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(54) Title: CD3 BINDING POLYPEPTIDES

(57) Abstract: The present disclosure relates to protein molecules that specifically bind to CD3, which may have at least one humanized CD3-binding domain. Such molecules are useful for the treatment of cancer. The protein molecule binding to CD3 may have a second binding domain that binds to another target. In one embodiment, multispecific polypeptide molecules bind both tumor antigen-expressing cells and the CD3 subunit of a T-cell receptor complex on T-cells to induce target-dependent T-cell cytotoxicity, activation, and proliferation. The disclosure also provides pharmaceutical compositions comprising the CD3-binding polypeptide molecules, nucleic acid molecules encoding these polypeptides and methods of making these molecules.



CD3 BINDING POLYPEPTIDES

[001] This application claims priority to and benefit of U.S. Provisional Patent Application No. 62/221,190, filed on September 21, 2015. The contents of this application are herein
5 incorporated by reference in their entirety.

DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONICALLY

[002] The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (filename: APVO_052_01WO_SeqList_ST25.txt, date recorded: September 21, 2016, file size 544
10 kilobytes).

FIELD OF THE DISCLOSURE

[003] The present disclosure relates to molecules that specifically bind to CD3, which may have at least one humanized CD3-binding domain. A protein therapeutic binding to CD3 may be a monospecific protein therapeutic or a multispecific protein therapeutic. A multispecific protein
15 therapeutic may bind both a tumor antigen and CD3 subunits of the T-cell receptor complex on T-cells to induce target-dependent T-cell cytotoxicity, activation and proliferation.

BACKGROUND OF THE DISCLOSURE

[004] Targeting the T-cell receptor complex (TCR) on human T-cells with anti-CD3 antibodies has been proposed for treatment of autoimmune disease and related disorders, such as for
20 treatment of organ allograft rejection. In addition to monospecific therapeutics that target CD3, multispecific polypeptides that bind selectively to both T-cells and tumor cells could offer a mechanism to redirect T-cell cytotoxicity towards the tumor cells. Such multispecific polypeptides may be useful for treatment of cancer.

[005] Clinical use of some anti-CD3 antibodies has been hampered by serious side effects. For
25 example, OKT3, a mouse monoclonal antibody specific for human CD3, induced T-cell proliferation and cytokine production in vitro and led to a large scale release of cytokine *in vivo* (Hirsch et al. (1989) J. Immunol 142: 737-43). The cytokine release (also referred to as "cytokine storm") in turn led to a "flu-like" syndrome, characterized by fever, chills, headaches, nausea, vomiting, diarrhea, respiratory distress, septic meningitis and hypotension (Chatenoud
30 (2003) Nature Reviews 3:123-132).

[006] There is a need for CD3-binding molecules that have improved thermal stability with a favorable manufacturability profile and reduced adverse effects.

SUMMARY OF THE DISCLOSURE

[007] The disclosure encompasses CD3-binding domains and polypeptides that have an advantageous manufacturability profile. Polypeptides comprising CD3-binding domains disclosed herein may be thermally stable. In some cases, a polypeptide has an improved thermal stability compared to another CD3-binding polypeptide. CD3-binding domains and polypeptides disclosed herein may have reduced side effects (for example, may lead to release of low levels of cytokines when administered to a subject).

[007a] In one embodiment, the disclosure relates to a CD3-binding polypeptide comprising a CD3-binding domain that binds specifically to human CD3 and that comprises a humanized immunoglobulin light chain region and a humanized immunoglobulin heavy chain region, wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93.

[007b] In another embodiment, there is provided a CD3-binding polypeptide comprising a CD3-binding domain that binds specifically to human CD3 and that comprises a humanized immunoglobulin light chain region and a humanized immunoglobulin heavy chain region, wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93; wherein the amino acid at position 9 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is proline; and wherein the amino acid at position 21 according to the IMGT numbering system of the immunoglobulin light chain variable region is methionine; and wherein the amino acid at position 87 according to the IMGT numbering system of the immunoglobulin light chain variable region is tyrosine, and wherein (a) the immunoglobulin light chain variable region comprises an amino acid sequence that is at least 95% identical to

SEQ ID NO:88 and the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least 95% identical to SEQ ID NO:86 ; or (b) the immunoglobulin light chain variable region comprises an amino acid sequence that is at least 95% identical to SEQ ID NO:89 and the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least 95% identical to SEQ ID NO:86.

[007c] In one embodiment, the disclosure relates to a CD3-binding polypeptide comprising a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain region and an immunoglobulin heavy chain region, wherein the immunoglobulin light chain variable region is humanised and comprises framework regions based on the human IGKV3D-20*1 germline amino acid sequence; wherein the immunoglobulin heavy chain variable region is humanized and comprises framework regions based on the human IGHV1-69*02 germline amino acid sequence; and (a) wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93; or (b) wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:202, an LCDR2 amino acid sequence of SEQ ID NO:203, and an LCDR3 amino acid sequence of SEQ ID NO:204 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:199, an HCDR2 amino acid sequence of SEQ ID NO:200, and an HCDR3 amino acid sequence of SEQ ID NO:201.

[007d] In another embodiment, the disclosure relates to a CD3-binding polypeptide comprising, in order from amino-terminus to carboxyl-terminus, (i) a second binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) a carboxyl-terminus linker, and (v) a CD3-binding domain, wherein said immunoglobulin constant region comprises a human IgG1 CH2 domain containing the substitutions L234A, L235A, G237A, and K322A, according to the EU numbering system.

[007e] In yet another embodiment, the disclosure relates to a heterodimeric CD3-binding protein comprising (i) a first polypeptide chain comprising, in order from amino-terminus to carboxyl-terminus or from carboxyl-terminus to amino-terminus, (a) a CD3-binding polypeptide of any one of claims 1-14, (b) a first hinge region, (c) a

first immunoglobulin constant region, and (d) a first immunoglobulin heterodimerization domain; and (ii) a second polypeptide chain comprising, in order from amino-terminus to carboxyl-terminus or from carboxyl-terminus to amino-terminus, (a') a second hinge region, (b') a second immunoglobulin constant region, and (c') a second immunoglobulin heterodimerization domain that is different from the first immunoglobulin heterodimerization domain of the first single chain polypeptide, wherein the first and second immunoglobulin heterodimerization domains associate with each other to form a heterodimer.

[008] In certain embodiments, the disclosure relates to a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region; wherein the immunoglobulin light chain variable region comprises an amino acid sequence that is (a) at least about 93% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:88; or (b) at least about 94% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:89; and wherein the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least about 82% identical, at least about 85% identical, at least about 87% identical, at least about 90% identical, at least about 92% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:86. A CD3-binding domain may comprise an amino acid sequence that is at least about 87% identical, at least about 90% identical, at least about 92% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:83 or SEQ ID NO:84. A CD3-binding domain may comprise SEQ ID NO:83 or SEQ ID NO:84.

[009] In one embodiment, a CD3-binding domain comprises an immunoglobulin light chain variable region that comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and an immunoglobulin heavy chain variable region that comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93. In another embodiment, a CD3-binding domain comprises an immunoglobulin light chain variable region that comprises an LCDR1 amino acid sequence of SEQ ID NO:202, an LCDR2 amino acid sequence of SEQ ID NO:203,

and an LCDR3 amino acid sequence of SEQ ID NO:204 and an immunoglobulin heavy chain variable region that comprises an HCDR1 amino acid sequence of SEQ ID NO:199, an HCDR2 amino acid sequence of SEQ ID NO:200, and an HCDR3 amino acid sequence of SEQ ID NO:201.

5 **[0010]** In certain aspects, a CD3-binding domain may comprise an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region that comprise framework regions and at least one of the immunoglobulin light chain variable region and the immunoglobulin heavy chain variable region may be humanized. In one embodiment, an immunoglobulin light chain variable region comprises framework regions based on the human IGKV3D-20*1 germline amino acid sequence. In another embodiment, an immunoglobulin heavy chain variable region comprises framework regions based on the human IGHV1-69*02 germline amino acid sequence.

10 **[0011]** In some embodiments, the amino acid residue at position 52 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain is arginine and/or the amino acid residue at position 53 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain is tryptophan. The amino acid residue at position 27 according to the IMGT numbering system of the immunoglobulin heavy chain variable region of a CD3-binding domain may be tyrosine. In some embodiments, a CD3-binding domain comprises one or more of the following: (a) the amino acid residue at position 9 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is proline; (b) the amino acid residue at position 53 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is isoleucine; and (c) the amino acid residue at position 21 according to the IMGT numbering system of the immunoglobulin light chain variable region is methionine. The amino acid residue at position 87 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain may be tyrosine. The amino acid residue at position 86 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain may be aspartic acid. In one embodiment, the amino acid residue at position 86 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain is aspartic acid and the amino acid residue at position 87 according to the IMGT numbering system of the immunoglobulin light chain variable region of a CD3-binding domain is tyrosine.

20 **[0012]** The disclosure encompasses a CD3-binding domain that is a single chain variable fragment (scFv). In some aspects, an scFv may comprise a linker between the heavy chain

variable region and the light chain variable region. In one embodiment, a linker between the heavy chain variable region and the light chain variable region comprises the amino acid sequence QRHNSSLNTGTQMAGHSPNS (SEQ ID NO:148). In some embodiments, the heavy chain variable region of an scFv is amino-terminal to the light chain variable region of the scFv. In other embodiments, the light chain variable region of an scFv is amino-terminal to the heavy chain variable region of the scFv.

[0013] The disclosure encompasses a CD3-binding domain that has a thermal stability that is increased at least about 10% when compared to the thermal stability of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87. The thermal transition midpoint (T_m) of a CD3-binding domain may be increased at least about 3°C, at least about 4°C, at least about 5°C, or at least about 6°C increased and up to about 20°C when compared to the T_m of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87. The thermal transition midpoint of a CD3-binding domain may be at least about 54°C, at least about 55°C, at least about 56°C, or at least about 57°C and up to about 72°C. The thermal stability or the thermal transition midpoint of a CD3-binding domain may be measured by differential scanning calorimetry or differential scanning fluorimetry.

[0014] A CD3-binding domain as disclosed herein may have storage stability that is increased at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% and up to about 100% when compared to the storage stability of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87. Storage stability may be measured after a CD3-binding domain is stored in PBS at about 25°C. In one embodiment, a CD3-binding domain is stable in storage in PBS at about 25°C for at least about 6 days, at least about 10 days, or at least about 13 days and up to about 90 days.

[0015] In some aspects, a CD3-binding domain as disclosed herein has a level of high molecular weight aggregates produced during recombinant expression that is at least about 5%, at least about 10%, at least about 20% decreased, at least about 30% decreased and up to about 50% decreased when compared to the level of high molecular weight aggregates produced during recombinant expression of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87.

[0016] The disclosure also relates to a CD3-binding domain that binds to human CD3 with an EC₅₀ of about 10 nM or lower. In some embodiments, a CD3-binding domain of the disclosure may also bind specifically to cynomolgus CD3. For example, a CD3-binding domain may bind to cynomolgus CD3 with an EC₅₀ of about 30 nM or lower.

5 [0017] The disclosure encompasses a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region, wherein (a) the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the
10 immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93; or (b) the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:202, an LCDR2 amino acid sequence of SEQ ID NO:203, and an LCDR3 amino acid sequence of SEQ ID NO:204 and wherein the
15 immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:199, an HCDR2 amino acid sequence of SEQ ID NO:200, and an HCDR3 amino acid sequence of SEQ ID NO:201; and wherein the CD3-binding domain has any one or more of the properties described herein. For example, (i) the thermal transition midpoint of the CD3-binding domain (or a protein comprising the CD3-binding domain) is at least about 54°C, at least
20 about 55°C, at least about 56°C, or at least about 57°C and up to about 72°C; (ii) the CD3-binding domain (or a protein comprising the CD3-binding domain) is stable in storage in PBS at about 25°C for at least about 6 days, at least about 10 days, or at least about 13 days and up to about 90 days; (iii) the CD3-binding domain (or a protein comprising the CD3-binding domain) binds to human CD3 with an EC₅₀ of about 10 nM or lower; and (iv) the CD3-binding domain
25 (or a protein comprising the CD3-binding domain) binds to cynomolgus CD3 with an EC₅₀ of about 30 nM or lower.

[0018] The disclosure also relates to a CD3-binding polypeptide comprising any of the CD3-binding domains described herein. In some variations, a CD3-binding polypeptide may comprise an immunoglobulin constant region. This immunoglobulin constant region may comprise
30 immunoglobulin CH2 and CH3 domains of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2 or IgD. In some embodiments, an immunoglobulin constant region comprises a human IgG1 CH2 domain comprising the substitutions L234A, L235A, G237A, and K322A, according to the EU numbering system. In certain embodiments, an immunoglobulin constant region comprises a human IgG1 CH2 domain comprising one or more of the substitutions L234A, L235A, G237A, and K322A,

according to the EU numbering system. In some embodiments, a CD3-binding polypeptide when bound to a CD3 protein on a T cell does not induce or induces a minimally detectable cytokine release from said T cell. In certain aspects, a CD3-binding protein or polypeptide exhibits reduced cytokine release in a patient as compared to the cytokine released when anti-
5 CD3 antibody OKT3 is administered to a patient. In some cases, a CD3-binding polypeptide may induce T-cell activation or T-cell proliferation.

[0019] In certain aspects, a CD3-binding polypeptide further comprises a second binding domain. The second binding domain may be a single chain variable fragment (scFv). In some embodiments, the second binding domain binds or interacts with a tumor associated antigen
10 (e.g., PSMA, CD19, CD20, CD37, CD38, CD123, Her2, ROR1, RON, glycoprotein A33 antigen (gpA33) or CEA).

[0020] The disclosure further encompasses a CD3-binding polypeptide comprising: (i) a CD3-binding domain and (ii) a second binding domain. In some embodiments, a CD3-binding polypeptide comprises, in order from amino-terminus to carboxyl-terminus or in order from
15 carboxyl-terminus to amino-terminus, (i) a CD3-binding domain, (ii) a hinge region and (iii) an immunoglobulin constant region. In some embodiments, a CD3-binding polypeptide comprises, in order from amino-terminus to carboxyl-terminus, (i) a second binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) a carboxyl-terminus linker, and (v) a CD3-binding domain. In other embodiments, a CD3-binding polypeptide comprises, in order from
20 carboxyl-terminus to amino-terminus, (i) a second binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) an amino-terminus linker, and (v) a CD3-binding domain. In certain variations, the first and/or the second binding domain is an scFv. Non-limiting examples of carboxyl-terminus and amino-terminus linkers include flexible linkers comprising glycine-serine (e.g., (Gly₄Ser)) repeats and linkers derived from (i) a stalk region of a type II C
25 lectin or (ii) an immunoglobulin hinge region. In certain aspects, a carboxyl-terminus linker (or an amino-terminus linker) comprises or consists of SEQ ID NO:196. In some aspects, the disclosure relates to a CD3-binding polypeptide (e.g., multispecific), wherein (i) the CD3-binding domain comprises (a) an immunoglobulin light chain variable region comprising LCDR1, LCDR2, and LCDR3, and (b) an immunoglobulin heavy chain variable region comprising
30 HCDR1, HCDR2, and HCDR3; and (ii) the second binding domain comprises (a) an immunoglobulin light chain variable region comprising LCDR1, LCDR2, and LCDR3, and (b) an immunoglobulin heavy chain variable region comprising HCDR1, HCDR2, and HCDR3.

