-496	**Sequences**		
3-496-1	Sequence Number [ID]	496	
3-496-2	Molecule Type	AA	
3-496-3	Length	5	
3-496-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-496-5	Residues	SHYIY	5
3-497	**Sequences**		
3-497-1	Sequence Number [ID]	497	
3-497-2	Molecule Type	AA	
3-497-3	Length	7	
3-497-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-497-5	Residues	GFTFTSH	7
3-498	**Sequences**		
3-498-1	Sequence Number [ID]	498	
3-498-2	Molecule Type	AA	
3-498-3	Length	10	
3-498-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-498-5	Residues	GFTFTSHYIY	10
3-499	**Sequences**		
3-499-1	Sequence Number [ID]	499	
3-499-2	Molecule Type	AA	
3-499-3	Length	17	
3-499-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-499-5	Residues	WINPNSGGTK YAQKFQD	17
3-500	**Sequences**		
3-500-1	Sequence Number [ID]	500	
3-500-2	Molecule Type	AA	
3-500-3	Length	6	
3-500-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-500-5	Residues	NPNSGG	6
3-501	**Sequences**		
3-501-1	Sequence Number [ID]	501	
3-501-2	Molecule Type	AA	
3-501-3	Length	14	
3-501-4	Features	**REGION 1..14**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..14	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-501-5	Residues	DRKREYYYNF GMDV	14
3-502	**Sequences**		
3-502-1	Sequence Number [ID]	502	
3-502-2	Molecule Type	AA	
3-502-3	Length	5	
3-502-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-502-5	Residues	IYAIH	5
3-503	**Sequences**		
3-503-1	Sequence Number [ID]	503	
3-503-2	Molecule Type	AA	
3-503-3	Length	7	
3-503-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-503-5	Residues	GFTLSIY	7
3-504	**Sequences**		
3-504-1	Sequence Number [ID]	504	
3-504-2	Molecule Type	AA	
3-504-3	Length	10	
3-504-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-504-5	Residues	GFTLSIYAIH	10
3-505	**Sequences**		
3-505-1	Sequence Number [ID]	505	
3-505-2	Molecule Type	AA	
3-505-3	Length	17	
3-505-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-505-5	Residues	SFGGRGSSTY FADSVKG	17
3-506	**Sequences**		
3-506-1	Sequence Number [ID]	506	
3-506-2	Molecule Type	AA	
3-506-3	Length	6	
3-506-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-506-5	Residues	GGRGSS	6
3-507	**Sequences**		
3-507-1	Sequence Number [ID]	507	
3-507-2	Molecule Type	AA	
3-507-3	Length	10	
3-507-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-507-5	Residues	EKDWGRGFDY	10
3-508	**Sequences**		
3-508-1	Sequence Number [ID]	508	
3-508-2	Molecule Type	AA	
3-508-3	Length	5	
3-508-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-508-5	Residues	NYSMN	5
3-509	**Sequences**		
3-509-1	Sequence Number [ID]	509	
3-509-2	Molecule Type	AA	
3-509-3	Length	7	
3-509-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-509-5	Residues	GFTFSNY	7
3-510	**Sequences**		
3-510-1	Sequence Number [ID]	510	
3-510-2	Molecule Type	AA	
3-510-3	Length	10	
3-510-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-510-5	Residues	GFTFSNYSMN	10
3-511	**Sequences**		
3-511-1	Sequence Number [ID]	511	
3-511-2	Molecule Type	AA	
3-511-3	Length	17	
3-511-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-511-5	Residues	SISSSTIYIY YADSVKG	17
3-512	**Sequences**		
3-512-1	Sequence Number [ID]	512	
3-512-2	Molecule Type	AA	
3-512-3	Length	6	
3-512-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-512-5	Residues	SSSTIY	6
3-513	**Sequences**		
3-513-1	Sequence Number [ID]	513	
3-513-2	Molecule Type	AA	
3-513-3	Length	13	
3-513-4	Features	**REGION 1..13**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..13	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-513-5	Residues	DIGWEVFTLG FDY	13
3-514	**Sequences**		
3-514-1	Sequence Number [ID]	514	
3-514-2	Molecule Type	AA	
3-514-3	Length	11	
3-514-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-514-5	Residues	RASQSISTWL A	11
3-515	**Sequences**		
3-515-1	Sequence Number [ID]	515	
3-515-2	Molecule Type	AA	
3-515-3	Length	7	
3-515-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-515-5	Residues	KASSLES	7
3-516	**Sequences**		
3-516-1	Sequence Number [ID]	516	
3-516-2	Molecule Type	AA	
3-516-3	Length	9	
3-516-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-516-5	Residues	QQYKSYSHT	9
3-517	**Sequences**		
3-517-1	Sequence Number [ID]	517	
3-517-2	Molecule Type	AA	
3-517-3	Length	11	
3-517-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-517-5	Residues	RASQSISSWL A	11
3-518	**Sequences**		
3-518-1	Sequence Number [ID]	518	
3-518-2	Molecule Type	AA	
3-518-3	Length	7	
3-518-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-518-5	Residues	KASSLES	7
3-519	**Sequences**		
3-519-1	Sequence Number [ID]	519	
3-519-2	Molecule Type	AA	
3-519-3	Length	9	
3-519-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-519-5	Residues	QQYKSFSLT	9
3-520	**Sequences**		

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3-520-1	Sequence Number [ID]	520	
3-520-2	Molecule Type	AA	
3-520-3	Length	11	
3-520-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-520-5	Residues	RASQSISSWL A	11
3-521	**Sequences**		
3-521-1	Sequence Number [ID]	521	
3-521-2	Molecule Type	AA	
3-521-3	Length	7	
3-521-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-521-5	Residues	KASTLES	7
3-522	**Sequences**		
3-522-1	Sequence Number [ID]	522	
3-522-2	Molecule Type	AA	
3-522-3	Length	9	
3-522-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-522-5	Residues	QQYNSYSYT	9
3-523	**Sequences**		
3-523-1	Sequence Number [ID]	523	
3-523-2	Molecule Type	AA	
3-523-3	Length	11	
3-523-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-523-5	Residues	RASQSVSSWL A	11
3-524	**Sequences**		
3-524-1	Sequence Number [ID]	524	
3-524-2	Molecule Type	AA	
3-524-3	Length	7	
3-524-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-524-5	Residues	KASSLES	7
3-525	**Sequences**		
3-525-1	Sequence Number [ID]	525	
3-525-2	Molecule Type	AA	
3-525-3	Length	9	
3-525-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-525-5	Residues	QQYNTYSHT	9
3-526	**Sequences**		
3-526-1	Sequence Number [ID]	526	
3-526-2	Molecule Type	AA	

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3-526-3	Length	11	
3-526-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-526-5	Residues	RASQGIRNDL G	11
3-527	**Sequences**		
3-527-1	Sequence Number [ID]	527	
3-527-2	Molecule Type	AA	
3-527-3	Length	7	
3-527-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-527-5	Residues	AASSLQS	7
3-528	**Sequences**		
3-528-1	Sequence Number [ID]	528	
3-528-2	Molecule Type	AA	
3-528-3	Length	9	
3-528-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-528-5	Residues	LQDYNYPFT	9
3-529	**Sequences**		
3-529-1	Sequence Number [ID]	529	
3-529-2	Molecule Type	AA	
3-529-3	Length	11	
3-529-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-529-5	Residues	RASQDIDNYL A	11
3-530	**Sequences**		
3-530-1	Sequence Number [ID]	530	
3-530-2	Molecule Type	AA	
3-530-3	Length	7	
3-530-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-530-5	Residues	AASALQS	7
3-531	**Sequences**		
3-531-1	Sequence Number [ID]	531	
3-531-2	Molecule Type	AA	
3-531-3	Length	9	
3-531-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-531-5	Residues	QNYNSGPRT	9
3-532	**Sequences**		
3-532-1	Sequence Number [ID]	532	
3-532-2	Molecule Type	AA	
3-532-3	Length	11	
3-532-4	Features	**REGION 1..11**	

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-532-5	Residues	RASQDISNYL T	11
3-533	**Sequences**		
3-533-1	Sequence Number [ID]	533	
3-533-2	Molecule Type	AA	
3-533-3	Length	7	
3-533-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-533-5	Residues	AASALQS	7
3-534	**Sequences**		
3-534-1	Sequence Number [ID]	534	
3-534-2	Molecule Type	AA	
3-534-3	Length	9	
3-534-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-534-5	Residues	QNYNSAPRT	9
3-535	**Sequences**		
3-535-1	Sequence Number [ID]	535	
3-535-2	Molecule Type	AA	
3-535-3	Length	16	
3-535-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-535-5	Residues	RSSQSLLHSN GYNYLD	16
3-536	**Sequences**		
3-536-1	Sequence Number [ID]	536	
3-536-2	Molecule Type	AA	
3-536-3	Length	7	
3-536-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-536-5	Residues	LGSNRAS	7
3-537	**Sequences**		
3-537-1	Sequence Number [ID]	537	
3-537-2	Molecule Type	AA	
3-537-3	Length	9	
3-537-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-537-5	Residues	MQTLQTPFT	9
3-538	**Sequences**		
3-538-1	Sequence Number [ID]	538	
3-538-2	Molecule Type	AA	
3-538-3	Length	11	
3-538-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	

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		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-538-5	Residues	RASQGINSHL A	11
3-539	**Sequences**		
3-539-1	Sequence Number [ID]	539	
3-539-2	Molecule Type	AA	
3-539-3	Length	7	
3-539-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-539-5	Residues	YASTLPS	7
3-540	**Sequences**		
3-540-1	Sequence Number [ID]	540	
3-540-2	Molecule Type	AA	
3-540-3	Length	9	
3-540-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-540-5	Residues	QQLNHYPIT	9
3-541	**Sequences**		
3-541-1	Sequence Number [ID]	541	
3-541-2	Molecule Type	AA	
3-541-3	Length	11	
3-541-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-541-5	Residues	RASQGISNYL A	11
3-542	**Sequences**		
3-542-1	Sequence Number [ID]	542	
3-542-2	Molecule Type	AA	
3-542-3	Length	7	
3-542-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-542-5	Residues	AASTLHS	7
3-543	**Sequences**		
3-543-1	Sequence Number [ID]	543	
3-543-2	Molecule Type	AA	
3-543-3	Length	9	
3-543-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-543-5	Residues	QKYNSAPRT	9
3-544	**Sequences**		
3-544-1	Sequence Number [ID]	544	
3-544-2	Molecule Type	AA	
3-544-3	Length	11	
3-544-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value		
3-544-5	Residues	RASQDISNYL A	11
3-545	**Sequences**		
3-545-1	Sequence Number [ID]	545	
3-545-2	Molecule Type	AA	
3-545-3	Length	7	
3-545-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-545-5	Residues	AASTLHS	7
3-546	**Sequences**		
3-546-1	Sequence Number [ID]	546	
3-546-2	Molecule Type	AA	
3-546-3	Length	9	
3-546-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-546-5	Residues	QKYNSAPRT	9
3-547	**Sequences**		
3-547-1	Sequence Number [ID]	547	
3-547-2	Molecule Type	AA	
3-547-3	Length	11	
3-547-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-547-5	Residues	RASQDISSFL A	11
3-548	**Sequences**		
3-548-1	Sequence Number [ID]	548	
3-548-2	Molecule Type	AA	
3-548-3	Length	7	
3-548-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-548-5	Residues	VASTLQS	7
3-549	**Sequences**		
3-549-1	Sequence Number [ID]	549	
3-549-2	Molecule Type	AA	
3-549-3	Length	9	
3-549-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-549-5	Residues	QQLHVYPIT	9
3-550	**Sequences**		
3-550-1	Sequence Number [ID]	550	
3-550-2	Molecule Type	AA	
3-550-3	Length	17	
3-550-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-550-5	Residues	RSSQSLLDSD DGNTYLD	17

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3-551	**Sequences**		
3-551-1	Sequence Number [ID]	551	
3-551-2	Molecule Type	AA	
3-551-3	Length	7	
3-551-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-551-5	Residues	TLSYRAS	7
3-552	**Sequences**		
3-552-1	Sequence Number [ID]	552	
3-552-2	Molecule Type	AA	
3-552-3	Length	9	
3-552-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-552-5	Residues	MQRIEFPFT	9
3-553	**Sequences**		
3-553-1	Sequence Number [ID]	553	
3-553-2	Molecule Type	AA	
3-553-3	Length	11	
3-553-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-553-5	Residues	RASQTISTWL A	11
3-554	**Sequences**		
3-554-1	Sequence Number [ID]	554	
3-554-2	Molecule Type	AA	
3-554-3	Length	7	
3-554-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-554-5	Residues	KASNLES	7
3-555	**Sequences**		
3-555-1	Sequence Number [ID]	555	
3-555-2	Molecule Type	AA	
3-555-3	Length	9	
3-555-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-555-5	Residues	QQYQTFSHT	9
3-556	**Sequences**		
3-556-1	Sequence Number [ID]	556	
3-556-2	Molecule Type	AA	
3-556-3	Length	11	
3-556-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-556-5	Residues	RASQGISNYL A	11
3-557	**Sequences**		
3-557-1	Sequence Number [ID]	557	

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3-557-2	Molecule Type	AA	
3-557-3	Length	7	
3-557-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-557-5	Residues	AASTLQS	7
3-558	**Sequences**		
3-558-1	Sequence Number [ID]	558	
3-558-2	Molecule Type	AA	
3-558-3	Length	9	
3-558-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-558-5	Residues	QKYNSAPLT	9
3-559	**Sequences**		
3-559-1	Sequence Number [ID]	559	
3-559-2	Molecule Type	AA	
3-559-3	Length	16	
3-559-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-559-5	Residues	RSSQTLVHSN GYNYLN	16
3-560	**Sequences**		
3-560-1	Sequence Number [ID]	560	
3-560-2	Molecule Type	AA	
3-560-3	Length	7	
3-560-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-560-5	Residues	LGSNRAS	7
3-561	**Sequences**		
3-561-1	Sequence Number [ID]	561	
3-561-2	Molecule Type	AA	
3-561-3	Length	9	
3-561-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-561-5	Residues	MQAIQTPYT	9
3-562	**Sequences**		
3-562-1	Sequence Number [ID]	562	
3-562-2	Molecule Type	AA	
3-562-3	Length	11	
3-562-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-562-5	Residues	RASQSISSWL A	11
3-563	**Sequences**		
3-563-1	Sequence Number [ID]	563	
3-563-2	Molecule Type	AA	
3-563-3	Length	7	

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3-563-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-563-5	Residues	KASNLES	7
3-564	**Sequences**		
3-564-1	Sequence Number [ID]	564	
3-564-2	Molecule Type	AA	
3-564-3	Length	9	
3-564-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-564-5	Residues	QQYNSYSCT	9
3-565	**Sequences**		
3-565-1	Sequence Number [ID]	565	
3-565-2	Molecule Type	AA	
3-565-3	Length	11	
3-565-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-565-5	Residues	QASQDINNYL H	11
3-566	**Sequences**		
3-566-1	Sequence Number [ID]	566	
3-566-2	Molecule Type	AA	
3-566-3	Length	7	
3-566-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-566-5	Residues	DASDWET	7
3-567	**Sequences**		
3-567-1	Sequence Number [ID]	567	
3-567-2	Molecule Type	AA	
3-567-3	Length	9	
3-567-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-567-5	Residues	QQYDHLPIT	9
3-568	**Sequences**		
3-568-1	Sequence Number [ID]	568	
3-568-2	Molecule Type	AA	
3-568-3	Length	11	
3-568-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-568-5	Residues	QASQDISNYL H	11
3-569	**Sequences**		
3-569-1	Sequence Number [ID]	569	
3-569-2	Molecule Type	AA	
3-569-3	Length	7	
3-569-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	

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		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-569-5	Residues	DASDLET	7
3-570	**Sequences**		
3-570-1	Sequence Number [ID]	570	
3-570-2	Molecule Type	AA	
3-570-3	Length	9	
3-570-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-570-5	Residues	QQYDHLPIT	9
3-571	**Sequences**		
3-571-1	Sequence Number [ID]	571	
3-571-2	Molecule Type	AA	
3-571-3	Length	11	
3-571-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-571-5	Residues	QASQDISNYL H	11
3-572	**Sequences**		
3-572-1	Sequence Number [ID]	572	
3-572-2	Molecule Type	AA	
3-572-3	Length	7	
3-572-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-572-5	Residues	DASDLET	7
3-573	**Sequences**		
3-573-1	Sequence Number [ID]	573	
3-573-2	Molecule Type	AA	
3-573-3	Length	9	
3-573-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-573-5	Residues	QQYDHLPIT	9
3-574	**Sequences**		
3-574-1	Sequence Number [ID]	574	
3-574-2	Molecule Type	AA	
3-574-3	Length	11	
3-574-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-574-5	Residues	QASQDISNYL N	11
3-575	**Sequences**		
3-575-1	Sequence Number [ID]	575	
3-575-2	Molecule Type	AA	
3-575-3	Length	7	
3-575-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-575-5	Residues	DASNLET	7
3-576	**Sequences**		
3-576-1	Sequence Number [ID]	576	
3-576-2	Molecule Type	AA	
3-576-3	Length	9	
3-576-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-576-5	Residues	QQYDNLPYT	9
3-577	**Sequences**		
3-577-1	Sequence Number [ID]	577	
3-577-2	Molecule Type	AA	
3-577-3	Length	16	
3-577-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-577-5	Residues	RSSQSLLYSN GYNYLD	16
3-578	**Sequences**		
3-578-1	Sequence Number [ID]	578	
3-578-2	Molecule Type	AA	
3-578-3	Length	7	
3-578-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-578-5	Residues	LNSNRAS	7
3-579	**Sequences**		
3-579-1	Sequence Number [ID]	579	
3-579-2	Molecule Type	AA	
3-579-3	Length	9	
3-579-4	Features	**REGION 1..9**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..9	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-579-5	Residues	MQALQTPLT	9
3-580	**Sequences**		
3-580-1	Sequence Number [ID]	580	
3-580-2	Molecule Type	AA	
3-580-3	Length	489	
3-580-4	Features	**REGION 1..489**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct	
		source 1..489	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-580-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SYYYWTWIRQ 60 PPGKGLEWIG HIYYSGSTNY NPSLKSRVTI SIDTSKNLFS LKLSSVTAAD TAVYYCARAE 120 GSLDAFDFWG QGTMVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSTL SASVGDRVTI 180 TCRASQSIST WLAWYQQKPG KAPKVLIYKA SSLESGVPSR FSGSGSGTEF ILTINSLQPD 240 DFASYYCQQY KSYSHTFGQG TKLEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR	489
3-581	**Sequences**		
3-581-1	Sequence Number [ID]	581	
3-581-2	Molecule Type	AA	

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3-581-3	Length	484
3-581-4	Features	**REGION 1..484**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..484
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-581-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLIQPGGSLR LSCAASGFTV SSNYMTWVRQ 60 APGKGLEWVS VIYSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARNW 120 GDYWGQGTLV TVSSGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSTLSASVG DRVTITCRAS 180 QSISSWLAWY QQKPGKAPKV LIYKASSLES GVPSRFSGSG SGTEFTLTIN SLQPDDFATY 240 YCQQYKSFSL TFGQGTKLEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP AAGGAVHTRG 300 LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC 360 RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR RGRDPEMGGK 420 PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA 480 LPPR 484
3-582	**Sequences**	
3-582-1	Sequence Number [ID]	582
3-582-2	Molecule Type	AA
3-582-3	Length	489
3-582-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-582-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSGTLS LTCTVSGGSI DYYFWNWFRQ 60 SPVKGLEWIG HVYDIGNTKY NPSLKSRVTI SIDTSENQFS LKLNSVTAAD TAVYYCARGE 120 GALDAFDIWG QGTMVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSTL SASVGDRVTI 180 TCRASQSISS WLAWYQQKPG KAPKVLIYKA STLESGVPSR FSGSGSGTEF TLTISSLQPD 240 DFATYYCQQY NSYSYTFGHG TKLEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-583	**Sequences**	
3-583-1	Sequence Number [ID]	583
3-583-2	Molecule Type	AA
3-583-3	Length	489
3-583-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-583-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LNCTVSGGSI SYYYWTWIRQ 60 PPGKGLEWIG HVIYSGTTNY NPSLKSRVTI SVDTSKNQFS LKLNSVTAAD TAVYYCVRAE 120 GSLDAFDLWG QGTMVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSIL SASVGDRVTI 180 TCRASQSVSS WLAWYQQKPG KAPKVLIYKA SSLESGVPSR FSGTGSGTEF TLTISSLQSD 240 DFATYYCQQY NTYSHTFGQG TKLEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-584	**Sequences**	
3-584-1	Sequence Number [ID]	584
3-584-2	Molecule Type	AA
3-584-3	Length	491
3-584-4	Features	**REGION 1..491**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..491
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-584-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCVASGFTF SDYGIHWVRQ 60 APGMGQEWVA VIWYDGSIKK YSDSVKGRFI ISRDNSENTV YLQMNSLRGE DTAIYYCARD 120 EVGTFGAFDF WGQGTKVTVS SGGGGSGGGG SGGGGSGGGG SAIQMTQSPS SLSASVGDRV 180 TITCRASQGI RNDLGWYQQK PGKAPKLLIY AASSLQSGVP SRFSGSGSGT DFTLTISSLQ 240 PEDFATYYCL QDYNYPFTFG PGTKVDIKTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG 300 GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG RKKLLYIFKQ PFMRPVQTTQ 360 EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR 420