[0021] The disclosure encompasses a CD3-binding polypeptide that induces redirected T-cell cytotoxicity (RTCC). For example, a CD3-binding polypeptide may induce RTCC with an EC₅₀

of about 30 pM or lower. In some embodiments, a CD3-binding polypeptide does not exhibit or exhibits minimal antibody-dependent cell-mediated cytotoxicity (ADCC) activity and/or complement-dependent cytotoxicity (CDC) activity. In certain aspects, null ADCC and/or CDC activity is accomplished through mutations in the hinge region and Ig constant region (e.g., Fc).

5 **[0022]** A CD3-binding polypeptide may further comprise an immunoglobulin heterodimerization domain. In some embodiments, an immunoglobulin heterodimerization domain comprises an immunoglobulin CH1 domain or an immunoglobulin CL domain. In some aspects, a CD3-binding polypeptide is a heterodimeric CD3-binding protein comprising (i) a first polypeptide chain comprising, in order from amino-terminus to carboxyl-terminus or from carboxyl-terminus
10 to amino-terminus, (a) a CD3-binding domain that specifically binds human CD3, (b) a first hinge region, (c) a first immunoglobulin constant region, and (d) a first immunoglobulin heterodimerization domain; and (ii) a second polypeptide chain comprising, in order from amino-terminus to carboxyl-terminus or from carboxyl-terminus to amino-terminus, (a') a second hinge region, (b') a second immunoglobulin constant region, and (c') a second immunoglobulin
15 heterodimerization domain that is different from the first immunoglobulin heterodimerization domain of the first single chain polypeptide, wherein the first and second immunoglobulin heterodimerization domains associate with each other to form a heterodimer. In one embodiment, the first immunoglobulin heterodimerization domain comprises an immunoglobulin CH1 domain and the second immunoglobulin heterodimerization domain comprises an
20 immunoglobulin CL domain, or wherein the first immunoglobulin heterodimerization domain comprises an immunoglobulin CL domain and the second immunoglobulin heterodimerization domain comprises an immunoglobulin CH1 domain. At least one of the first and second immunoglobulin constant regions may comprise immunoglobulin CH2 and CH3 domains of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD or any combination thereof; an immunoglobulin CH3
25 domain of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, IgM or any combination thereof; or immunoglobulin CH3 and CH4 domains of IgE, IgM or a combination thereof. In some aspects, the second polypeptide chain of a heterodimeric CD3-binding protein may further comprise a second binding domain. In certain embodiments, the second binding domain may be amino-terminal or carboxy-terminal to the second hinge region.

30 **[0023]** In some variations, a CD3-binding polypeptide may be a bispecific single chain antibody molecule comprising a CD3-binding domain and a second binding domain, wherein the binding domains are arranged in the order VH CD3-VL CD3-VH second binding domain-VL second binding domain or VL CD3-VH CD3-VH second binding domain -VL second binding domain or

VH second binding domain-VL second binding domain-VH CD3-VL CD3 or VH second binding domain-VL second binding domain-VL CD3-VH CD3.

[0024] The disclosure also relates to an isolated nucleic acid molecule encoding a CD3-binding domain or a CD3-binding polypeptide described herein or a portion of said CD3-binding domain or polypeptide. In some aspects, the disclosure encompasses an expression vector comprising a nucleic acid segment encoding a CD3-binding domain or a CD3-binding polypeptide described herein, wherein the nucleic acid segment is operatively linked to regulatory sequences suitable for expression of the nucleic acid segment in a host cell. A recombinant host cell comprising an expression vector is included in the disclosure.

[0025] The disclosure encompasses an expression vector comprising first and second expression units, wherein the first and second expression units respectively comprise first and second nucleic acid segments encoding the first and second polypeptide chains of a heterodimeric CD3-binding polypeptide, and wherein the first and second nucleic acid segments are operably linked to regulatory sequences suitable for expression of the nucleic acid segments in a host cell. A recombinant host cell comprising an expression vector comprising first and second expression units is part of the disclosure.

[0026] The disclosure further relates to a method for producing a CD3-binding polypeptide, the method comprising: culturing a recombinant host cell comprising an expression vector described herein under conditions whereby the nucleic acid segment is expressed, thereby producing the CD3-binding polypeptide. In some embodiments, a method for producing a heterodimeric CD3-binding protein comprises: culturing a recombinant host cell comprising first and second expression units, wherein the first and second expression units respectively comprise first and second nucleic acid segments encoding the first and second polypeptide chains of a heterodimeric CD3-binding protein, wherein the first and second nucleic acid segments are operably linked to regulatory sequences suitable for expression of the nucleic acid segments in a host cell, and wherein said culturing is under conditions whereby the first and second nucleic acid segments are expressed and the encoded polypeptide chains are produced as the heterodimeric CD3-binding protein. These methods may further comprise recovering the CD3-binding polypeptide or the heterodimeric CD3-binding protein.

[0027] The disclosure encompasses a pharmaceutical composition comprising a CD3-binding polypeptide disclosed herein and a pharmaceutically acceptable carrier, diluent, or excipient. The disclosure also relates to a method for inducing redirected T-cell cytotoxicity (RTCC) against a cell expressing a tumor associated antigen, the method comprising: contacting said tumor associated antigen-expressing cell with a CD3-binding polypeptide, wherein said

contacting is under conditions whereby RTCC against the tumor associated antigen-expressing cell is induced. One aspect of the disclosure includes a method for inhibiting tumor growth in a subject in need thereof, comprising administering a therapeutically effective amount of a CD3-binding polypeptide or a pharmaceutical composition described herein to the subject. The disclosure encompasses a method for treating cancer or an autoimmune disorder in a subject in need thereof, comprising administering a therapeutically effective amount of a CD3-binding polypeptide or a pharmaceutical composition described herein to the subject. Non-limiting examples of cancer that may be treated by methods and CD3-binding polypeptides described herein include prostate cancer, colorectal cancer, renal cell carcinoma, bladder cancer, salivary gland cancer, pancreatic cancer, ovarian cancer, non-small cell lung cancer, breast cancer (e.g., triple negative breast cancer), melanoma, adrenal cancer, mantle cell lymphoma, acute lymphoblastic leukemia, chronic lymphocytic leukemia, Non-Hodgkin's lymphoma, acute myeloid leukemia (AML), B-lymphoid leukemia, blastic plasmacytoid dendritic neoplasm (BPDCN), and hairy cell leukemia.

[0028] The disclosure encompasses a CD3-binding domain that binds specifically to human CD3 and that comprises SEQ ID NO: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, or 60.

[0029] The disclosure also relates to a CD3-binding protein that is a dimer of two identical polypeptides, wherein each polypeptide is any of the CD3-binding polypeptides disclosed herein.

[0030] These and other embodiments and/or other aspects of the disclosure will become evident upon reference to the following detailed description of the disclosure and the attached drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

[0031] Figure 1 (top panel) is a graph showing the results of a flow cytometry study measuring the binding of CD3-binding domain constructs to Jurkat T-cells. Mean fluorescence intensity (MFI) of bound molecules on live cells is shown on the y-axis. Concentration (nM) of the CD3-binding domain constructs is shown on the x-axis. The table (bottom panel) shows the EC₅₀ values obtained from the data in the graph.

[0032] Figure 2 (top panel) is a graph showing the results of a flow cytometry study measuring the binding of CD3-binding domain constructs to a subclone of the Jurkat T-cell line with higher levels of CD3 expression. Mean fluorescence intensity (MFI) of bound molecules on live cells is

shown on the y-axis. Concentration (nM) of the CD3-binding domain constructs is shown on the x-axis. The table (bottom panel) shows the EC₅₀ values obtained from the data in the graph.

[0033] Figure 3 is a graph showing the results of a differential scanning fluorimetry study performed with CD3-binding domain constructs. The figure also shows the thermal transition midpoint (T_m) values obtained from the data in the graph.

[0034] Figure 4 is a graph showing the results of a flow cytometry study measuring the binding of CD3-binding domain constructs to a subclone of the Jurkat T-cell line with higher levels of CD3 expression. Mean fluorescence intensity (MFI) of bound molecules on live cells is shown on the y-axis. Concentration (nM) of the CD3-binding domain constructs is shown on the x-axis.

[0035] Figure 5 is a graph showing the results of a flow cytometry study measuring the binding of CD3-binding domain constructs to a subclone of the Jurkat T-cell line with higher levels of CD3 expression. Mean fluorescence intensity (MFI) of bound molecules on live cells is shown on the y-axis. Concentration (nM) of the CD3-binding domain constructs is shown on the x-axis.

[0036] Figure 6 (top panel) is a graph showing the results of a chromium-51 release assay measuring the effectiveness of bispecific anti-PSMA and anti-CD3 constructs at inducing target-dependent T-cell cytotoxicity with human PBMC in 4 hours against C4-2B cells. Percent specific lysis relative to a total lysis control is shown on the y-axis. Concentration (pM) of the CD3-binding domain constructs is shown on the x-axis. The table (bottom panel) shows the EC₅₀ values obtained from the data in the graph.

[0037] Figure 7A and Figure 7B are graphs showing the results of a flow cytometry study measuring the binding of CD3-binding domain constructs to Cynomolgus T-cells. Mean fluorescence intensity (MFI) of bound molecules on live cells is shown on the y-axis of each graph. Concentration (nM) of the CD3-binding domain constructs is shown on the x-axis of each graph.

[0038] Figure 8A and Figure 8B are graphs showing the results of a chromium-51 release assay measuring the effectiveness of CD3-binding domain constructs at inducing target-dependent T-cell cytotoxicity with Cynomolgus PBMC in 4 hours against C4-2B cells. Percent specific lysis relative to a total lysis control is shown on the y-axis of each graph. Concentration (pM) of the CD3-binding domain constructs is shown on the x-axis of each graph.

[0039] Figure 9 is a graph showing the results of a flow cytometry study measuring the binding of bispecific anti-CD37 and anti-CD3 constructs to Cynomolgus T-cells. Mean fluorescence intensity (MFI) of bound molecules on live cells is shown on the y-axis. Concentration (nM) of

the CD3-binding domain constructs is shown on the x-axis. TSC394 DY refers to the TSC394 construct including the E86D and F87Y substitutions.

[0040] Figure 10 (top panel) is a graph showing the results of a chromium-51 release assay measuring the effectiveness of bispecific anti-CD37 and anti-CD3 constructs at inducing target-dependent T-cell cytotoxicity with Cynomolgus PBMC in 4 hours against Ramos cells. Percent specific lysis relative to a total lysis control is shown on the y-axis of each graph. Concentration (pM) of the CD3-binding domain constructs is shown on the x-axis of each graph. The table (bottom panel) shows the EC₅₀ values obtained from the data in the graph. TSC394 DY refers to the TSC394 construct including the E86D and F87Y substitutions.

[0041] Figure 11 is a graph showing the results of a study measuring the storage stability of CD3-binding domain constructs at 25°C over the number of days specified on the x-axis. CAS105 is a control construct comprising the DRA222 CD3-binding domain.

[0042] Figure 12 is a graph showing the results of a study measuring the serum stability in human serum of anti-ROR1 x anti-CD3 bispecific molecules over the number of days specified on the x-axis.

[0043] Figure 13 shows an alignment of the amino acid sequences of the DRA222 scFv (SEQ ID NO:85), TSC455 scFv (SEQ ID NO:83), and TSC456 scFv (SEQ ID NO:84). The sequences of these constructs are also shown in Table 14.

[0044] Figure 14 is a graph showing the results of a study measuring serum concentrations of anti-PSMA X anti-CD3 bispecific binding molecules in BALB/c mice as a function of time. Results are expressed as mean serum concentration (µg/mL) over time for each of the treatment groups. Each point shows the mean (+standard deviation) of individual animals.

[0045] Figure 15 is a table showing a comparison of pharmacokinetic parameters of anti-PSMA X anti-CD3 bispecific binding molecules in BALB/c mice.

[0046] Figure 16 is a graph showing the results of a study measuring serum concentrations of anti-ROR1 X anti-CD3 bispecific binding molecules in NSG mice as a function of time. Results are expressed as mean serum concentration (µg/mL) over time for each of the treatment groups.

[0047] Figure 17A and Figure 17B are tables showing a comparison of pharmacokinetic parameters of anti-ROR1 X anti-CD3 bispecific binding molecules in NSG mice. Figure 17A shows pharmacokinetic parameter estimates calculated using NCA for IV dosing with sparse sampling and uniform weighting for each treatment group. Figure 17B shows pharmacokinetic

parameter estimates determined using a 2 Compartment IV model with 1/Y weighting for each treatment group.

[0048] Figure 18 is a graph showing the results of a study analyzing the effects of anti-ROR1 X anti-CD3 bispecific binding molecules on MDA-MB-231 xenograft tumor growth.

5 **[0049]** Figure 19 is a graph showing the results of a study analyzing the effects of anti-ROR1 X anti-CD3 bispecific binding molecules on Kasumi-2 xenograft tumor growth. Results are shown for human T-cell donor #336.

DETAILED DESCRIPTION OF THE DISCLOSURE

10 **[0050]** The disclosure provides binding domains that specifically bind to CD3 (cluster of differentiation 3) and binding molecules (e.g. polypeptides and proteins) that specifically bind to CD3. These binding molecules may bind specifically to CD3 and to at least one other target. In some embodiments, a CD3-binding molecule described herein has a favorable
manufacturability profile, having one or more of the properties described below. In certain
15 embodiments, CDRs from the Cris7 anti-CD3 antibody have been used to engineer CD3-binding molecules with improved and novel properties. Accordingly, the disclosure relates to humanized anti-CD3 binding domains and proteins that have improved properties (e.g., thermal stability, storage stability, serum half-life, reduced formation of high molecular weight
aggregates) compared to other anti-CD3 binding domains and proteins. In some aspects of the
20 disclosure, a CD3-binding molecule is thermally stable. For example, the molecule may have improved thermal stability compared to another CD3-binding molecule (e.g., DRA222). CD3-binding molecules may have a high production yield and a long serum half-life and long storage half-life. Further, CD3-binding molecules described herein may have a low risk of adverse side effects when administered to a subject. For example, CD3-binding molecules may lead to
25 release of low levels of cytokines.

[0051] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein
30 refer to "one or more" of the enumerated components unless otherwise indicated. The use of the alternative (e.g., "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include" and "comprise" are used synonymously. In addition, it should be understood that the polypeptides comprising the various combinations of the components (e.g., domains or regions) and substituents described herein,

are disclosed by the present application to the same extent as if each polypeptide was set forth individually. Thus, selection of particular components of individual polypeptides is within the scope of the present disclosure.