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		DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY 480 DALHMQALPP R 491
3-585	**Sequences**	
3-585-1	Sequence Number [ID]	585
3-585-2	Molecule Type	AA
3-585-3	Length	489
3-585-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-585-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPLQTLS LTCTVSGGSI SSDGYYWSWI 60 RQNPGKGLEW IGYMYYSGST YYNPSLKSRV TISVDTSKNQ FSLKLRSVTA ADTAVYYCTR 120 DFGWYFDLWG RGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDSITI 180 TCRASQDIDN YLAWYQQKTG KVPKVLIYAA SALQSGVPSR FSGSGSGTDF TLTISSLQPE 240 DVATYYCQNY NSGPRTFGQG TKVEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-586	**Sequences**	
3-586-1	Sequence Number [ID]	586
3-586-2	Molecule Type	AA
3-586-3	Length	489
3-586-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-586-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQSLS LTCSVSGGSV SSDGYYWSWI 60 RQHPGKGLEW IGYIYYRRIT DYNPSLKSRV NISLDTSKNQ FSLKLSSVTA ADTAVYYCAR 120 DFGWYFDLWG RGTLVAVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDRVTI 180 TCRASQDISN YLTWYQQKPG RVPEVLIYAA SALQSGVPSR FSGSGSGTDF TLTISSLQPE 240 DVATYYCQNY NSAPRTFGQG TKVEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-587	**Sequences**	
3-587-1	Sequence Number [ID]	587
3-587-2	Molecule Type	AA
3-587-3	Length	498
3-587-4	Features	**REGION 1..498**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..498
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-587-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCKASGYTF TGYYLHWVRQ 60 APGQGLEWMG WINPNSGGTN YAQKFQGRVT MTRDTSITTA YMELSRLRID DTAVYYCARD 120 RGVTMIVDGM DDWGQGTTVT VSSGGGGSGG GGSGGGGSGG GGSDIVMTQS PLSLPVTPGE 180 PASISCRSSQ SLLHSNGYNY LDWYLQKPGQ SPQVLILLGS NRASGVPDRV SASGSGTDFT 240 LKISRMQAED VGIYYCMQTL QTPFTFGQGT KLEIKTTTPA PRPPTPAPTI ASQPLSLRPE 300 ACRPAAGGAV HTRGLDFACD IYIWAPLAGT CGVLLLSLVI TLYCKRGRKK LLYIFKQPFM 360 RPVQTTQEED GCSCRFPEEE EGGCELRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV 420 LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS 480 TATKDTYDAL HMQALPPR 498
3-588	**Sequences**	
3-588-1	Sequence Number [ID]	588
3-588-2	Molecule Type	AA
3-588-3	Length	491
3-588-4	Features	**REGION 1..491**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..491
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-588-5	Residues	MALPVTALLL PLALLLHAAR PEVELVESGG GMVQPGRSLR LSCAASGFTF SDYGMHWVRQ 60 APGMGLEWVT VIWYDGSNKY YADSVKGRFT ISRDNSKNTV FLQMNSLRAE DTAVYYCARD 120

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		EVGFVGAFDI WGQGTMVTVS SGGGGSGGGG SGGGGSGGGG SDIQLTQSPS FLSASVGDRV 180 IITCRASQGI NSHLAWYQQK PGKAPKLLIY YASTLPSGVP SRFSGSGSGT EFTLTVTSLQ 240 PEDFATYYCQ QLNHYPITFG QGTRLDINTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG 300 GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG RKKLLYIFKQ PFMRPVQTTQ 360 EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR 420 DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY 480 DALHMQALPP R 491
3-589	**Sequences**	
3-589-1	Sequence Number [ID]	589
3-589-2	Molecule Type	AA
3-589-3	Length	489
3-589-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-589-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI SSDGYYWSWI 60 RQHPGKGLEW IGYMYYSGIT YHNPSLKSRV TISVDTSKNQ FSLRLSSVTA ADTAVYYCAR 120 DFGWYFDLWG RGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDRVTI 180 TCRASQGISN YLAWYQQKPG KVPKLLIYAA STLHSGVPSR FSGSGSGTDF TLTISSLQPE 240 DVATYYCQKY NSAPRTFGQG TKVEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-590	**Sequences**	
3-590-1	Sequence Number [ID]	590
3-590-2	Molecule Type	AA
3-590-3	Length	489
3-590-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-590-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI SSDAYYWSWI 60 RQHPGKGLEW IGYMYYSGIT YYNPSLKSRV TISVDTSKNQ FSLKLSSVTA ADTAVYYCAR 120 DFGWYFDLWG RGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDRVTI 180 TCRASQDISN YLAWYQQKPG KVPKLLIYAA STLHSGVPSR FSGSGSGTDF TLTISSLQPD 240 DFAAYYCQKY NSAPRTFGQG TKVEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-591	**Sequences**	
3-591-1	Sequence Number [ID]	591
3-591-2	Molecule Type	AA
3-591-3	Length	491
3-591-4	Features	**REGION 1..491**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..491
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-591-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCVASGFTF SDYGIHWVRQ 60 APGMGQEWVA VIWYDGSIKK YSDSVKGRFI ISRDNSENTV YLQMNSLRGE DTAIYYCARD 120 EVGTFGAFDF WGQGTKVTVS SGGGGSGGGG SGGGGSGGGG SDIQLTQSPS FLSASVGDRV 180 SITCRASQDI SSFLAWYQQK PGKAPVLLIY VASTLQSGVP SRFSGSGSGT EFTLTVSSLQ 240 PEDFATYYCQ QLHVYPITFG QGTRLEIRTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG 300 GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG RKKLLYIFKQ PFMRPVQTTQ 360 EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR 420 DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY 480 DALHMQALPP R 491
3-592	**Sequences**	
3-592-1	Sequence Number [ID]	592
3-592-2	Molecule Type	AA
3-592-3	Length	499
3-592-4	Features	**REGION 1..499**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..499

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-592-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVKPGGSLR LSCAASGFTF SNAWMSWVRQ 60 APGKGLEWVG RIKSKTGGGT TDYAAPVKGR FTISRDDSKN TLYLQMNSLK TEDTAVYYCT 120 SLIVGAISLF DYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSDIVMTQT PLSLPVTPGE 180 PASISCRSSQ SLLDSDDGNT YLDWYLQKPG QSPQLLIYTL SYRASGVPDR FSGSGSGTDF 240 TLKISRVEAE DVGVYYCMQR IEFPFTFGPG TKVDIKTTTP APRPPTPAPT IASQPLSLRP 300 EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF 360 MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD 420 VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL 480 STATKDTYDA LHMQALPPR 499
3-593	**Sequences**	
3-593-1	Sequence Number [ID]	593
3-593-2	Molecule Type	AA
3-593-3	Length	489
3-593-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-593-5	Residues	MALPVTALLL PLALLLHAAR PQVQLRESGP GLVKPSETLS LTCTISGGSI SYYFWTWIRQ 60 PPGRGLEWIG QIYYSGNTNS NPSLKSRVTI SIDTSKNQFS LKLTSVTVAD TAVYYCVRAE 120 GSLDAFDIWG QGTMVAVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSAL SASVGDRVAI 180 TCRASQTIST WLAWYQQKPG KAPKVLIYKA SNLESGVPSR FSGSGSGTEF TLTINSLQPD 240 DFATYYCQQY QTFSHTFGQG TKLEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-594	**Sequences**	
3-594-1	Sequence Number [ID]	594
3-594-2	Molecule Type	AA
3-594-3	Length	493
3-594-4	Features	**REGION 1..493**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..493
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-594-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVKPGGSLR LSCVASGFTF SSYSMNWVRQ 60 FPGKGLEWVS SISTSSNYIH YADSLQGRFT ISRDNAKNSL YLQMSSLRVE DTAVYYCVRD 120 KGTTLTNWYF DLWGRGTLVT VSSGGGGSGG GGSGGGGSGG GGSDMQMTQS PSSLSASVGD 180 RVTLTCRASQ GISNYLAWFQ LKPGKVPKLL IYAASTLQSG VPSRFSGSGS GTDFALTISS 240 LQPEDVATYY CQKYNSAPLT FGGGTKVEIK TTTPAPRPPT PAPTIASQPL SLRPEACRPA 300 AGGAVHTRGL DFACDIYIWA PLAGTCGVLL LSLVITLYCK RGRKKLLYIF KQPFMRPVQT 360 TQEEDGCSCR FPEEEEGGCE LRVKFSRSAD APAYQQGQNQ LYNELNLGRR EEYDVLDKRR 420 GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD 480 TYDALHMQAL PPR 493
3-595	**Sequences**	
3-595-1	Sequence Number [ID]	595
3-595-2	Molecule Type	AA
3-595-3	Length	497
3-595-4	Features	**REGION 1..497**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..497
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-595-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCGASGFTF SSYGMHWVRQ 60 APGKGLEWVA VIWYDGSNKY YADSLKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARD 120 GYSGSSDAFD IWGQGTMVTV SSGGGGSGGG GSGGGGSGGG GSDIVMTQSP LSLPVTPGEP 180 ASISCRSSQT LVHSNGYNYL NWYLQKPGQS PQLLIYLGSN RASGVPDRFS GSGSGSDFTL 240 KISRMEAEDV GVYYCMQAIQ TPYTFGQGTN VEIKTTTPAP RPPTPAPTIA SQPLSLRPEA 300 CRPAAGGAVH TRGLDFACDI YIWAPLAGTC GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR 360 PVQTTQEEDG CSCRFPEEEE GGCELRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL 420 DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST 480 ATKDTYDALH MQALPPR 497
3-596	**Sequences**	
3-596-1	Sequence Number [ID]	596
3-596-2	Molecule Type	AA

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3-596-3	Length	489
3-596-4	Features	**REGION 1..489**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..489
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-596-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVQPSETLS LTCTVSGGSI SYYYWSWIRQ 60 PPGKGLEWIG NINYMGNTIY NPSLKSRVTI SVDTSKDQFS LKLTSVSAAD TAVYYCVRAE 120 GSLDAFDFWG QGTLVAVSLG GGGSGGGGSG GGGSGGGGSD IQMTQSPSTL SASVGDRVTI 180 TCRASQSISS WLAWYQQKPG KAPKVLIYKA SNLESGVPSR FSGSGSGTEF TLTISSLQPD 240 DFATYYCQQY NSYSCTFGQG TKLEIKTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR 489
3-597	**Sequences**	
3-597-1	Sequence Number [ID]	597
3-597-2	Molecule Type	AA
3-597-3	Length	494
3-597-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-597-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVTKPGASVK VSCKASGYIF TGYYIYWVRQ 60 APGQGLEWMG WINPSSGGTN YAQKFQGRVT MARDTSISTA YMELSSLRSD DTAVYYCARD 120 RKREYYYNFG MDVWGQGTTV TVSTGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSSLSASVG 180 DRIIFTCQAS QDINNYLHWY QQKPGKAPKL LIYDASDWET GVPSRFSGSG SGTDFTFTIS 240 SLQPEDIATY YCQQYDHLPI TFGQGTRVEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-598	**Sequences**	
3-598-1	Sequence Number [ID]	598
3-598-2	Molecule Type	AA
3-598-3	Length	494
3-598-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-598-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQSGA EVTKPGASVK VSCKASGYTF TSHYIYWVRQ 60 APGQGLEWMG WINPNSGGTN YAQKFQDRVT MARDTSISTA YMELSRLRSD DTAVYYCAKD 120 RKREYYYNFG MDVWGQGTTV TVSAGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSSLSASVG 180 DRVILTCQAS QDISNYLHWY QQKPGKAPKL LIYDASDLET GVPSRFSGSG SGADFTFTIS 240 NLQPEDFATY YCQQYDHLPI TFGQGTRLEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-599	**Sequences**	
3-599-1	Sequence Number [ID]	599
3-599-2	Molecule Type	AA
3-599-3	Length	494
3-599-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-599-5	Residues	MALPVTALLL PLALLLHAAR PQVQLVQFGV EVRKPGASVK VSCKVSGFTF TSHYIYWVRQ 60 APGQGLEWMG WINPNSGGTK YAQKFQDRVT MARDTSISTA YMELSRLRSD DTSVYYCVKD 120 RKREYYYNFG MDVWGQGTTV TVSSGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSSLSASVG 180 DRVILTCQAS QDISNYLHWY QQKPGKAPKL LIYDASDLET GVPSRFSGSG SGADFTFTIS 240 NLQPEDFATY YCQQYDHLPI TFGQGTRLEI KTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420