[0052] All documents, or portions of documents, cited herein, including but not limited to patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose. In the event that one or more of the incorporated documents or portions of documents define a term that contradicts that term's definition in the application, the definition that appears in this application controls. However, mention of any reference, article, publication, patent, patent publication, and patent application cited herein is not, and should not be taken as an acknowledgment, or any form of suggestion, that they constitute valid prior art or form part of the common general knowledge in any country in the world.

[0053] As used herein, the term "binding domain" or "binding region" refers to the domain, region, portion, or site of a protein, polypeptide, oligopeptide, or peptide or antibody or binding domain derived from an antibody that possesses the ability to specifically recognize and bind to a target molecule, such as an antigen, ligand, receptor, substrate, or inhibitor (e.g., CD3). Exemplary binding domains include single-chain antibody variable regions (e.g., domain antibodies, sFv, scFv, scFab), receptor ectodomains, and ligands (e.g., cytokines, chemokines). In certain embodiments, the binding domain comprises or consists of an antigen binding site (e.g., comprising a variable heavy chain sequence and variable light chain sequence or three light chain complementary determining regions (CDRs) and three heavy chain CDRs from an antibody placed into alternative framework regions (FRs) (e.g., human FRs optionally comprising one or more amino acid substitutions). A variety of assays are known for identifying binding domains of the present disclosure that specifically bind a particular target, including Western blot, ELISA, phage display library screening, and BIACORE® interaction analysis. As used herein, a CD3-binding polypeptide can have a "first binding domain" and, optionally, a "second binding domain." In certain embodiments, the "first binding domain" is a CD3-binding domain and the format is an antibody or antibody-like protein or domain. In certain embodiments comprising both the first and second binding domains, the second binding domain is a tumor antigen-binding domain. In other embodiments, the second binding domain is a second CD3-binding domain. In yet other embodiments, the second binding domain is a binding domain other than a tumor antigen-binding domain.

[0054] A binding domain or protein “specifically binds” a target if it binds the target with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of $1/M$) equal to or greater than $10^5 M^{-1}$, while not significantly binding other components present in a test sample. Binding domains can be classified as “high affinity” binding domains and “low affinity” binding domains. “High affinity” binding domains refer to those binding domains with a K_a of at least $10^7 M^{-1}$, at least $10^8 M^{-1}$, at least $10^9 M^{-1}$, at least $10^{10} M^{-1}$, at least $10^{11} M^{-1}$, at least $10^{12} M^{-1}$, or at least $10^{13} M^{-1}$. “Low affinity” binding domains refer to those binding domains with a K_a of up to $10^7 M^{-1}$, up to $10^8 M^{-1}$, up to $10^9 M^{-1}$. Alternatively, affinity can be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, $10^{-5} M$ to $10^{-13} M$). Affinities of binding domain polypeptides and single chain polypeptides according to the present disclosure can be readily determined using conventional techniques (*see, e.g.*, Scatchard *et al.* (1949) *Ann. N.Y. Acad. Sci.* 51:660; and U.S. Patent Nos. 5,283,173, 5,468,614, or the equivalent).

[0055] “CD3” is known in the art as a multi-protein complex of six chains (*see, e.g.*, Abbas and Lichtman, 2003; Janeway *et al.*, p. 172 and 178, 1999), which are subunits of the T-cell receptor complex. In mammals, the CD3 subunits of the T-cell receptor complex are a CD3 γ chain, a CD3 δ chain, two CD3 ϵ chains, and a homodimer of CD3 ζ chains. The CD3 γ , CD3 δ , and CD3 ϵ chains are highly related cell surface proteins of the immunoglobulin superfamily containing a single immunoglobulin domain. The transmembrane regions of the CD3 γ , CD3 δ , and CD3 ϵ chains are negatively charged, which is a characteristic that allows these chains to associate with the positively charged T-cell receptor chains. The intracellular tails of the CD3 γ , CD3 δ , and CD3 ϵ chains each contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif or ITAM, whereas each CD3 ζ chain has three. It is believed the ITAMs are important for the signaling capacity of a TCR complex. CD3 as used in the present disclosure can be from various animal species, including human, monkey, mouse, rat, or other mammals.

[0056] As used herein, a “conservative substitution” is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are well-known in the art (*see, e.g.*, WO 97/09433, page 10, published March 13, 1997; Lehninger, *Biochemistry*, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77; Lewin, *Genes IV*, Oxford University Press, NY and Cell Press, Cambridge, MA (1990), p. 8). In certain embodiments, a conservative substitution includes a leucine to serine substitution.

[0057] As used herein, the term "derivative" refers to a modification of one or more amino acid residues of a peptide by chemical or biological means, either with or without an enzyme, e.g., by glycosylation, alkylation, acylation, ester formation, or amide formation.

[0058] As used herein, a polypeptide or amino acid sequence "derived from" a designated polypeptide or protein refers to the origin of the polypeptide. In certain embodiments, the polypeptide or amino acid sequence which is derived from a particular sequence (sometimes referred to as the "starting" or "parent" or "parental" sequence) has an amino acid sequence that is essentially identical to the starting sequence or a portion thereof, wherein the portion consists of at least 10-20 amino acids, at least 20-30 amino acids, or at least 30-50 amino acids, or at least 50-150 amino acids, or which is otherwise identifiable to one of ordinary skill in the art as having its origin in the starting sequence. For example, a binding domain can be derived from an antibody, e.g., a Fab, F(ab')₂, Fab', scFv, single domain antibody (sdAb), etc.

[0059] Polypeptides derived from another polypeptide can have one or more mutations relative to the starting polypeptide, e.g., one or more amino acid residues which have been substituted with another amino acid residue or which has one or more amino acid residue insertions or deletions. The polypeptide can comprise an amino acid sequence which is not naturally occurring. Such variations necessarily have less than 100% sequence identity or similarity with the starting polypeptide. In one embodiment, the variant will have an amino acid sequence from about 60% to less than 100% amino acid sequence identity or similarity with the amino acid sequence of the starting polypeptide. In another embodiment, the variant will have an amino acid sequence from about 75% to less than 100%, from about 80% to less than 100%, from about 85% to less than 100%, from about 90% to less than 100%, from about 95% to less than 100% amino acid sequence identity or similarity with the amino acid sequence of the starting polypeptide.

[0100] As used herein, unless otherwise provided, a position of an amino acid residue in a variable region of an immunoglobulin molecule is numbered using the IMGT criteria (Brochet, X, et al, Nucl. Acids Res. (2008) 36, W503-508), and a position of an amino acid residue in a constant region of an immunoglobulin molecule is numbered according to EU nomenclature (Ward et al., 1995 *Therap. Immunol.* 2:77-94). The Kabat numbering convention (Kabat, Sequences of Proteins of Immunological Interest, 5th ed. Bethesda, MD: Public Health Service, National Institutes of Health (1991)) is an alternative system used to refer to a position of an amino acid residue in a variable region of an immunoglobulin molecule.

[0060] As used herein, the term “dimer” refers to a biological entity that consists of two subunits associated with each other via one or more forms of intramolecular forces, including covalent bonds (e.g., disulfide bonds) and other interactions (e.g., electrostatic interactions, salt bridges, hydrogen bonding, and hydrophobic interactions), and is stable under appropriate conditions (e.g., under physiological conditions, in an aqueous solution suitable for expressing, purifying, and/or storing recombinant proteins, or under conditions for non-denaturing and/or non-reducing electrophoresis). A “heterodimer” or “heterodimeric protein,” as used herein, refers to a dimer formed from two different polypeptides. A heterodimer does not include an antibody formed from four polypeptides (*i.e.*, two light chains and two heavy chains). A “homodimer” or “homodimeric protein,” as used herein, refers to a dimer formed from two identical polypeptides.

[0061] In some embodiments, a CD3-binding polypeptide comprises, in order from amino-terminus to carboxyl-terminus or in order from carboxyl-terminus to amino-terminus, (i) a second binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) a carboxyl-terminus linker (or an amino-terminus linker), and (v) a CD3-binding domain. As used herein and depending on context, a “hinge region” or a “hinge” refers to a polypeptide region between a binding domain (e.g., a CD3-binding domain or a second binding domain) and an immunoglobulin constant region. As used herein and depending on context, a “linker” may refer to (1) a polypeptide region between V_H and V_L regions in a single-chain Fv (scFv) or (2) a polypeptide region between an immunoglobulin constant region and a second binding domain in a CD3-binding polypeptide comprising two binding domains. A polypeptide region between an immunoglobulin constant region and a CD3-binding domain in a CD3-binding polypeptide comprising two binding domains may also be referred to as a “carboxyl-terminus linker” or an “amino-terminus linker.” Non-limiting examples of carboxyl-terminus and amino-terminus linkers include flexible linkers comprising glycine-serine repeats, and linkers derived from (a) an interdomain region of a transmembrane protein (e.g., a type I transmembrane protein); (b) a stalk region of a type II C-lectin; or (c) an immunoglobulin hinge. Non-limiting examples of hinges and linkers are provided in Tables 1 and 2. In some embodiments, a “linker” provides a spacer function compatible with interaction of the two sub-binding domains so that the resulting polypeptide retains a specific binding affinity to the same target molecule as an antibody that comprises the same light and heavy chain variable regions. In certain embodiments, a linker is comprised of five to about 35 amino acids, for instance, about 15 to about 25 amino acids.

[0062] A “wild-type immunoglobulin hinge region” refers to a naturally occurring upper and middle hinge amino acid sequences interposed between and connecting the CH1 and CH2

domains (for IgG, IgA, and IgD) or interposed between and connecting the CH1 and CH3 domains (for IgE and IgM) found in the heavy chain of an antibody. In certain embodiments, a wild type immunoglobulin hinge region sequence is human, and can comprise a human IgG hinge region.

- 5 **[0063]** An “altered wild-type immunoglobulin hinge region” or “altered immunoglobulin hinge region” refers to (a) a wild type immunoglobulin hinge region with up to 30% amino acid changes (e.g., up to 25%, 20%, 15%, 10%, or 5% amino acid substitutions or deletions), or (b) a portion of a wild type immunoglobulin hinge region that has a length of about 5 amino acids (e.g., about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids) up to about 10 120 amino acids (for instance, having a length of about 10 to about 40 amino acids or about 15 to about 30 amino acids or about 15 to about 20 amino acids or about 20 to about 25 amino acids), has up to about 30% amino acid changes (e.g., up to about 25%, 20%, 15%, 10%, 5%, 4%, 3%, 2%, or 1% amino acid substitutions or deletions or a combination thereof), and has an IgG core hinge region as disclosed in US 2013/0129723 and US 2013/0095097.
- 15 **[0064]** As used herein, the term “humanized” refers to a process of making an antibody or immunoglobulin binding proteins and polypeptides derived from a non-human species (e.g., mouse or rat) less immunogenic to humans, while still retaining antigen-binding properties of the original antibody, using genetic engineering techniques. In some embodiments, the binding domain(s) of an antibody or immunoglobulin binding proteins and polypeptides (e.g., light and heavy chain variable regions, Fab, scFv) are humanized. Non-human binding domains can be 20 humanized using techniques known as CDR grafting (Jones *et al.*, *Nature* 321:522 (1986)) and variants thereof, including “reshaping” (Verhoeven, *et al.*, 1988 *Science* 239:1534-1536; Riechmann, *et al.*, 1988 *Nature* 332:323-337; Tempest, *et al.*, *Bio/Technol* 1991 9:266-271), “hyperchimerization” (Queen, *et al.*, 1989 *Proc Natl Acad Sci USA* 86:10029-10033; Co, *et al.*, 1991 *Proc Natl Acad Sci USA* 88:2869-2873; Co, *et al.*, 1992 *J Immunol* 148:1149-1154), and “veneering” (Mark, *et al.*, “Derivation of therapeutically active humanized and veneered anti-CD18 antibodies.” In: Metcalf BW, Dalton BJ, eds. *Cellular adhesion: molecular definition to therapeutic potential*. New York: Plenum Press, 1994: 291-312). If derived from a non-human source, other regions of the antibody or immunoglobulin binding proteins and polypeptides, such as the hinge region and constant region domains, can also be humanized. 30

[0065] An “immunoglobulin dimerization domain” or “immunoglobulin heterodimerization domain”, as used herein, refers to an immunoglobulin domain of a polypeptide chain that preferentially interacts or associates with a different immunoglobulin domain of a second

polypeptide chain, wherein the interaction of the different immunoglobulin heterodimerization domains substantially contributes to or efficiently promotes heterodimerization of the first and second polypeptide chains (*i.e.*, the formation of a dimer between two different polypeptide chains, which is also referred to as a “heterodimer”). The interactions between immunoglobulin heterodimerization domains “substantially contributes to or efficiently promotes” the heterodimerization of first and second polypeptide chains if there is a statistically significant reduction in the dimerization between the first and second polypeptide chains in the absence of the immunoglobulin heterodimerization domain of the first polypeptide chain and/or the immunoglobulin heterodimerization domain of the second polypeptide chain. In certain embodiments, when the first and second polypeptide chains are co-expressed, at least 60%, at least about 60% to about 70%, at least about 70% to about 80%, at least 80% to about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the first and second polypeptide chains form heterodimers with each other. Representative immunoglobulin heterodimerization domains include an immunoglobulin CH1 domain, an immunoglobulin CL domain (*e.g.*, C κ or C λ isotypes), or derivatives thereof, including wild type immunoglobulin CH1 and CL domains and altered (or mutated) immunoglobulin CH1 and CL domains, as provided therein.

[0066] An “immunoglobulin constant region” or “constant region” is a term defined herein to refer to a peptide or polypeptide sequence that corresponds to or is derived from part or all of one or more constant region domains. In certain embodiments, the immunoglobulin constant region corresponds to or is derived from part or all of one or more constant region domains, but not all constant region domains of a source antibody. In certain embodiments, the constant region comprises IgG CH2 and CH3 domains, *e.g.*, IgG1 CH2 and CH3 domains. In certain embodiments, the constant region does not comprise a CH1 domain. In certain embodiments, the constant region domains making up the constant region are human. In some embodiments (for example, in certain variations of a CD3-binding polypeptide or protein), the constant region domains of a fusion protein of this disclosure lack or have minimal effector functions of antibody-dependent cell-mediated cytotoxicity (ADCC) and complement activation and complement-dependent cytotoxicity (CDC), while retaining the ability to bind some F γ receptors (such as F γ Rn, the neonatal Fc receptor) and retaining a relatively long half life *in vivo*. In other variations, a fusion protein of this disclosure includes constant domains that retain such effector function of one or both of ADCC and CDC. In certain embodiments, a binding domain of this disclosure is fused to a human IgG1 constant region, wherein the IgG1 constant region has one or more of the following amino acids mutated: leucine at position 234 (L234), leucine at position 235 (L235), glycine at position 237 (G237), glutamate at position 318 (E318), lysine at position

320 (K320), lysine at position 322 (K322), or any combination thereof (numbering according to EU). For example, any one or more of these amino acids can be changed to alanine. In a further embodiment, an IgG1 Fc domain has each of L234, L235, G237, E318, K320, and K322 (according to EU numbering) mutated to an alanine (*i.e.*, L234A, L235A, G237A, E318A, K320A, and K322A, respectively), and optionally an N297A mutation as well (*i.e.*, essentially eliminating glycosylation of the CH2 domain).