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		RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-600	**Sequences**	
3-600-1	Sequence Number [ID]	600
3-600-2	Molecule Type	AA
3-600-3	Length	490
3-600-4	Features	**REGION 1..490**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..490
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-600-5	Residues	MALPVTALLL PLALLLHAAR PEVQMLESGG GLIQPGGSLR LSCKTSGFTL SIYAIHWVRQ 60 APGRGLEWVS SFGGRGSSTY FADSVKGRFT ISRDASENSL YLHMNSLRAE DTAVYYCAKE 120 KDWGRGFDYW GQGTLVTVSS GGGGSGGGGS GGGGSGGGGS DIQMTQSPSS LSASVGDRVT 180 ITCQASQDIS NYLNWYQQKP GKAPKLLIYD ASNLETGVPS RFSGSGSGTD FTFTISSLQP 240 EDIATYYCQQ YDNLPYTFGQ GTKLEIKTTT PAPRPPTPAP TIASQPLSLR PEACRPAAGG 300 AVHTRGLDFA CDIYIWAPLA GTCGVLLLSL VITLYCKRGR KKLLYIFKQP FMRPVQTTQE 360 EDGCSCRFPE EEEGGCELRV KFSRSADAPA YQQGQNQLYN ELNLGRREEY DVLDKRRGRD 420 PEMGGKPRRK NPQEGLYNEL QKDKMAEAYS EIGMKGERRR GKGHDGLYQG LSTATKDTYD 480 ALHMQALPPR 490
3-601	**Sequences**	
3-601-1	Sequence Number [ID]	601
3-601-2	Molecule Type	AA
3-601-3	Length	498
3-601-4	Features	**REGION 1..498**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic construct
		source 1..498
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-601-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVESGG GLVKPGGSLR LSCAASGFTF SNYSMNWVRQ 60 APGKGLEWVS SISSSTIYIY YADSVKGRFT ISRDNAKKSL YLQMNSLRAE DTAVYYCARD 120 IGWEVFTLGF DYWGQGTQVT VSSGGGGSGG GGSGGGGSGG GGSDIVMTQS PLSLPVTPGE 180 PASISCRSSQ SLLYSNGYNY LDWYLQKPGQ SPQLLIFLNS NRASGVPDRF SGSGSGTDFT 240 LKISRVEAED VGVYFCMQAL QTPLTFGGGT KVEIKTTTPA PRPPTPAPTI ASQPLSLRPE 300 ACRPAAGGAV HTRGLDFACD IYIWAPLAGT CGVLLLSLVI TLYCKRGRKK LLYIFKQPFM 360 RPVQTTQEED GCSCRFPEEE EGGCELRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV 420 LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS 480 TATKDTYDAL HMQALPPR 498
3-602	**Sequences**	
3-602-1	Sequence Number [ID]	602
3-602-2	Molecule Type	AA
3-602-3	Length	20
3-602-4	Features	**REGION 1..20**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..20
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-602-5	Residues	GGGGSGGGGS GGGGSGGGGS 20
3-603	**Sequences**	
3-603-1	Sequence Number [ID]	603
3-603-2	Molecule Type	AA
3-603-3	Length	12
3-603-4	Features	**REGION 1..12**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..12
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-603-5	Residues	CQFDLSTRRL KC 12
3-604	**Sequences**	
3-604-1	Sequence Number [ID]	604
3-604-2	Molecule Type	AA
3-604-3	Length	12
3-604-4	Features	**REGION 1..12**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..12
		mol_type=protein

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		organism=synthetic construct	
	NonEnglishQualifier Value		
3-604-5	Residues	CQYNLSSRAL KC	12
3-605	**Sequences**		
3-605-1	Sequence Number [ID]	605	
3-605-2	Molecule Type	AA	
3-605-3	Length	12	
3-605-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-605-5	Residues	CVWQRWQKSY VC	12
3-606	**Sequences**		
3-606-1	Sequence Number [ID]	606	
3-606-2	Molecule Type	AA	
3-606-3	Length	12	
3-606-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-606-5	Residues	CMWDRFSRWY KC	12
3-607	**Sequences**		
3-607-1	Sequence Number [ID]	607	
3-607-2	Molecule Type	AA	
3-607-3	Length	25	
3-607-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-607-5	Residues	SFVLNWYRMS PSNQTDKLAA FPEDR	25
3-608	**Sequences**		
3-608-1	Sequence Number [ID]	608	
3-608-2	Molecule Type	AA	
3-608-3	Length	19	
3-608-4	Features	**REGION 1..19**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..19	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-608-5	Residues	SGTYLCGAIS LAPKAQIKE	19
3-609	**Sequences**		
3-609-1	Sequence Number [ID]	609	
3-609-2	Molecule Type	AA	
3-609-3	Length	16	
3-609-4	Features	**REGION 1..16**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..16	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-609-5	Residues	ELPTQGTFSN VSTNVS	16
3-610	**Sequences**		
3-610-1	Sequence Number [ID]	610	
3-610-2	Molecule Type	AA	
3-610-3	Length	12	
3-610-4	Features	**REGION 1..12**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..12	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-610-5	Residues	GQNDTSQTSS PS	12
3-611	**Sequences**		
3-611-1	Sequence Number [ID]	611	
3-611-2	Molecule Type	AA	
3-611-3	Length	21	
3-611-4	Features	**REGION 1..21**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..21	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-611-5	Residues	MGTSLLCWMA LCLLGADHAD A	21
3-612	**Sequences**		
3-612-1	Sequence Number [ID]	612	
3-612-2	Molecule Type	AA	
3-612-3	Length	18	
3-612-4	Features	**REGION 1..18**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..18	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-612-5	Residues	GSTSGSGKPG SGEGSTKG	18
3-613	**Sequences**		
3-613-1	Sequence Number [ID]	613	
3-613-2	Molecule Type	AA	
3-613-3	Length	25	
3-613-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		REGION 1..25	
		note=MISC_FEATURE - This sequence may encompass 1-5 "Gly Gly Gly Gly Ser" repeating units	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-613-5	Residues	GGGGSGGGGS GGGGSGGGGS GGGGS	25
3-614	**Sequences**		
3-614-1	Sequence Number [ID]	614	
3-614-2	Molecule Type	AA	
3-614-3	Length	5	
3-614-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-614-5	Residues	SGGGG	5
3-615	**Sequences**		
3-615-1	Sequence Number [ID]	615	
3-615-2	Molecule Type	AA	
3-615-3	Length	5	
3-615-4	Features	**REGION 1..5**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..5	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-615-5	Residues	GGGGS	5
3-616	**Sequences**		
3-616-1	Sequence Number [ID]	616	
3-616-2	Molecule Type	AA	
3-616-3	Length	6	
3-616-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		

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3-616-5	Residues	SGGGGS	6
3-617	**Sequences**		
3-617-1	Sequence Number [ID]	617	
3-617-2	Molecule Type	AA	
3-617-3	Length	25	
3-617-4	Features	**REGION 1..25**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..25	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-617-5	Residues	GGGGSCPYSN PSLCSGGGGS GGGGS	25
3-618	**Sequences**		
3-618-1	Sequence Number [ID]	618	
3-618-2	Molecule Type	AA	
3-618-3	Length	55	
3-618-4	Features	**REGION 1..55**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..55	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-618-5	Residues	GSGGGGSCPY SNPSLCSGGG GSELPTQGTF SNVSTNVSPA KPTTTACPYS NPSLC	55
3-619	**Sequences**		
3-619-1	Sequence Number [ID]	619	
3-619-2	Molecule Type	AA	
3-619-3	Length	489	
3-619-4	Features	**REGION 1..489**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..489	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-619-5	Residues	MALPVTALLL PLALLLHAAR PQVTLKESGP VLVKPTETLT LTCTVSGFSL SNARMGVTWI 60 RQPPGKALEW LAHIFSNDEK SYSTSLKSRL TISKDTSKTQ VVLTMTNMDP VDTATYYCAR 120 IRDYYDISSY YDYWGQGTLV SVSSGGGGSG GGGSGGGGSD IQMTQSPSAM SASVGDRVTI 180 TCRASQDISN YLAWFQQKPG KVPKRLIYAA SSLQSGVPSR FSGSGSGTEF TLTISSLLPE 240 DFATYYCLQL NSFPFTFGGG TKVEINTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA 300 VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE 360 DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP 420 EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA 480 LHMQALPPR	489
3-620	**Sequences**		
3-620-1	Sequence Number [ID]	620	
3-620-2	Molecule Type	AA	
3-620-3	Length	526	
3-620-4	Features	**REGION 1..526**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..526	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-620-5	Residues	MALPVTALLL PLALLLHAAR PQVTLKESGP VLVKPTETLT LTCTVSGFSL SNARMGVTWI 60 RQPPGKALEW LAHIFSNDEK SYSTSLKSRL TISKDTSKTQ VVLTMTNMDP VDTATYYCAR 120 IRDYYDISSY YDYWGQGTLV SVSSGGGGSG GGGSGGGGSD IQMTQSPSAM SASVGDRVTI 180 TCRASQDISN YLAWFQQKPG KVPKRLIYAA SSLQSGVPSR FSGSGSGTEF TLTISSLLPE 240 DFATYYCLQL NSFPFTFGGG TKVEINGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR	526
3-621	**Sequences**		
3-621-1	Sequence Number [ID]	621	
3-621-2	Molecule Type	AA	
3-621-3	Length	536	
3-621-4	Features	**REGION 1..536**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide	
		source 1..536	
		mol_type=protein	
		organism=synthetic construct	

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	NonEnglishQualifier Value	
3-621-5	Residues	MALPVTALLL PLALLLHAAR PEVQLVQSGA EVKKPGESLK ISCKGSGYGF TSYWIGWVRQ 60 MPGKGLEWMG IIHPDDSDTK YSPSFQGQVT ISADKSISTA YLQWSSLKAS DTAMYYCASS 120 YLRGLWGGYF DYWGQGTLVT VSSGGGGSGG GGSGGGGSGG GGSELQSVLT QPPSASGTPG 180 QRVTISCSGS SSNIGSNYVN WYQQLPGTAP KLLIYGDYQR PSGVPDRFSG SKSGTSASLA 240 ISGLRSEDEA DYYCATRDDS LSGSVVFGTG TKLTVLGSGG GGSCPYSNPS LCSGGGGSCP 300 YSNPSLCSGG GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY 360 IWAPLAGTCG VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG 420 GCELRVKFSR SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE 480 GLYNELQKDK MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 536
3-622	**Sequences**	
3-622-1	Sequence Number [ID]	622
3-622-2	Molecule Type	AA
3-622-3	Length	526
3-622-4	Features	**REGION 1..526**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..526** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-622-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LTCTVSGGSI SYYYWTWIRQ 60 PPGKGLEWIG HIYYSGSTNY NPSLKSRVTI SIDTSKNLFS LKLSSVTAAD TAVYYCARAE 120 GSLDAFDFWG QGTMVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSTL SASVGDRVTI 180 TCRASQSIST WLAWYQQKPG KAPKVLIYKA SSLESGVPSR FSGSGSGTEF ILTINSLQPD 240 DFASYYCQQY KSYSHTFGQG TKLEIKGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 526
3-623	**Sequences**	
3-623-1	Sequence Number [ID]	623
3-623-2	Molecule Type	AA
3-623-3	Length	526
3-623-4	Features	**REGION 1..526**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..526** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-623-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSETLS LNCTVSGGSI SYYYWTWIRQ 60 PPGKGLEWIG HVIYSGTTNY NPSLKSRVTI SVDTSKNQFS LKLNSVTAAD TAVYYCVRAE 120 GSLDAFDLWG QGTMVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSIL SASVGDRVTI 180 TCRASQSVSS WLAWYQQKPG KAPKVLIYKA SSLESGVPSR FSGTGSGTEF TLTISSLQSD 240 DFATYYCQQY NTYSHTFGQG TKLEIKGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 526
3-624	**Sequences**	
3-624-1	Sequence Number [ID]	624
3-624-2	Molecule Type	AA
3-624-3	Length	526
3-624-4	Features	**REGION 1..526**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..526** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-624-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPLQTLS LTCTVSGGSI SSDGYYWSWI 60 RQNPGKGLEW IGYMYYSGST YYNPSLKSRV TISVDTSKNQ FSLKLRSVTA ADTAVYYCTR 120 DFGWYFDLWG RGTLVTVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDSITI 180 TCRASQDIDN YLAWYQQKTG KVPKVLIYAA SALQSGVPSR FSGSGSGTDF TLTISSLQPE 240 DVATYYCQNY NSGPRTFGQG TKVEIKGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 526
3-625	**Sequences**	
3-625-1	Sequence Number [ID]	625
3-625-2	Molecule Type	AA
3-625-3	Length	526
3-625-4	Features	**REGION 1..526**