[0067] "Fc region" or "Fc domain" refers to a polypeptide sequence corresponding to or derived from the portion of a source antibody that is responsible for binding to antibody receptors on cells and the C1q component of complement. Fc stands for "fragment crystalline," the fragment of an antibody that will readily form a protein crystal. Distinct protein fragments, which were originally described by proteolytic digestion, can define the overall general structure of an immunoglobulin protein. As originally defined in the literature, the Fc fragment consists of the disulfide-linked heavy chain hinge regions, CH2, and CH3 domains. However, more recently the term has been applied to a single chain consisting of CH3, CH2, and at least a portion of the hinge sufficient to form a disulfide-linked dimer with a second such chain. For a review of immunoglobulin structure and function, see Putnam, *The Plasma Proteins*, Vol. V (Academic Press, Inc., 1987), pp. 49-140; and Padlan, *Mol. Immunol.* 31:169-217, 1994. As used herein, the term Fc includes variants of naturally occurring sequences.

[0068] In some embodiments, a CD3-binding protein comprises a protein scaffold as generally disclosed in, for example, in US Patent Application Publication Nos. 2003/0133939, 2003/0118592, and 2005/0136049. A CD3-binding protein may comprise, in order from amino-terminus to carboxyl-terminus, a first binding domain, a hinge region, and an immunoglobulin constant constant region. In other embodiments, a CD3-binding protein comprises a protein scaffold as generally disclosed in, for example, in US Patent Application Publication No. 2009/0148447. A CD3-binding protein may comprise, in order from carboxyl-terminus to amino-terminus, an immunoglobulin constant region, a hinge region and a first binding domain.

[0069] CD3-binding polypeptides and proteins disclosed herein may incorporate a multi-specific binding protein scaffold. Multi-specific binding proteins and polypeptides using scaffolds are disclosed, for instance, in PCT Application Publication No. WO 2007/146968, U.S. Patent Application Publication No. 2006/0051844, PCT Application Publication No. WO 2010/040105, PCT Application Publication No. WO 2010/003108, U.S. Patent No. 7,166,707 and U.S. Patent No. 8,409,577, which are each incorporated herein by reference in their entirety. A CD3-binding protein may comprise two binding domains (the domains can be designed to specifically bind

the same or different targets), two hinge regions, and an immunoglobulin constant region. A CD3-binding protein may be a homodimeric protein comprising two identical, disulfide-bonded polypeptides.

[0070] As used herein, the “stalk region” of a type II C-lectin refers to the portion of the extracellular domain of the type II C-lectin that is located between the C-type lectin-like domain (CTLD; e.g., similar to CTLD of natural killer cell receptors) and the transmembrane domain. For example, in the human CD94 molecule (GenBank Accession No. AAC50291.1, PRI November 30, 1995), the extracellular domain corresponds to amino acid residues 34-179, whereas the CTLD corresponds to amino acid residues 61-176. Accordingly, the stalk region of the human CD94 molecule includes amino acid residues 34-60, which is found between the membrane and the CTLD (see Boyington *et al.*, *Immunity* 10:75, 1999; for descriptions of other stalk regions, see also Beavil *et al.*, *Proc. Nat'l. Acad. Sci. USA* 89:753, 1992; and Figdor *et al.*, *Nature Rev. Immunol.* 2:77, 2002). These type II C-lectins can also have from six to 10 junction amino acids between the stalk region and the transmembrane region or the CTLD. In another example, the 233 amino acid human NKG2A protein (GenBank Accession No. P26715.1, PRI June 15, 2010) has a transmembrane domain ranging from amino acids 71-93 and an extracellular domain ranging from amino acids 94-233. The CTLD is comprised of amino acids 119-231, and the stalk region comprises amino acids 99-116, which is flanked by junctions of five and two amino acids. Other type II C-lectins, as well as their extracellular ligand-bind domains, interdomain or stalk regions, and CTLDs are known in the art (see, e.g., GenBank Accession Nos. NP_001993.2; AAH07037.1, PRI July 15, 2006; NP_001773.1, PRI June 20, 1010; AAL65234.1, PRI January 17, 2002, and CAA04925.1, PRI November 14, 2006, for the sequences of human CD23, CD69, CD72, NKG2A and NKG2D and their descriptions, respectively).

[0071] As used herein, the “interdomain region” of a transmembrane protein (e.g., a type I transmembrane protein) refers to a portion of the extracellular domain of the transmembrane protein that is located between two adjacent domains. Examples of interdomain regions include regions linking adjacent Ig domains of immunoglobulin superfamily members (e.g., an immunoglobulin hinge region from IgG, IgA, IgD, or IgE; the region linking the IgV and IgC2 domains of CD2; or the region linking the IgV and IgC domains of CD80 or CD86). Another example of an interdomain region is the region linking the non-Ig and IgC2 domain of CD22, a type I sialic acid-binding Ig-like lectin.

[0072] A polypeptide region “derived from” a stalk region of a type II C-lectin, or “derived from” a transmembrane protein interdomain region (e.g., an immunoglobulin hinge region), refers to an about five to about 150 amino acid sequence, an about 5 to about 100 amino acid sequence, an about 5 to about 50 amino acid sequence, an about 5 to about 40 amino acid sequence, an about 5 to about 30 amino acid sequence, an about 5 to about 25 amino acid sequence, an about 5 to about 20 amino acid sequence, an about 10 to about 25 amino acid sequence, an about 10 to about 20 amino acid sequence, about 8 to about 20 amino acid sequence, about 9 to about 20 amino acid sequence, about 10 to about 20 amino acid sequence, about 11 to about 20 amino acid sequence, about 12 to about 20 amino acid sequence, about 13 to about 20 amino acid sequence, about 14 to about 20 amino acid sequence, about 15 to about 20 amino acid sequence, or an about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid sequence, wherein all or at least a portion of which includes (i) a wild-type stalk region or interdomain region sequence; (ii) a fragment of the wild-type stalk region or interdomain region sequence; (iii) a polypeptide having at least 80%, 85%, 90%, or 95% amino acid sequence identity with either (i) or (ii); or (iv) either (i) or (ii) in which one, two, three, four, or five amino acids have a deletion, insertion, substitution, or any combination thereof, for instance, the one or more changes are substitutions or the one or more mutations include only one deletion. In some embodiments, a derivative of a stalk region is more resistant to proteolytic cleavage as compared to the wild-type stalk region sequence, such as those derived from about eight to about 20 amino acids of NKG2A, NKG2D, CD23, CD64, CD72, or CD94.

[0073] As used herein, the term “junction amino acids” or “junction amino acid residues” refers to one or more (e.g., about 2-10) amino acid residues between two adjacent regions or domains of a polypeptide, such as between a hinge and an adjacent immunoglobulin constant region or between a hinge and an adjacent binding domain or between a peptide linker and an adjacent immunoglobulin variable domain or an adjacent immunoglobulin constant region. Junction amino acids can result from the construct design of a polypeptide (e.g., amino acid residues resulting from the use of a restriction enzyme site during the construction of a nucleic acid molecule encoding a polypeptide).

[0074] As used herein, the phrase a “linker between CH3 and CH1 or CL” refers to one or more (e.g., about 2-12, about 2-10, about 4-10, about 5-10, about 6-10, about 7-10, about 8-10, about 9-10, about 8-12, about 9-12, or about 10-12) amino acid residues between the C-terminus of a CH3 domain (e.g., a wild type CH3 or a mutated CH3) and the N-terminus of a CH1 domain or CL domain (e.g., Ck).

[0075] As used herein, the term "patient in need" or "subject in need" refers to a patient or a subject at risk of, or suffering from, a disease, disorder or condition that is amenable to treatment or amelioration with a CD3-binding protein or polypeptide or a composition thereof provided herein.

5 [0076] As used herein, the term "pharmaceutically acceptable" refers to molecular entities and compositions that do not generally produce allergic or other serious adverse reactions when administered using routes well known in the art. Molecular entities and compositions approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans
10 are considered to be "pharmaceutically acceptable."

[0077] As used herein, the term "promoter" refers to a region of DNA involved in binding RNA polymerase to initiate transcription.

[0078] As used herein, the terms "nucleic acid," "nucleic acid molecule," or "polynucleotide" refer to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-
15 stranded form. Unless specifically limited, the terms encompass nucleic acids containing analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and
20 complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions can be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.* (1991) *Nucleic Acid Res.* 19:5081; Ohtsuka *et al.* (1985) *J. Biol. Chem.* 260:2605-2608; Cassol *et al.* (1992); Rossolini *et al.* (1994) *Mol. Cell. Probes* 8:91-98). The term nucleic
25 acid is used interchangeably with gene, cDNA, and mRNA encoded by a gene. As used herein, the terms "nucleic acid," "nucleic acid molecule," or "polynucleotide" are intended to include DNA molecules (e.g., cDNA or genomic DNA), RNA molecules (e.g., mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof.

30 [0079] The term "expression" refers to the biosynthesis of a product encoded by a nucleic acid. For example, in the case of nucleic acid segment encoding a polypeptide of interest, expression involves transcription of the nucleic acid segment into mRNA and the translation of mRNA into one or more polypeptides.

[0080] The terms "expression unit" and "expression cassette" are used interchangeably herein and denote a nucleic acid segment encoding a polypeptide of interest and capable of providing expression of the nucleic acid segment in a host cell. An expression unit typically comprises a transcription promoter, an open reading frame encoding the polypeptide of interest, and a transcription terminator, all in operable configuration. In addition to a transcriptional promoter and terminator, an expression unit can further include other nucleic acid segments such as, *e.g.*, an enhancer or a polyadenylation signal.

[0081] The term "expression vector," as used herein, refers to a nucleic acid molecule, linear or circular, comprising one or more expression units. In addition to one or more expression units, an expression vector can also include additional nucleic acid segments such as, for example, one or more origins of replication or one or more selectable markers. Expression vectors are generally derived from plasmid or viral DNA, or can contain elements of both.

[0082] As used herein, the term "sequence identity" refers to a relationship between two or more polynucleotide sequences or between two or more polypeptide sequences. When a position in one sequence is occupied by the same nucleic acid base or amino acid residue in the corresponding position of the comparator sequence, the sequences are said to be "identical" at that position. The percentage "sequence identity" is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of "identical" positions. The number of "identical" positions is then divided by the total number of positions in the comparison window and multiplied by 100 to yield the percentage of "sequence identity." Percentage of "sequence identity" is determined by comparing two optimally aligned sequences over a comparison window. The comparison window for nucleic acid sequences can be, for instance, at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more nucleic acids in length. The comparison window for polypeptide sequences can be, for instance, at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300 or more amino acids in length. In order to optimally align sequences for comparison, the portion of a polynucleotide or polypeptide sequence in the comparison window can comprise additions or deletions termed gaps while the reference sequence is kept constant. An optimal alignment is that alignment which, even with gaps, produces the greatest possible number of "identical" positions between the reference and comparator sequences. Percentage "sequence identity" between two sequences can be determined using the version of the program "BLAST 2 Sequences" which was available from the National Center for Biotechnology

Information as of September 1, 2004, which program incorporates the programs BLASTN (for nucleotide sequence comparison) and BLASTP (for polypeptide sequence comparison), which programs are based on the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90(12):5873-5877, 1993). When utilizing "BLAST 2 Sequences," parameters that were default
5 parameters as of September 1, 2004, can be used for word size (3), open gap penalty (11), extension gap penalty (1), gap dropoff (50), expect value (10) and any other required parameter including but not limited to matrix option. Two nucleotide or amino acid sequences are considered to have "substantially similar sequence identity" or "substantial sequence identity" if the two sequences have at least 80%, at least 85%, at least 90%, at least 95%, at
10 least 96%, at least 97%, at least 98%, or at least 99% sequence identity relative to each other.

[0083] As used herein, a "polypeptide" or "polypeptide chain" is a single, linear and contiguous arrangement of covalently linked amino acids. It does not include two polypeptide chains that link together in a non-linear fashion, such as via an interchain disulfide bond (e.g., a half immunoglobulin molecule in which a light chain links with a heavy chain via a disulfide bond).

15 Polypeptides can have or form one or more intrachain disulfide bonds. With regard to polypeptides as described herein, reference to amino acid residues corresponding to those specified by SEQ ID NO includes post-translational modifications of such residues.

[0084] As used herein, "CD3-binding protein" may be used interchangeably with "CD3-binding polypeptide." Such molecules specifically bind to cluster of differentiation 3 protein (CD3) (e.g.,
20 human CD3).

[0085] A "protein" is a macromolecule comprising one or more polypeptide chains. A protein can also comprise non-peptidic components, such as carbohydrate groups. Carbohydrates and other non-peptidic substituents can be added to a protein by the cell in which the protein is produced, and will vary with the type of cell. Proteins are defined herein in terms of their amino
25 acid backbone structures; substituents such as carbohydrate groups are generally not specified, but may be present nonetheless. A protein may be an antibody or an antigen-binding fragment of an antibody. In some embodiments, a protein may also be an scFv-Fc-scFv molecule, scFv-scFv dimer, or a diabody.

[0086] The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions
30 within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a

polypeptide is located proximal to the carboxyl-terminus of the reference sequence, but is not necessarily at the carboxyl-terminus of the complete polypeptide.

[0087] "T-cell receptor" (TCR) is a molecule found on the surface of T-cells that, along with CD3, is generally responsible for recognizing antigens bound to major histocompatibility complex (MHC) molecules. It consists of a disulfide-linked heterodimer of the highly variable α and β chains in most T-cells. In other T-cells, an alternative receptor made up of variable γ and δ chains is expressed. Each chain of the TCR is a member of the immunoglobulin superfamily and possesses one N-terminal immunoglobulin variable domain, one immunoglobulin constant domain, a transmembrane region, and a short cytoplasmic tail at the C-terminal end (see Abbas and Lichtman, *Cellular and Molecular Immunology* (5th Ed.), Editor: Saunders, Philadelphia, 2003; Janeway *et al.*, *Immunobiology: The Immune System in Health and Disease*, 4th Ed., Current Biology Publications, p148, 149, and 172, 1999). TCR as used in the present disclosure can be from various animal species, including human, mouse, rat, or other mammals.

[0088] "TCR complex," as used herein, refers to a complex formed by the association of CD3 chains with other TCR chains. For example, a TCR complex can be composed of a CD3 γ chain, a CD3 δ chain, two CD3 ϵ chains, a homodimer of CD3 ζ chains, a TCR α chain, and a TCR β chain. Alternatively, a TCR complex can be composed of a CD3 γ chain, a CD3 δ chain, two CD3 ϵ chains, a homodimer of CD3 ζ chains, a TCR γ chain, and a TCR δ chain.