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	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..526
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-625-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQSLS LTCSVSGGSV SSDGYYWSWI 60 RQHPGKGLEW IGYIYYRRIT DYNPSLKSRV NISLDTSKNQ FSLKLSSVTA ADTAVYYCAR 120 DFGWYFDLWG RGTLVAVSSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDRVTI 180 TCRASQDISN YLTWYQQKPG RVPEVLIYAA SALQSGVPSR FSGSGSGTDF TLTISSLQPE 240 DVATYYCQNY NSAPRTFGQG TKVEIKGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 526
3-626	**Sequences**	
3-626-1	Sequence Number [ID]	626
3-626-2	Molecule Type	AA
3-626-3	Length	528
3-626-4	Features	**REGION 1..528**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..528
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-626-5	Residues	MALPVTALLL PLALLLHAAR PEVELVESGG GMVQPGRSLR LSCAASGFTF SDYGMHWVRQ 60 APGMGLEWVT VIWYDGSNKY YADSVKGRFT ISRDNSKNTV FLQMNSLRAE DTAVYYCARD 120 EVGFVGAFDI WGQGTMVTVS SGGGGSGGGG SGGGGSGGGG SDIQLTQSPS FLSASVGDRV 180 IITCRASQGI NSHLAWYQQK PGKAPKLLIY YASTLPSGVP SRFSGSGSGT EFTLTVTSLQ 240 PEDFATYYCQ QLNHYPITFG QGTRLDINGS GGGGSCPYSN PSLCSGGGGS CPYSNPSLCS 300 GGGGSTTTPA PRPPTPAPTI ASQPLSLRPE ACRPAAGGAV HTRGLDFACD IYIWAPLAGT 360 CGVLLLSLVI TLYCKRGRKK LLYIFKQPFM RPVQTTQEED GCSCRFPEEE EGGCELRVKF 420 SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK 480 DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR 528
3-627	**Sequences**	
3-627-1	Sequence Number [ID]	627
3-627-2	Molecule Type	AA
3-627-3	Length	526
3-627-4	Features	**REGION 1..526**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..526
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-627-5	Residues	MALPVTALLL PLALLLHAAR PQVQLQESGP GLVQPSETLS LTCTVSGGSI SYYYWSWIRQ 60 PPGKGLEWIG NINYMGNTIY NPSLKSRVTI SVDTSKDQFS LKLTSVSAAD TAVYYCVRAE 120 GSLDAFDFWG QGTLVAVSLG GGGSGGGGSG GGGSGGGGSD IQMTQSPSTL SASVGDRVTI 180 TCRASQSISS WLAWYQQKPG KAPKVLIYKA SNLESGVPSR FSGSGSGTEF TLTISSLQPD 240 DFATYYCQQY NSYSCTFGQG TKLEIKGSGG GGSCPYSNPS LCSGGGGSCP YSNPSLCSGG 300 GGSTTTPAPR PPTPAPTIAS QPLSLRPEAC RPAAGGAVHT RGLDFACDIY IWAPLAGTCG 360 VLLLSLVITL YCKRGRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GCELRVKFSR 420 SADAPAYQQG QNQLYNELNL GRREEYDVLD KRRGRDPEMG GKPRRKNPQE GLYNELQKDK 480 MAEAYSEIGM KGERRRGKGH DGLYQGLSTA TKDTYDALHM QALPPR 526
3-628	**Sequences**	
3-628-1	Sequence Number [ID]	628
3-628-2	Molecule Type	AA
3-628-3	Length	569
3-628-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..569
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-628-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVTL KESGPVLVKP 60 TETLTLTCTV SGFSLSNARM GVTWIRQPPG KALEWLAHIF SNDEKSYSTS LKSRLTISKD 120 TSKTQVVLTM TNMDPVDTAT YYCARIRDYY DISSYYDYWG QGTLVSVSSG GGGSGGGGSG 180 GGGSDIQMTQ SPSAMSASVG DRVTITCRAS QDISNYLAWF QQKPGKVPKR LIYAASSLQS 240 GVPSRFSGSG SGTEFTLTIS SLLPEDFATY YCLQLNSFPF TFGGGTKVEI NGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569

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3-629	**Sequences**	
3-629-1	Sequence Number [ID]	629
3-629-2	Molecule Type	AA
3-629-3	Length	579
3-629-4	Features	**REGION 1..579**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..579
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-629-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSEVQL VQSGAEVKKP 60 GESLKISCKG SGYGFTSYWI GWVRQMPGKG LEWMGIIHPD DSDTKYSPSF QGQVTISADK 120 SISTAYLQWS SLKASDTAMY YCASSYLRGL WGGYFDYWGQ GTLVTVSSGG GGSGGGGSGG 180 GGSGGGGSEL QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG SNYVNWYQQL PGTAPKLLIY 240 GDYQRPSGVP DRFSGSKSGT SASLAISGLR SEDEADYYCA TRDDSLSGSV VFGTGTKLTV 300 LGSGGGGSCP YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP 360 APRPPTPAPT IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV 420 ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY 480 QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE 540 IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQALPPR 579
3-630	**Sequences**	
3-630-1	Sequence Number [ID]	630
3-630-2	Molecule Type	AA
3-630-3	Length	569
3-630-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..569
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-630-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVQL QESGPGLVKP 60 SETLSLTCTV SGGSISYYYW TWIRQPPGKG LEWIGHIYYS GSTNYNPSLK SRVTISIDTS 120 KNLFSLKLSS VTAADTAVYY CARAEGSLDA FDFWGQGTMV TVSSGGGGSG GGGSGGGGSG 180 GGGSDIQMTQ SPSTLSASVG DRVTITCRAS QSISTWLAWY QQKPGKAPKV LIYKASSLES 240 GVPSRFSGSG SGTEFILTIN SLQPDDFASY YCQQYKSYSH TFGQGTKLEI KGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569
3-631	**Sequences**	
3-631-1	Sequence Number [ID]	631
3-631-2	Molecule Type	AA
3-631-3	Length	569
3-631-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..569
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-631-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVQL QESGPGLVKP 60 SETLSLNCTV SGGSISYYYW TWIRQPPGKG LEWIGHVIYS GTTNYNPSLK SRVTISVDTS 120 KNQFSLKLNS VTAADTAVYY CVRAEGSLDA FDLWGQGTMV TVSSGGGGSG GGGSGGGGSG 180 GGGSDIQMTQ SPSILSASVG DRVTITCRAS QSVSSWLAWY QQKPGKAPKV LIYKASSLES 240 GVPSRFSGTG SGTEFTLTIS SLQSDDFATY YCQQYNTYSH TFGQGTKLEI KGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569
3-632	**Sequences**	
3-632-1	Sequence Number [ID]	632
3-632-2	Molecule Type	AA
3-632-3	Length	569
3-632-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..569
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-632-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVQL QESGPGLVKP 60

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		LQTLSLTCTV SGGSISSDGY YWSWIRQNPG KGLEWIGYMY YSGSTYYNPS LKSRVTISVD 120 TSKNQFSLKL RSVTAADTAV YYCTRDFGWY FDLWGRGTLV TVSSGGGGSG GGGSGGGGSG 180 GGGSDIQMTQ SPSSLSASVG DSITITCRAS QDIDNYLAWY QQKTGKVPKV LIYAASALQS 240 GVPSRFSGSG SGTDFTLTIS SLQPEDVATY YCQNYNSGPR TFGQGTKVEI KGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569
3-633	**Sequences**	
3-633-1	Sequence Number [ID]	633
3-633-2	Molecule Type	AA
3-633-3	Length	569
3-633-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..569** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-633-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVQL QESGPGLVKP 60 SQSLSLTCSV SGGSVSSDGY YWSWIRQHPG KGLEWIGYIY YRRITDYNPS LKSRVNISLD 120 TSKNQFSLKL SSVTAADTAV YYCARDFGWY FDLWGRGTLV AVSSGGGGSG GGGSGGGGSG 180 GGGSDIQMTQ SPSSLSASVG DRVTITCRAS QDISNYLTWY QQKPGRVPEV LIYAASALQS 240 GVPSRFSGSG SGTDFTLTIS SLQPEDVATY YCQNYNSAPR TFGQGTKVEI KGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569
3-634	**Sequences**	
3-634-1	Sequence Number [ID]	634
3-634-2	Molecule Type	AA
3-634-3	Length	571
3-634-4	Features	**REGION 1..571**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..571** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-634-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSEVEL VESGGGMVQP 60 GRSLRLSCAA SGFTFSDYGM HWVRQAPGMG LEWVTVIWYD GSNKYYADSV KGRFTISRDN 120 SKNTVFLQMN SLRAEDTAVY YCARDEVGFV GAFDIWGQGT MVTVSSGGGG SGGGGSGGGG 180 SGGGGSDIQL TQSPSFLSAS VGDRVIITCR ASQGINSHLA WYQQKPGKAP KLLIYYASTL 240 PSGVPSRFSG SGSGTEFTLT VTSLQPEDFA TYYCQQLNHY PITFGQGTRL DINGSGGGGS 300 CPYSNPSLCS GGGGSELPTQ GTFSNVSTNV SPAKPTTTAC PYSNPSLCTT TPAPRPPTPA 360 PTIASQPLSL RPEACRPAAG GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG 420 RKKLLYIFKQ PFMRPVQTTQ EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY 480 NELNLGRREE YDVLDKRRGR DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR 540 RGKGHDGLYQ GLSTATKDTY DALHMQALPP R 571
3-635	**Sequences**	
3-635-1	Sequence Number [ID]	635
3-635-2	Molecule Type	AA
3-635-3	Length	569
3-635-4	Features	**REGION 1..569**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..569** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-635-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVQL QESGPGLVQP 60 SETLSLTCTV SGGSISYYYW SWIRQPPGKG LEWIGNINYM GNTIYNPSLK SRVTISVDTS 120 KDQFSLKLTS VSAADTAVYY CVRAEGSLDA FDFWGQGTLV AVSLGGGGSG GGGSGGGGSG 180 GGGSDIQMTQ SPSTLSASVG DRVTITCRAS QSISSWLAWY QQKPGKAPKV LIYKASNLES 240 GVPSRFSGSG SGTEFTLTIS SLQPDDFATY YCQQYNSYSC TFGQGTKLEI KGSGGGGSCP 300 YSNPSLCSGG GGSELPTQGT FSNVSTNVSP AKPTTTACPY SNPSLCTTTP APRPPTPAPT 360 IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG TCGVLLLSLV ITLYCKRGRK 420 KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK FSRSADAPAY QQGQNQLYNE 480 LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG 540 KGHDGLYQGL STATKDTYDA LHMQALPPR 569
3-636	**Sequences**	
3-636-1	Sequence Number [ID]	636
3-636-2	Molecule Type	AA