[0089] "A component of a TCR complex," as used herein, refers to a TCR chain (*i.e.*, TCR α , TCR β , TCR γ or TCR δ), a CD3 chain (*i.e.*, CD3 γ , CD3 δ , CD3 ϵ or CD3 ζ), or a complex formed by two or more TCR chains or CD3 chains (*e.g.*, a complex of TCR α and TCR β , a complex of TCR γ and TCR δ , a complex of CD3 ϵ and CD3 δ , a complex of CD3 γ and CD3 ϵ , or a sub-TCR complex of TCR α , TCR β , CD3 γ , CD3 δ , and two CD3 ϵ chains).

[0090] "Antibody-dependent cell-mediated cytotoxicity" and "ADCC," as used herein, refer to a cell-mediated process in which nonspecific cytotoxic cells that express Fc γ Rs (*e.g.*, monocytic cells such as Natural Killer (NK) cells and macrophages) recognize bound antibody (or other protein capable of binding Fc γ Rs) on a target cell and subsequently cause lysis of the target cell. In principle, any effector cell with an activating Fc γ R can be triggered to mediate ADCC. The primary cells for mediating ADCC are NK cells, which express only Fc γ RIII, whereas monocytes, depending on their state of activation, localization, or differentiation, can express Fc γ RI, Fc γ RII, and Fc γ RIII. For a review of Fc γ R expression on hematopoietic cells, see, *e.g.*, Ravetch *et al.*, 1991, *Annu. Rev. Immunol.*, 9:457-92.

[0091] The term "having ADCC activity," as used herein in reference to a polypeptide or protein, means that the polypeptide or protein (for example, one comprising an immunoglobulin hinge region and an immunoglobulin constant region having CH2 and CH3 domains, such as derived from IgG (e.g., IgG1)), is capable of mediating antibody-dependent cell-mediated cytotoxicity (ADCC) through binding of a cytolytic Fc receptor (e.g., FcγRIII) on a cytolytic immune effector cell expressing the Fc receptor (e.g., an NK cell).

[0092] "Complement-dependent cytotoxicity" and "CDC," as used herein, refer to a process in which components in normal serum ("complement"), together with an antibody or other C1q-complement-binding protein bound to a target antigen, exhibit lysis of a target cell expressing the target antigen. Complement consists of a group of serum proteins that act in concert and in an orderly sequence to exert their effect.

[0093] The terms "classical complement pathway" and "classical complement system," as used herein, are synonymous and refer to a particular pathway for the activation of complement. The classical pathway requires antigen-antibody complexes for initiation and involves the activation, in an orderly fashion, of nine major protein components designated C1 through C9. For several steps in the activation process, the product is an enzyme that catalyzes the subsequent step. This cascade provides amplification and activation of large amounts of complement by a relatively small initial signal.

[0094] The term "having CDC activity," as used herein in reference to a polypeptide or protein, means that the polypeptide or protein (for example, one comprising an immunoglobulin hinge region and an immunoglobulin constant region having CH2 and CH3 domains, such as derived from IgG (e.g., IgG1)) is capable of mediating complement-dependent cytotoxicity (CDC) through binding of C1q complement protein and activation of the classical complement system.

[0095] "Redirected T-cell cytotoxicity" and "RTCC," as used herein, refer to a T-cell-mediated process in which a cytotoxic T-cell is recruited to a target cell using a multi-specific protein that is capable of specifically binding both the cytotoxic T-cell and the target cell, and whereby a target-dependent cytotoxic T-cell response is elicited against the target cell. Polypeptides and proteins comprising CD3-binding domains, as disclosed herein, and tumor antigen-binding domains are capable of RTCC.

[0096] As used herein, the term "treatment," "treating," or "ameliorating" refers to either a therapeutic treatment or prophylactic/preventative treatment. A treatment is therapeutic if at least one symptom of disease in an individual receiving treatment improves or a treatment can

delay worsening of a progressive disease in an individual, or prevent onset of additional associated diseases.

[0097] As used herein, the term “therapeutically effective amount (or dose)” or “effective amount (or dose)” of a specific binding molecule or compound refers to that amount of the compound sufficient to result in amelioration of one or more symptoms of the disease being treated in a statistically significant manner or a statistically significant improvement in organ function. When referring to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When referring to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered serially or simultaneously (in the same formulation or concurrently in separate formulations).

[0098] As used herein, the term “transformation,” “transfection,” and “transduction” refer to the transfer of nucleic acid (i.e., a nucleotide polymer) into a cell. As used herein, the term “genetic transformation” refers to the transfer and incorporation of DNA, especially recombinant DNA, into a cell. The transferred nucleic acid can be introduced into a cell via an expression vector.

[0099] As used herein, the term “variant” or “variants” refers to a nucleic acid or polypeptide differing from a reference nucleic acid or polypeptide, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the reference nucleic acid or polypeptide. For instance, a variant may exhibit at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98% or at least about 99% sequence identity compared to the active portion or full length reference nucleic acid or polypeptide.

[00100] The terms “light chain variable region” (also referred to as “light chain variable domain” or “VL” or V_L) and “heavy chain variable region” (also referred to as “heavy chain variable domain” or “VH” or V_H) refer to the variable binding region from an antibody light and heavy chain, respectively. The variable binding regions are made up of discrete, well-defined sub-regions known as “complementarity determining regions” (CDRs) and “framework regions” (FRs), generally comprising in order FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4 from amino-terminus to carboxyl-terminus. In one embodiment, the FRs are humanized. The term “CL” refers to an “immunoglobulin light chain constant region” or a “light chain constant region,” i.e., a constant region from an antibody light chain. The term “CH” refers to an “immunoglobulin heavy chain constant region” or a “heavy chain constant region,” which is further divisible, depending on the antibody isotype into CH1, CH2, and CH3 (IgA, IgD, IgG), or CH1, CH2, CH3, and CH4

domains (IgE, IgM). A "Fab" (fragment antigen binding) is the part of an antibody that binds to antigens and includes the variable region and CH1 domain of the heavy chain linked to the light chain via an inter-chain disulfide bond.

[00101] The present disclosure describes binding domains that specifically bind CD3 (e.g., human CD3), as well as polypeptides and proteins comprising these binding domains. In some embodiments, the CD3-binding proteins and polypeptides comprise a second binding domain, which may bind to a tumor antigen (e.g., PSMA, CD19, CD20, CD37, CD38, CD123, Her2, ROR1, RON, glycoprotein A33 antigen (gpA33) or CEA). The polypeptides and proteins comprising binding domains of this disclosure can further comprise immunoglobulin constant regions, linker peptides, hinge regions, immunoglobulin dimerization/heterodimerization domains, junctional amino acids, tags, *etc.* These components of the disclosed polypeptides and proteins are described in further detail below.

[00102] Additionally, the CD3-binding polypeptides and proteins disclosed herein can be in the form of an antibody or a fusion protein of any of a variety of different formats (e.g., the fusion protein can be in the form of a CD3-binding bispecific or multispecific molecule). Non-limiting examples of bispecific molecules include a scFv-Fc-scFv molecule. Some bispecific molecules typically comprise or consist of an anti-tumor antigen scFv linked to an anti-CD3 scFv and typically do not include other sequences such as an immunoglobulin constant region. In other embodiments, a CD3-binding protein is a diabody.

[00103] A CD3-binding protein in accordance with the present disclosure generally includes at least one CD3-binding polypeptide chain comprising (a) a CD3-binding domain as set forth herein. In certain variations, the CD3-binding polypeptide further includes (b) a hinge region carboxyl-terminal to the CD3-binding domain, and (c) an immunoglobulin constant region. In further variations, the ROR1-binding polypeptide further includes (d) a carboxyl-terminus linker carboxyl-terminal to the immunoglobulin constant region, and (e) a second binding domain carboxyl-terminal to the carboxyl-terminus linker.

[00104] In yet other variations, the CD3-binding polypeptide comprises (b) a hinge region amino-terminal to the CD3-binding domain, and (c) an immunoglobulin sub-region amino-terminal to the hinge region. In some variations, the CD3-binding polypeptide comprises (b) a hinge region carboxyl-terminal to the CD3-binding domain, and (c) an immunoglobulin sub-region carboxyl-terminal to the hinge region

[00105] In some embodiments, CD3-binding polypeptides are capable of homodimerization, typically through disulfide bonding, via the immunoglobulin constant region and/or hinge region (e.g., via an immunoglobulin constant region comprising IgG CH2 and CH3 domains and an IgG hinge region). Thus, in certain embodiments of the present disclosure, two identical single
5 chain CD3-binding polypeptides homodimerize to form a dimeric CD3-binding protein.

[00106] In other embodiments, a CD3-binding polypeptide includes a heterodimerization domain that is capable of heterodimerization with a different heterodimerization domain in a second, non-identical polypeptide chain. In certain variations, the second polypeptide chain for heterodimerization includes a second binding domain. Accordingly, in certain embodiments of
10 the present disclosure, two non-identical polypeptide chains, one comprising the CD3-binding domain and the second optionally comprising a second binding domain, dimerize to form a heterodimeric CD3-binding protein. Examples of types of heterodimers include those described in US 2013/0095097 and US 2013/0129723.

[00107] In some embodiments, a CD3-binding domain, protein or polypeptide is conjugated to a
15 drug or a toxic moiety.

[00108] CD3-binding polypeptides, proteins, and their various components used in the present disclosure are further described below.

[00109] As indicated above, the disclosure relates to binding domains that specifically bind CD3 (e.g., human CD3). A CD3-binding domain may comprise amino acid sequences shown in
20 Table 14. In some embodiments, a CD3-binding polypeptide or protein comprises a signal sequence. The disclosure also encompasses CD3-binding domains and proteins comprising or encoded by any of the sequences shown in Table 14, excluding the signal sequences that are part of these sequences. CD3-binding domains and polypeptides, their internal designations, and their sequences are summarized in Table 15. In some cases, CD3-binding domains of the
25 disclosure contain amino acid substitutions. For example, TSC370 has the amino acid sequence of TSC342 with the glycine residue at position 27 according to the IMGT numbering system substituted with tyrosine.

[00110] In certain embodiments, the disclosure relates to a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain variable region and
30 an immunoglobulin heavy chain variable region; wherein the immunoglobulin light chain variable region comprises an amino acid sequence that is (a) at least about 93% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99%

identical to the amino acid sequence in SEQ ID NO:88; or (b) at least about 94% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:89; and wherein the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least
5 about 82% identical, at least about 85% identical, at least about 87% identical, at least about 90% identical, at least about 92% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:86. A CD3-binding domain may comprise an amino acid sequence that is at least about 87% identical, at least about 90% identical, at least about 92% identical, at
10 least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:83 or SEQ ID NO:84. A CD3-binding domain may comprise or consist of SEQ ID NO:83 or SEQ ID NO:84. In some embodiments, a CD3-binding domain comprises an amino acid sequence that is at least about 87% identical, at least about 90% identical, at least about 92% identical, at least about 95%
15 identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, or 100% identical to the amino acid sequence in SEQ ID NO:4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, or 60.

[00111] In some embodiments, a CD3-binding domain may comprise an immunoglobulin light chain variable region that comprises an LCDR1 amino acid sequence that differs from SEQ ID
20 NO:94 by at least one amino acid substitution, an LCDR2 amino acid sequence that differs from SEQ ID NO:95 by at least one amino acid substitution, and an LCDR3 amino acid sequence that differs from SEQ ID NO:96 by at least one amino acid substitution, and an immunoglobulin heavy chain variable region that comprises an HCDR1 amino acid sequence that differs from SEQ ID NO:91 by at least one amino acid substitution, an HCDR2 amino acid sequence that
25 differs from SEQ ID NO:92 by at least one amino acid substitution, and an HCDR3 amino acid sequence that differs from SEQ ID NO:93 by at least one amino acid substitution. In other embodiments, a CD3-binding domain may comprise an immunoglobulin light chain variable region that comprises an LCDR1 amino acid sequence that differs from SEQ ID NO:202 by at least one amino acid substitution, an LCDR2 amino acid sequence that differs from SEQ ID
30 NO:203 by at least one amino acid substitution, and an LCDR3 amino acid sequence that differs from SEQ ID NO:204 by at least one amino acid substitution, and an immunoglobulin heavy chain variable region that comprises an HCDR1 amino acid sequence that differs from SEQ ID NO:199 by at least one amino acid substitution, an HCDR2 amino acid sequence that differs from SEQ ID NO:200 by at least one amino acid substitution, and an HCDR3 amino acid

sequence that differs from SEQ ID NO:201 by at least one amino acid substitution. The CDR amino acid sequence of a CD3-binding domain may differ from the recited sequence by at least one amino acid substitution. The at least one amino acid substitution may be a conservative or a non-conservative amino acid substitution. In some embodiments, a LCDR1, LCDR2, LCDR3, HCDR1, HCDR2, and/or HCDR3 differs from an above-listed CDR sequence by 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, a CDR of the present disclosure contains about one or more (*e.g.*, about 2, 3, 4, 5, 6, 7, 8, 9, 10) insertions, about one or more (*e.g.*, about 2, 3, 4, 5, 6, 7, 8, 9, 10) deletions, about one or more (*e.g.*, about 2, 3, 4, 5, 6, 7, 8, 9, 10) amino acid substitutions (*e.g.*, conservative amino acid substitutions or non-conservative amino acid substitutions), or a combination of the above-noted changes, when compared to the CDR sequence of a known monoclonal antibody.

[00112] When describing the amino acid substitutions in this disclosure, a position of an amino acid residue in a variable region of an immunoglobulin molecule is usually numbered using the IMGT criteria (Brochet, X, et al, Nucl. Acids Res. (2008) 36, W503-508). In some embodiments, the amino acid residue at position 52 of the immunoglobulin light chain variable region of a CD3-binding domain is arginine and/or the amino acid residue at position 53 of the immunoglobulin light chain variable region of a CD3-binding domain is tryptophan. The amino acid residue at position 27 of the immunoglobulin heavy chain variable region of a CD3-binding domain may be tyrosine. In some embodiments, a CD3-binding domain comprises one or more of the following: (a) the amino acid residue at position 9 of the immunoglobulin heavy chain variable region is proline; (b) the amino acid residue at position 53 of the immunoglobulin heavy chain variable region is isoleucine; and (c) the amino acid residue at position 21 of the immunoglobulin light chain variable region is methionine. The amino acid residue at position 87 of the immunoglobulin light chain variable region of a CD3-binding domain may be tyrosine. The amino acid residue at position 86 of the immunoglobulin light chain variable region of a CD3-binding domain may be aspartic acid. In one embodiment, the amino acid residue at position 86 of the immunoglobulin light chain variable region of a CD3-binding domain is aspartic acid and the amino acid residue at position 87 of the immunoglobulin light chain variable region of a CD3-binding domain is tyrosine.

[00113] In certain embodiments, a CD3-binding domain comprises humanized immunoglobulin VL and/or VH regions. Techniques for humanizing immunoglobulin VL and VH regions are known in the art and are discussed, for example, in U.S. Patent Application Publication No. 2006/0153837. In certain aspects, a CD3-binding domain may comprise an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region that comprise

framework regions and at least one of the immunoglobulin light chain variable region and the immunoglobulin heavy chain variable region may be humanized. In one embodiment, an immunoglobulin light chain variable region comprises framework regions based on the human IGKV3D-20*1 germline amino acid sequence. In another embodiment, an immunoglobulin heavy chain variable region comprises framework regions based on the human IGHV1-69*02 germline amino acid sequence. In some aspects, an immunoglobulin heavy chain variable region comprises framework regions based on the human IGHV1-2*02 (H7), IGHV1-46*02 (H8), IGHV1-3*01 (H9), or IGHV1-69*02 (H10) germline amino acid sequence. An immunoglobulin light chain variable region may comprise framework regions based on the human IGKV3-11*01 (L4), IGKV1-33*01 (L5), IGKV1-39*01 (L7), or IGKV3D-20*1 (L8) germline amino acid sequence.

[00114] The disclosure relates to CD3-binding domains that have improved properties compared to the DRA222 CD3-binding domain. DRA222 has a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87.

DRA222 is described in WO 2013/158856. DRA222 is sometimes referred to as TSC311 or TSC312 in this disclosure. Fc DRA222 has the amino acid sequence of SEQ ID NO:2. The disclosure encompasses a CD3-binding domain (or a protein comprising said domain) that has a thermal stability that is increased at least about 10% when compared to the thermal stability of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87. The thermal transition midpoint (T_m) of a CD3-binding domain (or a protein comprising said domain) may be at least about 3°C, at least about 4°C, at least about 5°C, or at least about 6°C increased and up to about 20°C increased when compared to the T_m of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87. The thermal transition midpoint of a CD3-binding domain (or a protein comprising said domain) may be at least about 54°C, at least about 55°C, at least about 56°C, or at least about 57°C and up to about 72°C. The thermal stability or the thermal transition midpoint of a CD3-binding domain (or a protein comprising said domain) may be measured by differential scanning calorimetry or differential scanning fluorimetry.

[00115] A CD3-binding domain as disclosed herein (or a protein comprising said domain) may have storage stability that is increased at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% and up to about 100% when compared to the storage stability of a CD3-binding domain comprising a light chain variable region

comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87.

Storage stability may be measured after a CD3-binding domain (or a protein comprising said domain) is stored in PBS at about 25°C. In one embodiment, a CD3-binding domain (or a protein comprising said domain) is stable in storage in PBS at about 25°C for at least about 6 days, at least about 10 days, or at least about 13 days and up to about 90 days.

[00116] In some aspects, a CD3-binding domain as disclosed herein (or a protein comprising said domain) has a level of high molecular weight aggregates produced during recombinant expression that are at least about 5%, at least about 10%, at least about 20% decreased, at least about 30% decreased and up to about 50% decreased when compared to the level of high molecular weight aggregates produced during recombinant expression of a CD3-binding domain comprising a light chain variable region comprising SEQ ID NO:90 and a heavy chain variable region comprising SEQ ID NO:87.

[00117] The disclosure also relates to a CD3-binding domain that binds to human CD3 with an EC₅₀ of about 10 nM or lower. A CD3-binding domain of the disclosure may bind specifically to both human CD3 and cynomolgus CD3. For example, a CD3-binding domain may bind to cynomolgus CD3 with an EC₅₀ of about 30 nM or lower. Binding to cynomolgus CD3 allows the anti-CD3 therapeutic to be tested in non-human primates.

[00118] The disclosure encompasses a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region, wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93, and wherein the CD3-binding domain has any one or more of the properties described herein. For example, (i) the thermal transition midpoint of the CD3-binding domain (or a protein comprising the CD3-binding domain) is at least about 54°C, at least about 55°C, at least about 56°C, or at least about 57°C and up to about 72°C; (ii) the CD3-binding domain (or a protein comprising the CD3-binding domain) is stable in storage in PBS at about 25°C for at least about 6 days, at least about 10 days, or at least about 13 days and up to about 90 days; (iii) the CD3-binding domain (or a protein comprising the CD3-binding domain) binds to human CD3 with an EC₅₀ of about 10 nM or lower; and (iv) the CD3-binding domain (or a protein comprising the CD3-binding domain) binds to cynomolgus CD3 with an EC₅₀ of about 30 nM or lower.

[00119] In some embodiments, a CD3-binding polypeptide when bound to a CD3 protein on a T cell does not induce or induces a minimally detectable cytokine release from said T cell. In certain aspects, a CD3-binding protein or polypeptide exhibits reduced cytokine release in a patient as compared to the cytokine released when anti-CD3 antibody OKT3 is administered to a patient. A CD3-binding polypeptide may induce T-cell activation or T-cell proliferation.

[00120] In certain embodiments, a CD3-binding protein can comprise one or more additional binding domains (e.g., second binding domain) that bind a target other than CD3. These other binding domains can comprise, for example, a particular cytokine or a molecule that targets the binding domain polypeptide to a particular cell type, a toxin, an additional cell receptor, an antibody, *etc.*

[00121] In certain embodiments, a CD3-binding polypeptide used in the methods and compositions described herein is a bispecific single chain molecule comprising a CD3-binding domain and a second binding domain. In some embodiments, a CD3- and/or a second binding domain is derived from an antibody and comprises a variable heavy chain (VH) and a variable light chain (VL). These binding domains and variable chains may be arranged in any order that still retains some binding to the target(s). For example, the variable domains may be arranged in the order such as VH SBD-VL SBD-VH CD3-VL CD3; VL SBD-VH SBD-VH CD3-VL CD3; VH SBD-VL SBD-VL CD3-VH CD3; VL SBD-VH SBD-VL CD3-VH CD3; VH CD3-VL CD3-VH SBD-VL SBD; VL CD3-VH CD3-VL SBD-VH SBD; VH CD3-VL CD3-VL SBD-VH SBD; or VL CD3-VH CD3-VH SBD-VL SBD (where SBD refers to "second binding domain"). In certain aspects, the pairs of VH regions and VL regions in the binding domain binding to CD3 are in the format of a single chain antibody (scFv). The VH and VL regions may be arranged in the order VH-VL or VL-VH. In certain embodiments, the scFv may bind more effectively to CD3 in the VL-VH orientation than in the VH-VL orientation, or vice versa. The VH-region may be positioned N-terminally to a linker sequence. The VL region may be positioned C-terminally to the linker sequence. The domain arrangement in the CD3 binding domain of the bispecific single chain molecule may be VH-VL, with said CD3 binding domain located C-terminally to the second binding domain. In some cases, a bispecific molecule may comprise an scFv binding to a second binding domain linked to an scFv binding to CD3. These scFvs may be linked with a short peptide. In some embodiments, bispecific single chain molecules do not comprise a hinge region or a constant region (see, for example, US 2013/0295121, US 2013/0129730, US 2011/0293619, US 7,635,472, WO 2010/037836, WO 2004/106381 and WO 2011/121110; each incorporated herein by reference in its entirety).

[00122] In some embodiments, a binding domain is a single-chain Fv fragment (scFv) that comprises V_H and V_L regions specific for a target of interest. In certain embodiments, the V_H and V_L regions are human or humanized. In some variations, a binding domain is a single-chain Fv (scFv) comprising immunoglobulin V_L and V_H regions joined by a peptide linker. The use of peptide linkers for joining V_L and V_H regions is well-known in the art, and a large number of publications exist within this particular field. A linker may comprise the amino acid sequence QRHNNSSLNTGTQMAGHSPNS (SEQ ID NO:148). In some embodiments, a peptide linker is a 15mer consisting of three repeats of a Gly-Gly-Gly-Gly-Ser amino acid sequence ((Gly₄Ser)₃) (SEQ ID NO:193). Other linkers have been used, and phage display technology, as well as selective infective phage technology, has been used to diversify and select appropriate linker sequences (Tang *et al.*, *J. Biol. Chem.* 271, 15682-15686, 1996; Hennecke *et al.*, *Protein Eng.* 11, 405-410, 1998). In certain embodiments, the V_L and V_H regions are joined by a peptide linker having an amino acid sequence comprising the formula (Gly₄Ser)_n, wherein n = 1-5 (SEQ ID NO:194). In some embodiments, a Gly₄Ser sequence may be repeated between 6 and 10 times. Other suitable linkers can be obtained by optimizing a simple linker (e.g., (Gly₄Ser)_n (SEQ ID NO:194)) through random mutagenesis. In some embodiments, the heavy chain variable region of an scFv is amino-terminal to the light chain variable region of the scFv. In other embodiments, the light chain variable region of an scFv is amino-terminal to the heavy chain variable region of the scFv.

[00123] In some embodiments, a CD3-binding polypeptide comprises, in order from amino-terminus to carboxyl-terminus (or in order from carboxyl-terminus to amino-terminus), (i) a second binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) a carboxyl-terminus linker (or an amino-terminus linker), and (v) a CD3-binding domain. As used herein in the context of a polypeptide construct comprising a first binding domain and a second binding domain, a "hinge region" or a "hinge" refers to a polypeptide region between the first binding domain and the Fc region. A "carboxyl-terminus linker" or "an amino-terminus linker" refers to a polypeptide region between the Fc region and the second binding domain. In some embodiments, a carboxyl-terminus (or an amino-terminus linker) linker comprises or consists of SEQ ID NO:196. In certain embodiments, a hinge is a wild-type human immunoglobulin hinge region. In certain other embodiments, one or more amino acid residues can be added at the amino- or carboxyl-terminus of a wild type immunoglobulin hinge region as part of a fusion protein construct design. For example, additional junction amino acid residues at the hinge amino-terminus can be "RT," "RSS," "TG," or "T," or at the hinge carboxyl-terminus can be "SG",

or a hinge deletion can be combined with an addition, such as ΔP with "SG" added at the carboxyl-terminus.

[00124] In certain embodiments, a hinge, a carboxyl-terminus linker, or an amino-terminus linker is an altered immunoglobulin hinge in which one or more cysteine residues in a wild type immunoglobulin hinge region is substituted with one or more other amino acid residues (e.g., serine or alanine).

[00125] Exemplary altered immunoglobulin hinges, carboxyl-terminus linkers, and amino-terminus linkers include an immunoglobulin human IgG1 hinge region having one, two or three cysteine residues found in a wild type human IgG1 hinge substituted by one, two or three different amino acid residues (e.g., serine or alanine). An altered immunoglobulin hinge can additionally have a proline substituted with another amino acid (e.g., serine or alanine). For example, the above-described altered human IgG1 hinge can additionally have a proline located carboxyl-terminal to the three cysteines of wild type human IgG1 hinge region substituted by another amino acid residue (e.g., serine, alanine). In one embodiment, the prolines of the core hinge region are not substituted.

[00126] In certain embodiments, a hinge, a carboxyl-terminus linker, or an amino-terminus linker polypeptide comprises or is a sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a wild type immunoglobulin hinge region, such as a wild type human IgG1 hinge, a wild type human IgG2 hinge, or a wild type human IgG4 hinge.

[00127] In further embodiments, a hinge, a carboxyl-terminus linker, or an amino-terminus linker present in a CD3-binding polypeptide can be a hinge that is not based on or derived from an immunoglobulin hinge (i.e., not a wild-type immunoglobulin hinge or an altered immunoglobulin hinge). Examples for such hinges and carboxyl-terminus linkers include peptides of about five to about 150 amino acids derived from an interdomain region of a transmembrane protein or stalk region of a type II C-lectin, for instance, peptides of about eight to 25 amino acids and peptides of about seven to 18 amino acids.

[00128] In certain embodiments, interdomain or stalk region hinges, carboxyl-terminus linkers, and amino-terminus linkers have seven to 18 amino acids and can form an α -helical coiled coil structure. In certain embodiments, interdomain or stalk region hinges, carboxyl-terminus

linkers, or amino-terminus linkers contain 0, 1, 2, 3, or 4 cysteines. Exemplary interdomain or stalk region hinges, carboxyl-terminus linkers, and amino-terminus linkers are peptide fragments of the interdomain or stalk regions, such as ten to 150 amino acid fragments from the stalk regions of CD69, CD72, CD94, NKG2A and NKG2D. A hinge, a carboxyl-terminus linker, or an amino-terminus linker may also be a flexible linker sequence comprising (Gly₄Ser) repeats. In some embodiments, a hinge is a 15mer consisting of three repeats of a Gly-Gly-Gly-Gly-Ser amino acid sequence ((Gly₄Ser)₃) (SEQ ID NO:193). In certain embodiments, a hinge has an amino acid sequence comprising the formula (Gly₄Ser)_n, wherein n = 1-5 (SEQ ID NO:194). In some embodiments, a Gly₄Ser sequence may be repeated between 6 and 10 times. Other suitable hinges can be obtained by optimizing a simple linker (e.g., (Gly₄Ser)_n (SEQ ID NO:194)) through random mutagenesis.

[00129] In certain embodiments, hinge, carboxyl-terminus linker, and amino-terminal linker sequences have about 5 to 150 amino acids, 5 to 10 amino acids, 10 to 20 amino acids, 20 to 30 amino acids, 30 to 40 amino acids, 40 to 50 amino acids, 50 to 60 amino acids, 5 to 60 amino acids, 5 to 40 amino acids, 8 to 20 amino acids, or 10 to 15 amino acids. The hinge or linker can be primarily flexible, but can also provide more rigid characteristics or can contain primarily α -helical structure with minimal β -sheet structure. The lengths or the sequences of the hinges and linkers can affect the binding affinities of the binding domains to which the hinges are directly or indirectly (via another region or domain, such as an heterodimerization domain) connected as well as one or more activities of the Fc region portions to which the hinges or linkers are directly or indirectly connected.

[00130] In certain embodiments, hinge, carboxyl-terminus linker, and amino-terminal linker sequences are stable in plasma and serum and are resistant to proteolytic cleavage. The first lysine in the IgG1 upper hinge region can be mutated to minimize proteolytic cleavage, for instance, the lysine can be substituted with methionine, threonine, alanine or glycine, or is deleted.

[00131] In some embodiments of the disclosure, the CD3-binding polypeptide is capable of forming a heterodimer with a second polypeptide chain and comprises a hinge region (a) immediately amino-terminal to an immunoglobulin constant region (e.g., amino-terminal to a CH2 domain wherein the immunoglobulin constant region includes CH2 and CH3 domains, or amino-terminal to a CH3 domain wherein the immunoglobulin sub-regions includes CH3 and CH4 domains), (b) interposed between and connecting a binding domain (e.g., scFv) and a immunoglobulin heterodimerization domain, (c) interposed between and connecting a

immunoglobulin heterodimerization domain and an immunoglobulin constant region (e.g., wherein the immunoglobulin constant region includes CH2 and CH3 domains or CH3 and CH4 domains), (d) interposed between and connecting an immunoglobulin constant region and a binding domain, (e) at the amino-terminus of a polypeptide chain, or (f) at the carboxyl-terminus of a polypeptide chain. A polypeptide chain comprising a hinge region as described herein will be capable of associating with a different polypeptide chain to form a heterodimeric protein provided herein, and the heterodimer formed will contain a binding domain that retains its target specificity or its specific target binding affinity.