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3-636-3	Length	527
3-636-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-636-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVTLKESGPV LVKPTETLTL 60 TCTVSGFSLS NARMGVTWIR QPPGKALEWL AHIFSNDEKS YSTSLKSRLT ISKDTSKTQV 120 VLTMTNMDPV DTATYYCARI RDYYDISSYY DYWGQGTLVS VSSGGGGSGG GGSGGGGSDI 180 QMTQSPSAMS ASVGDRVTIT CRASQDISNY LAWFQQKPGK VPKRLIYAAS SLQSGVPSRF 240 SGSGSGTEFT LTISSLLPED FATYYCLQLN SFPFTFGGGT KVEINGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-637	**Sequences**	
3-637-1	Sequence Number [ID]	637
3-637-2	Molecule Type	AA
3-637-3	Length	537
3-637-4	Features	**REGION 1..537**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..537
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-637-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVQLVQSGAE VKKPGESLKI 60 SCKGSGYGFT SYWIGWVRQM PGKGLEWMGI IHPDDSDTKY SPSFQGQVTI SADKSISTAY 120 LQWSSLKASD TAMYYCASSY LRGLWGGYFD YWGQGTLVTV SSGGGGSGGG GSGGGGSGGG 180 GSELQSVLTQ PPSASGTPGQ RVTISCSGSS SNIGSNYVNW YQQLPGTAPK LLIYGDYQRP 240 SGVPDRFSGS KSGTSASLAI SGLRSEDEAD YYCATRDDSL SGSVVFGTGT KLTVLGGGGS 300 CPYSNPSLCG GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI 360 YIWAPLAGTC GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE 420 GGCELRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ 480 EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 537
3-638	**Sequences**	
3-638-1	Sequence Number [ID]	638
3-638-2	Molecule Type	AA
3-638-3	Length	527
3-638-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-638-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSETLSL 60 TCTVSGGSIS YYYWTWIRQP PGKGLEWIGH IYYSGSTNYN PSLKSRVTIS IDTSKNLFSL 120 KLSSVTAADT AVYYCARAEG SLDAFDFWGQ GTMVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSTLS ASVGDRVTIT CRASQSISTW LAWYQQKPGK APKVLIYKAS SLESGVPSRF 240 SGSGSGTEFI LTINSLQPDD FASYYCQQYK SYSHTFGQGT KLEIKGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-639	**Sequences**	
3-639-1	Sequence Number [ID]	639
3-639-2	Molecule Type	AA
3-639-3	Length	527
3-639-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-639-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSETLSL 60 NCTVSGGSIS YYYWTWIRQP PGKGLEWIGH VIYSGTTNYN PSLKSRVTIS VDTSKNQFSL 120 KLNSVTAADT AVYYCVRAEG SLDAFDLWGQ GTMVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSILS ASVGDRVTIT CRASQSVSSW LAWYQQKPGK APKVLIYKAS SLESGVPSRF 240 SGTGSGTEFT LTISSLQSDD FATYYCQQYN TYSHTFGQGT KLEIKGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420

		RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-640	**Sequences**	
3-640-1	Sequence Number [ID]	640
3-640-2	Molecule Type	AA
3-640-3	Length	527
3-640-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-640-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPLQTLSL 60 TCTVSGGSIS SDGYYWSWIR QNPGKGLEWI GYMYYSGSTY YNPSLKSRVT ISVDTSKNQF 120 SLKLRSVTAA DTAVYYCTRD FGWYFDLWGR GTLVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSSLS ASVGDSITIT CRASQDIDNY LAWYQQKTGK VPKVLIYAAS ALQSGVPSRF 240 SGSGSGTDFT LTISSLQPED VATYYCQNYN SGPRTFGQGT KVEIKGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-641	**Sequences**	
3-641-1	Sequence Number [ID]	641
3-641-2	Molecule Type	AA
3-641-3	Length	527
3-641-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-641-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSQSLSL 60 TCSVSGGSVS SDGYYWSWIR QHPGKGLEWI GYIYYRRITD YNPSLKSRVN ISLDTSKNQF 120 SLKLSSVTAA DTAVYYCARD FGWYFDLWGR GTLVAVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSSLS ASVGDRVTIT CRASQDISNY LTWYQQKPGR VPEVLIYAAS ALQSGVPSRF 240 SGSGSGTDFT LTISSLQPED VATYYCQNYN SAPRTFGQGT KVEIKGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-642	**Sequences**	
3-642-1	Sequence Number [ID]	642
3-642-2	Molecule Type	AA
3-642-3	Length	529
3-642-4	Features	**REGION 1..529**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..529
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-642-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVELVESGGG MVQPGRSLRL 60 SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY ADSVKGRFTI SRDNSKNTVF 120 LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS GGGGSGGGGS GGGGSGGGGS 180 DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 240 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLDINGGG GSCPYSNPSL 300 CGGGGSTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG 360 TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK 420 FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ 480 KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQALPPR 529
3-643	**Sequences**	
3-643-1	Sequence Number [ID]	643
3-643-2	Molecule Type	AA
3-643-3	Length	527
3-643-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-643-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVQPSETLSL 60 TCTVSGGSIS YYYWSWIRQP PGKGLEWIGN INYMGNTIYN PSLKSRVTIS VDTSKDQFSL 120

		KLTSVSAADT AVYYCVRAEG SLDAFDFWGQ GTLVAVSLGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSTLS ASVGDRVTIT CRASQSISSW LAWYQQKPGK APKVLIYKAS NLESGVPSRF 240 SGSGSGTEFT LTISSLQPDD FATYYCQQYN SYSCTFGQGT KLEIKGGGGS CPYSNPSLCG 300 GGGSTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-644	**Sequences**	
3-644-1	Sequence Number [ID]	644
3-644-2	Molecule Type	AA
3-644-3	Length	522
3-644-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-644-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVTLKESGPV LVKPTETLTL 60 TCTVSGFSLS NARMGVTWIR QPPGKALEWL AHIFSNDEKS YSTSLKSRLT ISKDTSKTQV 120 VLTMTNMDPV DTATYYCARI RDYYDISSYY DYWGQGTLVS VSSGGGGSGG GGSGGGGSDI 180 QMTQSPSAMS ASVGDRVTIT CRASQDISNY LAWFQQKPGK VPKRLIYAAS SLQSGVPSRF 240 SGSGSGTEFT LTISSLLPED FATYYCLQLN SFPFTFGGGT KVEINGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-645	**Sequences**	
3-645-1	Sequence Number [ID]	645
3-645-2	Molecule Type	AA
3-645-3	Length	532
3-645-4	Features	**REGION 1..532**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..532
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-645-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVQLVQSGAE VKKPGESLKI 60 SCKGSGYGFT SYWIGWVRQM PGKGLEWMGI IHPDDSDTKY SPSFQGQVTI SADKSISTAY 120 LQWSSLKASD TAMYYCASSY LRGLWGGYFD YWGQGTLVTV SSGGGGSGGG GSGGGGSGGG 180 GSELQSVLTQ PPSASGTPGQ RVTISCSGSS SNIGSNYVNW YQQLPGTAPK LLIYGDYQRP 240 SGVPDRFSGS KSGTSASLAI SGLRSEDEAD YYCATRDDSL SGSVVFGTGT KLTVLGGGGS 300 CPYSNPSLCT TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP 360 LAGTCGVLLL SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL 420 RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 480 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 532
3-646	**Sequences**	
3-646-1	Sequence Number [ID]	646
3-646-2	Molecule Type	AA
3-646-3	Length	522
3-646-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-646-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSETLSL 60 TCTVSGGSIS YYYWTWIRQP PGKGLEWIGH IYYSGSTNYN PSLKSRVTIS IDTSKNLFSL 120 KLSSVTAADT AVYYCARAEG SLDAFDFWGQ GTMVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSTLS ASVGDRVTIT CRASQSISTW LAWYQQKPGK APKVLIYKAS SLESGVPSRF 240 SGSGSGTEFI LTINSLQPDD FASYYCQQYK SYSHTFGQGT KLEIKGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-647	**Sequences**	
3-647-1	Sequence Number [ID]	647
3-647-2	Molecule Type	AA
3-647-3	Length	522
3-647-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522

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		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-647-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSETLSL 60 NCTVSGGSIS YYYWTWIRQP PGKGLEWIGH VIYSGTTNYN PSLKSRVTIS VDTSKNQFSL 120 KLNSVTAADT AVYYCVRAEG SLDAFDLWGQ GTMVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSILS ASVGDRVTIT CRASQSVSSW LAWYQQKPGK APKVLIYKAS SLESGVPSRF 240 SGTGSGTEFT LTISSLQSDD FATYYCQQYN TYSHTFGQGT KLEIKGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-648	**Sequences**	
3-648-1	Sequence Number [ID]	648
3-648-2	Molecule Type	AA
3-648-3	Length	522
3-648-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-648-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPLQTLSL 60 TCTVSGGSIS SDGYYWSWIR QNPGKGLEWI GYMYYSGSTY YNPSLKSRVT ISVDTSKNQF 120 SLKLRSVTAA DTAVYYCTRD FGWYFDLWGR GTLVTVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSSLS ASVGDSITIT CRASQDIDNY LAWYQQKTGK VPKVLIYAAS ALQSGVPSRF 240 SGSGSGTDFT LTISSLQPED VATYYCQNYN SGPRTFGQGT KVEIKGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-649	**Sequences**	
3-649-1	Sequence Number [ID]	649
3-649-2	Molecule Type	AA
3-649-3	Length	522
3-649-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-649-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVKPSQSLSL 60 TCSVSGGSVS SDGYYWSWIR QHPGKGLEWI GYIYYRRITD YNPSLKSRVN ISLDTSKNQF 120 SLKLSSVTAA DTAVYYCARD FGWYFDLWGR GTLVAVSSGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSSLS ASVGDRVTIT CRASQDISNY LTWYQQKPGR VPEVLIYAAS ALQSGVPSRF 240 SGSGSGTDFT LTISSLQPED VATYYCQNYN SAPRTFGQGT KVEIKGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-650	**Sequences**	
3-650-1	Sequence Number [ID]	650
3-650-2	Molecule Type	AA
3-650-3	Length	524
3-650-4	Features	**REGION 1..524**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..524
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-650-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVELVESGGG MVQPGRSLRL 60 SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY ADSVKGRFTI SRDNSKNTVF 120 LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS GGGGSGGGGS GGGGSGGGGS 180 DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 240 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLDINGGG GSCPYSNPSL 300 CTTTPAPRPP TPAPTIASQP LSLRPEACRP AAGGAVHTRG LDFACDIYIW APLAGTCGVL 360 LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA 420 DAPAYQQGQN QLYNELNLGR REEYDVLDKR RGRDPEMGGK PRRKNPQEGL YNELQKDKMA 480 EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 524
3-651	**Sequences**	
3-651-1	Sequence Number [ID]	651
3-651-2	Molecule Type	AA