[00132] In certain embodiments, a hinge present in a polypeptide that forms a heterodimer with another polypeptide chain can be an immunoglobulin hinge, such as a wild-type immunoglobulin hinge region or an altered immunoglobulin hinge region thereof. In certain embodiments, a hinge of one polypeptide chain of a heterodimeric protein is identical to a corresponding hinge of the other polypeptide chain of the heterodimer. In certain other embodiments, a hinge of one chain is different from that of the other chain (in their length or sequence). The different hinges in the different chains allow different manipulation of the binding affinities of the binding domains to which the hinges are connected, so that the heterodimer is able to preferentially bind to the target of one binding domain over the target of the other binding domain. For example, in certain embodiments, a heterodimeric protein has a CD3-binding domain in one chain and a second binding domain in another chain. Having two different hinges in the two chains may allow the heterodimer to bind to the second target first, and then to a CD3 component second. Thus, the heterodimer may recruit CD3⁺ T-cells to the second target-expressing cells (e.g., tumor or cancer cells), which in turn may damage or destroy the second target-expressing cells.

[00133] Some exemplary hinge, carboxyl-terminus linker, and amino-terminus linker sequences suitable for use in accordance with the present disclosure are shown in the Tables 1 and 2 below. Additional exemplary hinge and linker regions are set forth in SEQ ID NOs: 241-244, 601, 78, 763-791, 228, 379-434, 618-749 of US 2013/0129723 (said sequences incorporated by reference herein).

Table 1. Exemplary hinges and linkers

Hinge Region	Amino Acid Sequence	SEQ ID NO
sss(s)-hlgG1 hinge	EPKSSDKTHTSPPSS	SEQ ID NO:121
csc(s)-hlgG1 hinge	EPKSCDKTHTSPPCS	SEQ ID NO:122
ssc(s)-hlgG1 hinge	EPKSSDKTHTSPPCS	SEQ ID NO:123
scc(s)-hlgG1 hinge	EPKSSDKTHTCPPCS	SEQ ID NO:124

Hinge Region	Amino Acid Sequence	SEQ ID NO
css(s)-hlgG1 hinge	EPKSCDKTHTSPPSS	SEQ ID NO:125
scs(s)-hlgG1 hinge	EPKSSDKTHTCPPSS	SEQ ID NO:126
ccc(s)-hlgG1 hinge	EPKSCDKTHTSPPCS	SEQ ID NO:127
ccc(p)-hlgG1 hinge	EPKSCDKTHTSPPCP	SEQ ID NO:128
sss(p)-hlgG1 hinge	EPKSSDKTHTSPPSP	SEQ ID NO:129
csc(p)-hlgG1 hinge	EPKSCDKTHTSPPCP	SEQ ID NO:130
ssc(p)-hlgG1 hinge	EPKSSDKTHTSPPCP	SEQ ID NO:131
scc(p)-hlgG1 hinge	EPKSSDKTHTCPPCP	SEQ ID NO:132
css(p)-hlgG1 hinge	EPKSCDKTHTSPPSP	SEQ ID NO:133
scs(p)-hlgG1 hinge	EPKSSDKTHTCPPSP	SEQ ID NO:134
Scppcp	SCPPCP	SEQ ID NO:135
STD1	NYGGGGSGGGGSGGGGSGNS	SEQ ID NO:136
STD2	NYGGGGSGGGGSGGGGSGNY GGGGSGGGGSGGGGSGNS	SEQ ID NO:137
H1	NS	SEQ ID NO:138
H2	GGGGSGNS	SEQ ID NO:139
H3	NYGGGGSGNS	SEQ ID NO:140
H4	GGGGSGGGGSGNS	SEQ ID NO:141
H5	NYGGGGSGGGGSGNS	SEQ ID NO:142
H6	GGGGSGGGGSGGGGSGNS	SEQ ID NO:143
H7	GCPPCPNS	SEQ ID NO:144
(G ₄ S) ₃	GGGGSGGGGSGGGGS	SEQ ID NO:145
H105	SGGGGSGGGGSGGGGS	SEQ ID NO:146
(G ₄ S) ₄	GGGGSGGGGSGGGGSGGGGS	SEQ ID NO:147
H75 (NKG2A quadruple mutant)	QRHNNSSLNTGTQMAGHSPNS	SEQ ID NO:148
H83 (NKG2A derived)	SSLNTGTQMAGHSPNS	SEQ ID NO:149
H106 (NKG2A derived)	QRHNNSSLNTGTQMAGHS	SEQ ID NO:150
H81 (NKG2D derived)	EVQIPLTESYSPNS	SEQ ID NO:151
H91 (NKG2D derived)	NSLANQEVQIPLTESYSPNS	SEQ ID NO:152
H94	SGGGGSGGGGSGGGGSPNS	SEQ ID NO:153
H111	SGGGGSGGGGSGGGGSPGS	SEQ ID NO:196

Table 2. Exemplary hinges and linkers (derived from H7 hinge, stalk region of a type II C-lectin, or interdomain region of a type I transmembrane protein)

Hinge Region	Amino Acid Sequence	Molecule and/or hinge from which derived	SEQ ID NO:
H16	LSVKADFLTPSIGNS	CD80	SEQ ID NO:154
H17	LSVKADFLTPSISCPNPCNS	CD80 + H7	SEQ ID NO:155
H18	LSVLANFSQPEIGNS	CD86	SEQ ID NO:156
H19	LSVLANFSQPEISCPNPCNS	CD86 + H7	SEQ ID NO:157
H20	LKIQERVSKPKISNS	CD2	SEQ ID NO:158
H21	LKIQERVSKPKISCPNPCNS	CD2 + H7	SEQ ID NO:159
H22	LNVSERPFPPHIQNS	CD22	SEQ ID NO:160
H23	LDVSERPFPPHIQSCPPNPCNS	CD22 + H7	SEQ ID NO:161
H24	REQLAEVTLCLKANS	CD80	SEQ ID NO:162
H25	REQLAEVTLCLKACPPNPCNS	CD80 + H7	SEQ ID NO:163
H26	RIHQMNSELSVLANS	CD86	SEQ ID NO:164
H27	RIHQMNSELSVLACPPNPCNS	CD86 + H7	SEQ ID NO:165
H28	DTKGKNVLEKIFSNS	CD2	SEQ ID NO:166
H30	LPPETQESQEVTLNS	CD22	SEQ ID NO:167
H32	RIHLNVSERPFPPNS	CD22	SEQ ID NO:168
H33	RIHLNVSERPFPPCPNPCNS	CD22 + H7	SEQ ID NO:169
H36	GCPPCPGGGGSNS	H7	SEQ ID NO:170
H40	GCPPCPANS	H7	SEQ ID NO:171
H41	GCPPCPANS	H7	SEQ ID NO:172
H42	GCPPCPNS	H7	SEQ ID NO:173
H44	GGGASCPPCPGNS	H7	SEQ ID NO:174
H45	GGGASCPPCAGNS	H7	SEQ ID NO:175
H46	GGGASCPPCANS	H7	SEQ ID NO:176
H47	LSVKADFLTPSIGNS	CD80	SEQ ID NO:177
H48	ADFLTPSIGNS	CD80	SEQ ID NO:178
H50	LSVLANFSQPEIGNS	CD86	SEQ ID NO:179
H51	LSVLANFSQPEIGNS	CD86	SEQ ID NO:180
H52	SQPEIVPISNS	CD86	SEQ ID NO:181
H53	SQPEIVPISCPNPCNS	CD86 + H7	SEQ ID NO:182
H54	SVLANFSQPEISCPNPCNS	CD86 + H7	SEQ ID NO:183
H55	RIHQMNSELSVLANS	CD86	SEQ ID NO:184
H56	QMNSELSVLANS	CD86	SEQ ID NO:185
H57	VSERPFPPNS	CD22	SEQ ID NO:186
H58	KPFFTCGSADTCPNS	CD72	SEQ ID NO:187

Hinge Region	Amino Acid Sequence	Molecule and/or hinge from which derived	SEQ ID NO:
H59	KPFFTCGSADTCPNS	CD72	SEQ ID NO:188
H60	QYNCPGQYTFSMPNS	CD69	SEQ ID NO:189
H61	EPAFTPGPNIELQKSDCPNS	CD94	SEQ ID NO:190
H62	QRHNSSLNTRTQKARHCPNS	NKG2A	SEQ ID NO:191
H63	NSLFNQEVQIPLTESYCPNS	NKG2D	SEQ ID NO:192

[00134] In certain embodiments, a CD3-binding polypeptide or protein of the disclosure can comprise an “immunoglobulin dimerization domain” or “immunoglobulin heterodimerization domain.”

5 **[00135]** An “immunoglobulin dimerization domain” or “immunoglobulin heterodimerization domain,” as used herein, refers to an immunoglobulin domain of a polypeptide chain that preferentially interacts or associates with a different immunoglobulin domain of another polypeptide chain, wherein the interaction of the different immunoglobulin heterodimerization domains substantially contributes to or efficiently promotes heterodimerization of the first and
10 second polypeptide chains (*i.e.*, the formation of a dimer between two different polypeptide chains, which is also referred to as a “heterodimer” or “heterodimeric protein”). The interactions between immunoglobulin heterodimerization domains “substantially contributes to or efficiently promotes” the heterodimerization of first and second polypeptide chains if there is a statistically significant reduction in the dimerization between the first and second polypeptide chains in the
15 absence of the immunoglobulin heterodimerization domain of the first polypeptide chain and/or the immunoglobulin heterodimerization domain of the second polypeptide chain. In certain embodiments, when the first and second polypeptide chains are co-expressed, at least 60%, at least about 60% to about 70%, at least about 70% to about 80%, at least 80% to about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the first and second polypeptide chains
20 form heterodimers with each other. Representative immunoglobulin heterodimerization domains include an immunoglobulin CH1 domain, an immunoglobulin CL1 domain (*e.g.*, Cκ or Cλ isotypes), or derivatives thereof, including wild-type immunoglobulin CH1 and CL domains and altered (or mutated) immunoglobulin CH1 and CL domains, such as provided herein.

[00136] Dimerization/heterodimerization domains can be used where it is desired to form
25 heterodimers from two non-identical polypeptide chains, where one or both polypeptide chains comprise a binding domain. In certain embodiments, one polypeptide chain member of certain

heterodimers described herein does not contain a binding domain. As indicated above, a heterodimeric protein of the present disclosure comprises an immunoglobulin heterodimerization domain in each polypeptide chain. The immunoglobulin heterodimerization domains in the polypeptide chains of a heterodimer are different from each other and thus can be differentially modified to facilitate heterodimerization of both chains and to minimize homodimerization of either chain. Immunoglobulin heterodimerization domains provided herein allow for efficient heterodimerization between different polypeptides and facilitate purification of the resulting heterodimeric protein.

[00137] As provided herein, immunoglobulin heterodimerization domains useful for promoting heterodimerization of two different single chain polypeptides (*e.g.*, one short and one long) according to the present disclosure include immunoglobulin CH1 and CL domains, for instance, human CH1 and CL domains. In certain embodiments, an immunoglobulin heterodimerization domain is a wild-type CH1 domain, such as a wild type IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, or IgM CH1 domain. In further embodiments, an immunoglobulin heterodimerization domain is a wild-type human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, or IgM CH1 domain as set forth in SEQ ID NOS:114, 186-192 and 194, respectively, of US 2013/0129723 (said sequences incorporated by reference herein). In certain embodiments, an immunoglobulin heterodimerization domain is a wild-type human IgG1 CH1 domain as set forth in SEQ ID NO:114 of US 2013/0129723 (said sequence incorporated by reference herein).

[00138] In further embodiments, an immunoglobulin heterodimerization domain is an altered immunoglobulin CH1 domain, such as an altered IgG1, IgG2, IgG3, IgG4, IgA1, IgA2 IgD, IgE, or IgM CH1 domain. In certain embodiments, an immunoglobulin heterodimerization domain is an altered human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, or IgM CH1 domain. In still further embodiments, a cysteine residue of a wild-type CH1 domain (*e.g.*, a human CH1) involved in forming a disulfide bond with a wild type immunoglobulin CL domain (*e.g.*, a human CL) is deleted or substituted in the altered immunoglobulin CH1 domain such that a disulfide bond is not formed between the altered CH1 domain and the wild-type CL domain.

[00139] In certain embodiments, an immunoglobulin heterodimerization domain is a wild-type CL domain, such as a wild type C κ domain or a wild type C λ domain. In certain embodiments, an immunoglobulin heterodimerization domain is a wild type human C κ or human C λ domain as set forth in SEQ ID NOS:112 and 113, respectively, of US 2013/0129723 (said sequences incorporated by reference herein). In further embodiments, an immunoglobulin

heterodimerization domain is an altered immunoglobulin CL domain, such as an altered C κ or C λ domain, for instance, an altered human C κ or human C λ domain.

[00140] In certain embodiments, a cysteine residue of a wild-type CL domain (e.g., a human CL) involved in forming a disulfide bond with a wild type immunoglobulin CH1 domain (e.g., a human CH1) is deleted or substituted in the altered immunoglobulin CL domain. Such altered CL domains can further comprise an amino acid deletion at their amino-termini. An exemplary C κ domain is set forth in SEQ ID NO:141 of US 2013/0129723 (said sequence incorporated by reference herein), in which the first arginine and the last cysteine of the wild type human C κ domain are both deleted. In certain embodiments, only the last cysteine of the wild type human C κ domain is deleted in the altered C κ domain because the first arginine deleted from the wild type human C κ domain can be provided by a linker that has an arginine at its carboxyl-terminus and links the amino-terminus of the altered C κ domain with another domain (e.g., an immunoglobulin sub-region, such as a sub-region comprising immunoglobulin CH2 and CH3 domains). An exemplary C λ domain is set forth in SEQ ID NO:140 of US 2013/0129723 (said sequence incorporated by reference herein), in which the first arginine of a wild type human C λ domain is deleted and the cysteine involved in forming a disulfide bond with a cysteine in a CH1 domain is substituted by a serine.

[00141] In further embodiments, an immunoglobulin heterodimerization domain is an altered C κ domain that contains one or more amino acid substitutions, as compared to a wild type C κ domain, at positions that may be involved in forming the interchain-hydrogen bond network at a C κ -C κ interface. For example, in certain embodiments, an immunoglobulin heterodimerization domain is an altered human C κ domain having one or more amino acids at positions N29, N30, Q52, V55, T56, S68 or T70 that are substituted with a different amino acid. The numbering of the amino acids is based on their positions in the altered human C κ sequence as set forth in SEQ ID NO:141 of US 2013/0129723 (said sequence incorporated by reference herein). In certain embodiments, an immunoglobulin heterodimerization domain is an altered human C κ domain having one, two, three or four amino acid substitutions at positions N29, N30, V55, or T70. The amino acid used as a substitute at the above-noted positions can be an alanine, or an amino acid residue with a bulk side chain moiety such as arginine, tryptophan, tyrosine, glutamate, glutamine, or lysine. Additional amino acid residues that can be used to substitute amino acid residues of the wild type human C κ sequence at the above noted positions (e.g., N30) include aspartate, methionine, serine and phenylalanine. Exemplary altered human C κ domains are set forth in SEQ ID NOS:142-178 of US 2013/0129723 (said sequences

incorporated by reference herein). Altered human Ck domains are those that facilitate heterodimerization with a CH1 domain, but minimize homodimerization with another Ck domain. Representative altered human Ck domains are set forth in SEQ ID NOS:160 (N29W V55A T70A), 161 (N29Y V55A T70A), 202 (T70E N29A N30A V55A), 167 (N30R V55A T70A), 168 (N30K V55A T70A), 170 (N30E V55A T70A), 172 (V55R N29A N30A), 175 (N29W N30Y V55A T70E), 176 (N29Y N30Y V55A T70E), 177 (N30E V55A T70E), 178 (N30Y V55A T70E), 838 (N30D V55A T70E), 839 (N30M V55A T70E), 840 (N30S V55A T70E), and 841 (N30F V55A T70E) of US 2013/0129723 (said sequences incorporated by reference herein).