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3-651-3	Length	522
3-651-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-651-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVQLQESGPG LVQPSETLSL 60 TCTVSGGSIS YYYWSWIRQP PGKGLEWIGN INYMGNTIYN PSLKSRVTIS VDTSKDQFSL 120 KLTSVSAADT AVYYCVRAEG SLDAFDFWGQ GTLVAVSLGG GGSGGGGSGG GGSGGGGSDI 180 QMTQSPSTLS ASVGDRVTIT CRASQSISSW LAWYQQKPGK APKVLIYKAS NLESGVPSRF 240 SGSGSGTEFT LTISSLQPDD FATYYCQQYN SYSCTFGQGT KLEIKGGGGS CPYSNPSLCT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-652	**Sequences**	
3-652-1	Sequence Number [ID]	652
3-652-2	Molecule Type	AA
3-652-3	Length	522
3-652-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-652-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVTLKE 60 SGPVLVKPTE TLTLTCTVSG FSLSNARMGV TWIRQPPGKA LEWLAHIFSN DEKSYSTSLK 120 SRLTISKDTS KTQVVLTMTN MDPVDTATYY CARIRDYYDI SSYYDYWGQG TLVSVSSGGG 180 GSGGGGSGGG GSDIQMTQSP SAMSASVGDR VTITCRASQD ISNYLAWFQQ KPGKVPKRLI 240 YAASSLQSGV PSRFSGSGSG TEFTLTISSL LPEDFATYYC LQLNSFPFTF GGGTKVEINT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-653	**Sequences**	
3-653-1	Sequence Number [ID]	653
3-653-2	Molecule Type	AA
3-653-3	Length	532
3-653-4	Features	**REGION 1..532**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..532
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-653-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSEVQLVQ 60 SGAEVKKPGE SLKISCKGSG YGFTSYWIGW VRQMPGKGLE WMGIIHPDDS DTKYSPSFQG 120 QVTISADKSI STAYLQWSSL KASDTAMYYC ASSYLRGLWG GYFDYWGQGT LVTVSSGGGG 180 SGGGGSGGGG SGGGGSELQS VLTQPPSASG TPGQRVTISC SGSSSNIGSN YVNWYQQLPG 240 TAPKLLIYGD YQRPSGVPDR FSGSKSGTSA SLAISGLRSE DEADYYCATR DDSLSGSVVF 300 GTGTKLTVLT TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP 360 LAGTCGVLLL SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL 420 RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 480 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 532
3-654	**Sequences**	
3-654-1	Sequence Number [ID]	654
3-654-2	Molecule Type	AA
3-654-3	Length	522
3-654-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-654-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVQLQE 60 SGPGLVKPSE TLSLTCTVSG GSISYYYWTW IRQPPGKGLE WIGHIYYSGS TNYNPSLKSR 120 VTISIDTSKN LFSLKLSSVT AADTAVYYCA RAEGSLDAFD FWGQGTMVTV SSGGGGSGGG 180 GSGGGGSGGG GSDIQMTQSP STLSASVGDR VTITCRASQS ISTWLAWYQQ KPGKAPKVLI 240 YKASSLESGV PSRFSGSGSG TEFILTINSL QPDDFASYYC QQYKSYSHTF GQGTKLEIKT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420

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		PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-655	**Sequences**	
3-655-1	Sequence Number [ID]	655
3-655-2	Molecule Type	AA
3-655-3	Length	522
3-655-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..522** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-655-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVQLQE 60 SGPGLVKPSE TLSLNCTVSG GSISYYYWTW IRQPPGKGLE WIGHVIYSGT TNYNPSLKSR 120 VTISVDTSKN QFSLKLNSVT AADTAVYYCV RAEGSLDAFD LWGQGTMVTV SSGGGGSGGG 180 GSGGGGSGGG GSDIQMTQSP SILSASVGDR VTITCRASQS VSSWLAWYQQ KPGKAPKVLI 240 YKASSLESGV PSRFSGTGSG TEFTLTISSL QSDDFATYYC QQYNTYSHTF GQGTKLEIKT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-656	**Sequences**	
3-656-1	Sequence Number [ID]	656
3-656-2	Molecule Type	AA
3-656-3	Length	522
3-656-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..522** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-656-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVQLQE 60 SGPGLVKPLQ TLSLTCTVSG GSISSDGYYW SWIRQNPGKG LEWIGYMYYS GSTYYNPSLK 120 SRVTISVDTS KNQFSLKLRS VTAADTAVYY CTRDFGWYFD LWGRGTLVTV SSGGGGSGGG 180 GSGGGGSGGG GSDIQMTQSP SSLSASVGDS ITITCRASQD IDNYLAWYQQ KTGKVPKVLI 240 YAASALQSGV PSRFSGSGSG TDFTLTISSL QPEDVATYYC QNYNSGPRTF GQGTKVEIKT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-657	**Sequences**	
3-657-1	Sequence Number [ID]	657
3-657-2	Molecule Type	AA
3-657-3	Length	522
3-657-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..522** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-657-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVQLQE 60 SGPGLVKPSQ SLSLTCSVSG GSVSSDGYYW SWIRQHPGKG LEWIGYIYYR RITDYNPSLK 120 SRVNISLDTS KNQFSLKLSS VTAADTAVYY CARDFGWYFD LWGRGTLVAV SSGGGGSGGG 180 GSGGGGSGGG GSDIQMTQSP SSLSASVGDR VTITCRASQD ISNYLTWYQQ KPGRVPEVLI 240 YAASALQSGV PSRFSGSGSG TDFTLTISSL QPEDVATYYC QNYNSAPRTF GQGTKVEIKT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-658	**Sequences**	
3-658-1	Sequence Number [ID]	658
3-658-2	Molecule Type	AA
3-658-3	Length	524
3-658-4	Features	**REGION 1..524**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide **source 1..524** mol_type=protein organism=synthetic construct
	NonEnglishQualifier Value	
3-658-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSEVELVE 60 SGGGMVQPGR SLRLSCAASG FTFSDYGMHW VRQAPGMGLE WVTVIWYDGS NKYYADSVKG 120

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		RFTISRDNSK NTVFLQMNSL RAEDTAVYYC ARDEVGFVGA FDIWGQGTMV TVSSGGGGSG 180 GGGSGGGGSG GGGSDIQLTQ SPSFLSASVG DRVIITCRAS QGINSHLAWY QQKPGKAPKL 240 LIYYASTLPS GVPSRFSGSG SGTEFTLTVT SLQPEDFATY YCQQLNHYPI TFGQGTRLDI 300 NTTTPAPRPP TPAPTIASQP LSLRPEACRP AAGGAVHTRG LDFACDIYIW APLAGTCGVL 360 LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA 420 DAPAYQQGQN QLYNELNLGR REEYDVLDKR RGRDPEMGGK PRRKNPQEGL YNELQKDKMA 480 EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 524
3-659	**Sequences**	
3-659-1	Sequence Number [ID]	659
3-659-2	Molecule Type	AA
3-659-3	Length	522
3-659-4	Features	**REGION 1..522**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..522
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-659-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS CPYSNPSLCG GGGSQVQLQE 60 SGPGLVQPSE TLSLTCTVSG GSISYYYWSW IRQPPGKGLE WIGNINYMGN TIYNPSLKSR 120 VTISVDTSKD QFSLKLTSVS AADTAVYYCV RAEGSLDAFD FWGQGTLVAV SLGGGGSGGG 180 GSGGGGSGGG GSDIQMTQSP STLSASVGDR VTITCRASQS ISSWLAWYQQ KPGKAPKVLI 240 YKASNLESGV PSRFSGSGSG TEFTLTISSL QPDDFATYYC QQYNSYSCTF GQGTKLEIKT 300 TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP LAGTCGVLLL 360 SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL RVKFSRSADA 420 PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA 480 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 522
3-660	**Sequences**	
3-660-1	Sequence Number [ID]	660
3-660-2	Molecule Type	AA
3-660-3	Length	24
3-660-4	Features	**REGION 1..24**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..24
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-660-5	Residues	NSELLSLIND MPITNDQKKL MSNN 24
3-661	**Sequences**	
3-661-1	Sequence Number [ID]	661
3-661-2	Molecule Type	AA
3-661-3	Length	107
3-661-4	Features	**REGION 1..107**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..107
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-661-5	Residues	DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 60 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLEIK 107
3-662	**Sequences**	
3-662-1	Sequence Number [ID]	662
3-662-2	Molecule Type	AA
3-662-3	Length	120
3-662-4	Features	**REGION 1..120**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..120
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-662-5	Residues	EVELVESGGG MVQPGRSLRL SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY 60 ADSVKGRFTI SRDNSKNTVF LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS 120
3-663	**Sequences**	
3-663-1	Sequence Number [ID]	663
3-663-2	Molecule Type	AA
3-663-3	Length	5
3-663-4	Features	**REGION 1..5**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..5
		mol_type=protein
		organism=synthetic construct

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	NonEnglishQualifier Value		
3-663-5	Residues	DYGMH	5
3-664	**Sequences**		
3-664-1	Sequence Number [ID]	664	
3-664-2	Molecule Type	AA	
3-664-3	Length	7	
3-664-4	Features	**REGION 1..7**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..7	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-664-5	Residues	GFTFSDY	7
3-665	**Sequences**		
3-665-1	Sequence Number [ID]	665	
3-665-2	Molecule Type	AA	
3-665-3	Length	10	
3-665-4	Features	**REGION 1..10**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..10	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-665-5	Residues	GFTFSDYGMH	10
3-666	**Sequences**		
3-666-1	Sequence Number [ID]	666	
3-666-2	Molecule Type	AA	
3-666-3	Length	17	
3-666-4	Features	**REGION 1..17**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..17	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-666-5	Residues	VIWYDGSNKY YADSVKG	17
3-667	**Sequences**		
3-667-1	Sequence Number [ID]	667	
3-667-2	Molecule Type	AA	
3-667-3	Length	6	
3-667-4	Features	**REGION 1..6**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..6	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-667-5	Residues	WYDGSN	6
3-668	**Sequences**		
3-668-1	Sequence Number [ID]	668	
3-668-2	Molecule Type	AA	
3-668-3	Length	11	
3-668-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-668-5	Residues	DEVGFVGAFD I	11
3-669	**Sequences**		
3-669-1	Sequence Number [ID]	669	
3-669-2	Molecule Type	AA	
3-669-3	Length	11	
3-669-4	Features	**REGION 1..11**	
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide	
		source 1..11	
		mol_type=protein	
		organism=synthetic construct	
	NonEnglishQualifier Value		
3-669-5	Residues	RASQGINSHL A	11

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3-670	**Sequences**	
3-670-1	Sequence Number [ID]	670
3-670-2	Molecule Type	AA
3-670-3	Length	7
3-670-4	Features	**REGION 1..7**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..7
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-670-5	Residues	YASTLPS 7
3-671	**Sequences**	
3-671-1	Sequence Number [ID]	671
3-671-2	Molecule Type	AA
3-671-3	Length	9
3-671-4	Features	**REGION 1..9**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic peptide
		source 1..9
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-671-5	Residues	QQLNHYPIT 9
3-672	**Sequences**	
3-672-1	Sequence Number [ID]	672
3-672-2	Molecule Type	AA
3-672-3	Length	494
3-672-4	Features	**REGION 1..494**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..494
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-672-5	Residues	MALPVTALLL PLALLLHAAR PQVTLKESGP VLVKPTETLT LTCTVSGFSL SNARMGVTWI 60 RQPPGKALEW LAHIFSNDEK SYSTSLKSRL TISKDTSKTQ VVLTMTNMDP VDTATYYCAR 120 IRDYYDISSY YDYWGQGTLV SVSSGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSAMSASVG 180 DRVTITCRAS QDISNYLAWF QQKPGKVPKR LIYAASSLQS GVPSRFSGSG SGTEFTLTIS 240 SLLPEDFATY YCLQLNSFPF TFGGGTKVEI NTTTPAPRPP TPAPTIASQP LSLRPEACRP 300 AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ 360 TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN QLYNELNLGR REEYDVLDKR 420 RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG ERRRGKGHDG LYQGLSTATK 480 DTYDALHMQA LPPR 494
3-673	**Sequences**	
3-673-1	Sequence Number [ID]	673
3-673-2	Molecule Type	AA
3-673-3	Length	491
3-673-4	Features	**REGION 1..491**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..491
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-673-5	Residues	MALPVTALLL PLALLLHAAR PEVELVESGG GMVQPGRSLR LSCAASGFTF SDYGMHWVRQ 60 APGMGLEWVT VIWYDGSNKY YADSVKGRFT ISRDNSKNTV FLQMNSLRAE DTAVYYCARD 120 EVGFVGAFDI WGQGTMVTVS SGGGGSGGGG SGGGGSGGGG SDIQLTQSPS FLSASVGDRV 180 IITCRASQGI NSHLAWYQQK PGKAPKLLIY YASTLPSGVP SRFSGSGSGT EFTLTVTSLQ 240 PEDFATYYCQ QLNHYPITFG QGTRLEIKTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG 300 GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG RKKLLYIFKQ PFMRPVQTTQ 360 EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR 420 DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY 480 DALHMQALPP R 491
3-674	**Sequences**	
3-674-1	Sequence Number [ID]	674
3-674-2	Molecule Type	AA
3-674-3	Length	531
3-674-4	Features	**REGION 1..531**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..531
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	

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3-674-5	Residues	MALPVTALLL PLALLLHAAR PQVTLKESGP VLVKPTETLT LTCTVSGFSL SNARMGVTWI 60 RQPPGKALEW LAHIFSNDEK SYSTSLKSRL TISKDTSKTQ VVLTMTNMDP VDTATYYCAR 120 IRDYYDISSY YDYWGQGTLV SVSSGGGGSG GGGSGGGGSG GGGSDIQMTQ SPSAMSASVG 180 DRVTITCRAS QDISNYLAWF QQKPGKVPKR LIYAASSLQS GVPSRFSGSG SGTEFTLTIS 240 SLLPEDFATY YCLQLNSFPF TFGGGTKVEI NGSGGGGSCP YSNPSLCSGG GGSCPYSNPS 300 LCSGGGGSTT TPAPRPPTPA PTIASQPLSL RPEACRPAAG GAVHTRGLDF ACDIYIWAPL 360 AGTCGVLLLS LVITLYCKRG RKKLLYIFKQ PFMRPVQTTQ EEDGCSCRFP EEEEGGCELR 420 VKFSRSADAP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR KNPQEGLYNE 480 LQKDKMAEAY SEIGMKGERR RGKGHDGLYQ GLSTATKDTY DALHMQALPP R 531
3-675	**Sequences**	
3-675-1	Sequence Number [ID]	675
3-675-2	Molecule Type	AA
3-675-3	Length	528
3-675-4	Features	**REGION 1..528**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..528
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-675-5	Residues	MALPVTALLL PLALLLHAAR PEVELVESGG GMVQPGRSLR LSCAASGFTF SDYGMHWVRQ 60 APGMGLEWVT VIWYDGSNKY YADSVKGRFT ISRDNSKNTV FLQMNSLRAE DTAVYYCARD 120 EVGFVGAFDI WGQGTMVTVS SGGGGSGGGG SGGGGSGGGG SDIQLTQSPS FLSASVGDRV 180 IITCRASQGI NSHLAWYQQK PGKAPKLLIY YASTLPSGVP SRFSGSGSGT EFTLTVTSLQ 240 PEDFATYYCQ QLNHYPITFG QGTRLEIKGS GGGGSCPYSN PSLCSGGGGS CPYSNPSLCS 300 GGGGSTTTPA PRPPTPAPTI ASQPLSLRPE ACRPAAGGAV HTRGLDFACD IYIWAPLAGT 360 CGVLLLSLVI TLYCKRGRKK LLYIFKQPFM RPVQTTQEED GCSCRFPEEE EGGCELRVKF 420 SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK 480 DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR 528
3-676	**Sequences**	
3-676-1	Sequence Number [ID]	676
3-676-2	Molecule Type	AA
3-676-3	Length	574
3-676-4	Features	**REGION 1..574**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..574
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-676-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSQVTL KESGPVLVKP 60 TETLTLTCTV SGFSLSNARM GVTWIRQPPG KALEWLAHIF SNDEKSYSTS LKSRLTISKD 120 TSKTQVVLTM TNMDPVDTAT YYCARIRDYY DISSYYDYWG QGTLVSVSSG GGGSGGGGSG 180 GGGSGGGGSD IQMTQSPSAM SASVGDRVTI TCRASQDISN YLAWFQQKPG KVPKRLIYAA 240 SSLQSGVPSR FSGSGSGTEF TLTISSLLPE DFATYYCLQL NSFPFTFGGG TKVEINGSGG 300 GGSCPYSNPS LCSGGGGSEL PTQGTFSNVS TNVSPAKPTT TACPYSNPSL CTTTPAPRPP 360 TPAPTIASQP LSLRPEACRP AAGGAVHTRG LDFACDIYIW APLAGTCGVL LLSLVITLYC 420 KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA DAPAYQQGQN 480 QLYNELNLGR REEYDVLDKR RGRDPEMGGK PRRKNPQEGL YNELQKDKMA EAYSEIGMKG 540 ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 574
3-677	**Sequences**	
3-677-1	Sequence Number [ID]	677
3-677-2	Molecule Type	AA
3-677-3	Length	571
3-677-4	Features	**REGION 1..571**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..571
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-677-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCSGGGG SGGGGSEVEL VESGGGMVQP 60 GRSLRLSCAA SGFTFSDYGM HWVRQAPGMG LEWVTVIWYD GSNKYYADSV KGRFTISRDN 120 SKNTVFLQMN SLRAEDTAVY YCARDEVGFV GAFDIWGQGT MVTVSSGGGG SGGGGSGGGG 180 SGGGGSDIQL TQSPSFLSAS VGDRVIITCR ASQGINSHLA WYQQKPGKAP KLLIYYASTL 240 PSGVPSRFSG SGSGTEFTLT VTSLQPEDFA TYYCQQLNHY PITFGQGTRL EIKGSGGGGS 300 CPYSNPSLCS GGGGSELPTQ GTFSNVSTNV SPAKPTTTAC PYSNPSLCTT TPAPRPPTPA 360 PTIASQPLSL RPEACRPAAG GAVHTRGLDF ACDIYIWAPL AGTCGVLLLS LVITLYCKRG 420 RKKLLYIFKQ PFMRPVQTTQ EEDGCSCRFP EEEEGGCELR VKFSRSADAP AYQQGQNQLY 480 NELNLGRREE YDVLDKRRGR DPEMGGKPRR KNPQEGLYNE LQKDKMAEAY SEIGMKGERR 540 RGKGHDGLYQ GLSTATKDTY DALHMQALPP R 571
3-678	**Sequences**	
3-678-1	Sequence Number [ID]	678
3-678-2	Molecule Type	AA
3-678-3	Length	532

3-678-4	Features	**REGION 1..532**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..532
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-678-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVTLKESGPV LVKPTETLTL 60 TCTVSGFSLS NARMGVTWIR QPPGKALEWL AHIFSNDEKS YSTSLKSRLT ISKDTSKTQV 120 VLTMTNMDPV DTATYYCARI RDYYDISSYY DYWGQGTLVS VSSGGGGSGG GGSGGGGSGG 180 GGSDIQMTQS PSAMSASVGD RVTITCRASQ DISNYLAWFQ QKPGKVPKRL IYAASSLQSG 240 VPSRFSGSGS GTEFTLTISS LLPEDFATYY CLQLNSFPFT FGGGTKVEIN GGGGSCPYSN 300 PSLCGGGGST TTPAPRPPTP APTIASQPLS LRPEACRPAA GGAVHTRGLD FACDIYIWAP 360 LAGTCGVLLL SLVITLYCKR GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL 420 RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 480 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 532
3-679	**Sequences**	
3-679-1	Sequence Number [ID]	679
3-679-2	Molecule Type	AA
3-679-3	Length	529
3-679-4	Features	**REGION 1..529**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..529
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-679-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVELVESGGG MVQPGRSLRL 60 SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY ADSVKGRFTI SRDNSKNTVF 120 LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS GGGGSGGGGS GGGGSGGGGS 180 DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 240 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLEIKGGG GSCPYSNPSL 300 CGGGGSTTTP APRPPTPAPT IASQPLSLRP EACRPAAGGA VHTRGLDFAC DIYIWAPLAG 360 TCGVLLLSLV ITLYCKRGRK KLLYIFKQPF MRPVQTTQEE DGCSCRFPEE EEGGCELRVK 420 FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ 480 KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQALPPR 529
3-680	**Sequences**	
3-680-1	Sequence Number [ID]	680
3-680-2	Molecule Type	AA
3-680-3	Length	527
3-680-4	Features	**REGION 1..527**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..527
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-680-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS QVTLKESGPV LVKPTETLTL 60 TCTVSGFSLS NARMGVTWIR QPPGKALEWL AHIFSNDEKS YSTSLKSRLT ISKDTSKTQV 120 VLTMTNMDPV DTATYYCARI RDYYDISSYY DYWGQGTLVS VSSGGGGSGG GGSGGGGSGG 180 GGSDIQMTQS PSAMSASVGD RVTITCRASQ DISNYLAWFQ QKPGKVPKRL IYAASSLQSG 240 VPSRFSGSGS GTEFTLTISS LLPEDFATYY CLQLNSFPFT FGGGTKVEIN GGGGSCPYSN 300 PSLCTTTPAP RPPTPAPTIA SQPLSLRPEA CRPAAGGAVH TRGLDFACDI YIWAPLAGTC 360 GVLLLSLVIT LYCKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCELRVKFS 420 RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD 480 KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR 527
3-681	**Sequences**	
3-681-1	Sequence Number [ID]	681
3-681-2	Molecule Type	AA
3-681-3	Length	524
3-681-4	Features	**REGION 1..524**
	Location/Qualifiers	note=Description of Artificial Sequence: Synthetic polypeptide
		source 1..524
		mol_type=protein
		organism=synthetic construct
	NonEnglishQualifier Value	
3-681-5	Residues	MALPVTALLL PLALLLHAAR PGGGGSCPYS NPSLCGGGGS EVELVESGGG MVQPGRSLRL 60 SCAASGFTFS DYGMHWVRQA PGMGLEWVTV IWYDGSNKYY ADSVKGRFTI SRDNSKNTVF 120 LQMNSLRAED TAVYYCARDE VGFVGAFDIW GQGTMVTVSS GGGGSGGGGS GGGGSGGGGS 180 DIQLTQSPSF LSASVGDRVI ITCRASQGIN SHLAWYQQKP GKAPKLLIYY ASTLPSGVPS 240 RFSGSGSGTE FTLTVTSLQP EDFATYYCQQ LNHYPITFGQ GTRLEIKGGG GSCPYSNPSL 300 CTTTPAPRPP TPAPTIASQP LSLRPEACRP AAGGAVHTRG LDFACDIYIW APLAGTCGVL 360 LLSLVITLYC KRGRKKLLYI FKQPFMRPVQ TTQEEDGCSC RFPEEEEGGC ELRVKFSRSA 420 DAPAYQQGQN QLYNELNLGR REEYDVLDKR RGRDPEMGGK PRRKNPQEGL YNELQKDKMA 480 EAYSEIGMKG ERRRGKGHDG LYQGLSTATK DTYDALHMQA LPPR 524

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3-682	**Sequences**	
3-682-1	Sequence Number [ID]	682
3-682-2	Molecule Type	AA
3-682-3	Length	40
3-682-4	Features	**source 1..40**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-682-5	Residues	GRKKLLYIFK QPFMRPVQTT QEEDGCSCRF PEEEEGGCEL 40
3-683	**Sequences**	
3-683-1	Sequence Number [ID]	683
3-683-2	Molecule Type	AA
3-683-3	Length	112
3-683-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-683-5	Residues	RVKFSRSADA PAYKQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN 60 ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR 112