[00142] In certain embodiments, in addition to or alternative to the mutations in Ck domains described herein, both the immunoglobulin heterodimerization domains (*i.e.*, immunoglobulin CH1 and CL domains) of a polypeptide heterodimer have mutations so that the resulting immunoglobulin heterodimerization domains form salt bridges (*i.e.*, ionic interactions) between the amino acid residues at the mutated sites. For example, the immunoglobulin heterodimerization domains of a polypeptide heterodimer can be a mutated CH1 domain in combination with a mutated Ck domain. In the mutated CH1 domain, valine at position 68 (V68) of the wild type human CH1 domain is substituted by an amino acid residue having a negative charge (*e.g.*, aspartate or glutamate), whereas leucine at position 29 (L29) of a mutated human Ck domain in which the first arginine and the last cysteine have been deleted is substituted by an amino acid residue having a positive charge (*e.g.*, lysine, arginine or histidine). The charge-charge interaction between the amino acid residue having a negative charge of the resulting mutated CH1 domain and the amino acid residue having a positive charge of the resulting mutated Ck domain forms a salt bridge, which stabilizes the heterodimeric interface between the mutated CH1 and Ck domains. Alternatively, V68 of the wild type CH1 can be substituted by an amino acid residue having a positive charge, whereas L29 of a mutated human Ck domain in which the first arginine and the last cysteine have been deleted can be substituted by an amino acid residue having a negative charge. Exemplary mutated CH1 sequences in which V68 is substituted by an amino acid with either a negative or positive charge are set forth in SEQ ID NOS:844 and 845 of US 2013/0129723 (said sequences incorporated by reference herein). Exemplary mutated Ck sequences in which L29 is substituted by an amino acid with either a negative or positive charge are set forth in SEQ ID NOS:842 and 843 of US 2013/0129723 (said sequences incorporated by reference herein).

[00143] Positions other than V68 of human CH1 domain and L29 of human Ck domain can be substituted with amino acids having opposite charges to produce ionic interactions between the

amino acids in addition or alternative to the mutations in V68 of CH1 domain and L29 of Ck domain. Such positions can be identified by any suitable method, including random mutagenesis, analysis of the crystal structure of the CH1-Ck pair to identify amino acid residues at the CH1-Ck interface, and further identifying suitable positions among the amino acid
5 residues at the CH1-Ck interface using a set of criteria (e.g., propensity to engage in ionic interactions, proximity to a potential partner residue, etc.).

[00144] In certain embodiments, polypeptide heterodimers of the present disclosure contain only one pair of immunoglobulin heterodimerization domains. For example, a first chain of a polypeptide heterodimer can comprise a CH1 domain as an immunoglobulin heterodimerization
10 domain, while a second chain can comprise a CL domain (e.g., a Ck or CA) as an immunoglobulin heterodimerization domain. Alternatively, a first chain can comprise a CL domain (e.g., a Ck or CA) as an immunoglobulin heterodimerization domain, while a second chain can comprise a CH1 domain as an immunoglobulin heterodimerization domain. As set forth herein, the immunoglobulin heterodimerization domains of the first and second chains are
15 capable of associating to form a heterodimeric protein of this disclosure.

[00145] In certain other embodiments, heterodimeric proteins of the present disclosure can have two pairs of immunoglobulin heterodimerization domains. For example, a first chain of a heterodimer can comprise two CH1 domains, while a second chain can have two CL domains that associate with the two CH1 domains in the first chain. Alternatively, a first chain can
20 comprise two CL domains, while a second chain can have two CH1 domains that associate with the two CL domains in the first chain. In certain embodiments, a first polypeptide chain comprises a CH1 domain and a CL domain, while a second polypeptide chain comprises a CL domain and a CH1 domain that associate with the CH1 domain and the CL domain, respectively, of the first polypeptide chain.

[00146] In the embodiments where a heterodimeric protein comprises only one heterodimerization pair (i.e., one immunoglobulin heterodimerization domain in each chain), the immunoglobulin heterodimerization domain of each chain can be located amino-terminal to the immunoglobulin constant region of that chain. Alternatively, the immunoglobulin
25 heterodimerization domain in each chain can be located carboxyl-terminal to the immunoglobulin constant region of that chain.
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[00147] In the embodiments where a heterodimeric protein comprises two heterodimerization pairs (i.e., two immunoglobulin heterodimerization domains in each chain), both immunoglobulin heterodimerization domains in each chain can be located amino-terminal to the immunoglobulin

constant region of that chain. Alternatively, both immunoglobulin heterodimerization domains in each chain can be located carboxyl-terminal to the immunoglobulin constant region of that chain. In further embodiments, one immunoglobulin heterodimerization domain in each chain can be located amino-terminal to the immunoglobulin constant region of that chain, while the other immunoglobulin heterodimerization domain of each chain can be located carboxyl-terminal to the immunoglobulin constant region of that chain. In other words, in those embodiments, the immunoglobulin constant region is interposed between the two immunoglobulin heterodimerization domains of each chain.

[00148] As indicated herein, in certain embodiments, CD3-binding polypeptides of the present disclosure comprise an immunoglobulin constant region (also referred to as a constant region) in a polypeptide chain. The inclusion of an immunoglobulin constant region slows clearance of the homodimeric and heterodimeric proteins formed from two CD3-binding polypeptide chains from circulation after administration to a subject. By mutations or other alterations, an immunoglobulin constant region further enables relatively easy modulation of dimeric polypeptide effector functions (e.g., ADCC, ADCP, CDC, complement fixation, and binding to Fc receptors), which can either be increased or decreased depending on the disease being treated, as known in the art and described herein. In certain embodiments, an immunoglobulin constant region of one or both of the polypeptide chains of the polypeptide homodimers and heterodimers of the present disclosure will be capable of mediating one or more of these effector functions. In other embodiments, one or more of these effector functions are reduced or absent in an immunoglobulin constant region of one or both of the polypeptide chains of the polypeptide homodimers and heterodimers of the present disclosure, as compared to a corresponding wild-type immunoglobulin constant region. For example, for dimeric CD3-binding polypeptides designed to elicit RTCC, such as, e.g., via the inclusion of a second binding domain, an immunoglobulin constant region may have reduced or no effector function relative to a corresponding wild-type immunoglobulin constant region.

[00149] An immunoglobulin constant region present in CD3-binding polypeptides of the present disclosure can comprise or is derived from part or all of: a CH2 domain, a CH3 domain, a CH4 domain, or any combination thereof. For example, an immunoglobulin constant region can comprise a CH2 domain, a CH3 domain, both CH2 and CH3 domains, both CH3 and CH4 domains, two CH3 domains, a CH4 domain, two CH4 domains, and a CH2 domain and part of a CH3 domain.

[00150] A CH2 domain that can form an immunoglobulin constant region of a CD3-binding polypeptide of the present disclosure can be a wild type immunoglobulin CH2 domain or an altered immunoglobulin CH2 domain thereof from certain immunoglobulin classes or subclasses (e.g., IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, or IgD) and from various species (including human, mouse, rat, and other mammals).

[00151] In certain embodiments, a CH2 domain is a wild type human immunoglobulin CH2 domain, such as wild type CH2 domains of human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, or IgD, as set forth in SEQ ID NOS:115, 199-201 and 195-197, respectively, of US 2013/0129723 (said sequences incorporated by reference herein). In certain embodiments, the CH2 domain is a wild type human IgG1 CH2 domain as set forth in SEQ ID NO:115 of US 2013/0129723 (said sequence incorporated by reference herein).

[00152] In certain embodiments, a CH2 domain is an altered immunoglobulin CH2 region (e.g., an altered human IgG1 CH2 domain) that comprises an amino acid substitution at the asparagine of position 297 (e.g., asparagine to alanine). Such an amino acid substitution reduces or eliminates glycosylation at this site and abrogates efficient Fc binding to FcγR and C1q. The sequence of an altered human IgG1 CH2 domain with an Asn to Ala substitution at position 297 is set forth in SEQ ID NO:324 of US 2013/0129723 (said sequence incorporated by reference herein).

[00153] In certain embodiments, a CH2 domain is an altered immunoglobulin CH2 region (e.g., an altered human IgG1 CH2 domain) that comprises at least one substitution or deletion at positions 234 to 238. For example, an immunoglobulin CH2 region can comprise a substitution at position 234, 235, 236, 237 or 238, positions 234 and 235, positions 234 and 236, positions 234 and 237, positions 234 and 238, positions 234-236, positions 234, 235 and 237, positions 234, 236 and 238, positions 234, 235, 237, and 238, positions 236-238, or any other combination of two, three, four, or five amino acids at positions 234-238. In addition or alternatively, an altered CH2 region can comprise one or more (e.g., two, three, four or five) amino acid deletions at positions 234-238, for instance, at one of position 236 or position 237 while the other position is substituted. The above-noted mutation(s) decrease or eliminate the antibody-dependent cell-mediated cytotoxicity (ADCC) activity or Fc receptor-binding capability of a polypeptide heterodimer that comprises the altered CH2 domain. In certain embodiments, the amino acid residues at one or more of positions 234-238 has been replaced with one or more alanine residues. In further embodiments, only one of the amino acid residues at

positions 234-238 have been deleted while one or more of the remaining amino acids at positions 234-238 can be substituted with another amino acid (e.g., alanine or serine).

[00154] In certain other embodiments, a CH2 domain is an altered immunoglobulin CH2 region (e.g., an altered human IgG1 CH2 domain) that comprises one or more amino acid substitutions at positions 253, 310, 318, 320, 322, and 331. For example, an immunoglobulin CH2 region can comprise a substitution at position 253, 310, 318, 320, 322, or 331, positions 318 and 320, positions 318 and 322, positions 318, 320 and 322, or any other combination of two, three, four, five or six amino acids at positions 253, 310, 318, 320, 322, and 331. The above-noted mutation(s) decrease or eliminate the complement-dependent cytotoxicity (CDC) of a polypeptide heterodimer that comprises the altered CH2 domain.

[00155] In certain other embodiments, in addition to the amino acid substitution at position 297, an altered CH2 region (e.g., an altered human IgG1 CH2 domain) can further comprise one or more (e.g., two, three, four, or five) additional substitutions at positions 234-238. For example, an immunoglobulin CH2 region can comprise a substitution at positions 234 and 297, positions 234, 235, and 297, positions 234, 236 and 297, positions 234-236 and 297, positions 234, 235, 237 and 297, positions 234, 236, 238 and 297, positions 234, 235, 237, 238 and 297, positions 236-238 and 297, or any combination of two, three, four, or five amino acids at positions 234-238 in addition to position 297. In addition or alternatively, an altered CH2 region can comprise one or more (e.g., two, three, four or five) amino acid deletions at positions 234-238, such as at position 236 or position 237. The additional mutation(s) decreases or eliminates the antibody-dependent cell-mediated cytotoxicity (ADCC) activity or Fc receptor-binding capability of a polypeptide heterodimer that comprises the altered CH2 domain. In certain embodiments, the amino acid residues at one or more of positions 234-238 have been replaced with one or more alanine residues. In further embodiments, only one of the amino acid residues at positions 234-238 has been deleted while one or more of the remaining amino acids at positions 234-238 can be substituted with another amino acid (e.g., alanine or serine).

[00156] In certain embodiments, in addition to one or more (e.g., 2, 3, 4, or 5) amino acid substitutions at positions 234-238, a mutated CH2 region (e.g., an altered human IgG1 CH2 domain) in a fusion protein of the present disclosure can contain one or more (e.g., 2, 3, 4, 5, or 6) additional amino acid substitutions (e.g., substituted with alanine) at one or more positions involved in complement fixation (e.g., at positions I253, H310, E318, K320, K322, or P331). Examples of mutated immunoglobulin CH2 regions include human IgG1, IgG2, IgG4 and mouse IgG2a CH2 regions with alanine substitutions at positions 234, 235, 237 (if present), 318, 320

and 322. An exemplary mutated immunoglobulin CH2 region is mouse IGHG2c CH2 region with alanine substitutions at L234, L235, G237, E318, K320, and K322.

[00157] In still further embodiments, in addition to the amino acid substitution at position 297 and the additional deletion(s) or substitution(s) at positions 234-238, an altered CH2 region (e.g., an altered human IgG1 CH2 domain) can further comprise one or more (e.g., two, three, four, five, or six) additional substitutions at positions 253, 310, 318, 320, 322, and 331. For example, an immunoglobulin CH2 region can comprise a (1) substitution at position 297, (2) one or more substitutions or deletions or a combination thereof at positions 234-238, and one or more (e.g., 2, 3, 4, 5, or 6) amino acid substitutions at positions I253, H310, E318, K320, K322, and P331, such as one, two, three substitutions at positions E318, K320 and K322. The amino acids at the above-noted positions can be substituted by alanine or serine.

[00158] In certain embodiments, an immunoglobulin CH2 region polypeptide comprises: (i) an amino acid substitution at the asparagines of position 297 and one amino acid substitution at position 234, 235, 236 or 237; (ii) an amino acid substitution at the asparagine of position 297 and amino acid substitutions at two of positions 234-237; (iii) an amino acid substitution at the asparagine of position 297 and amino acid substitutions at three of positions 234-237; (iv) an amino acid substitution at the asparagine of position 297, amino acid substitutions at positions 234, 235 and 237, and an amino acid deletion at position 236; (v) amino acid substitutions at three of positions 234-237 and amino acid substitutions at positions 318, 320 and 322; or (vi) amino acid substitutions at three of positions 234-237, an amino acid deletion at position 236, and amino acid substitutions at positions 318, 320 and 322.

[00159] Exemplary altered immunoglobulin CH2 regions with amino acid substitutions at the asparagine of position 297 include: human IgG1 CH2 region with alanine substitutions at L234, L235, G237 and N297 and a deletion at G236 (SEQ ID NO:325 of US 2013/0129723, said sequence incorporated by reference herein), human IgG2 CH2 region with alanine substitutions at V234, G236, and N297 (SEQ ID NO:326 of US 2013/0129723, said sequence incorporated by reference herein), human IgG4 CH2 region with alanine substitutions at F234, L235, G237 and N297 and a deletion of G236 (SEQ ID NO:322 of US 2013/0129723, said sequence incorporated by reference herein), human IgG4 CH2 region with alanine substitutions at F234 and N297 (SEQ ID NO:343 of US 2013/0129723, said sequence incorporated by reference herein), human IgG4 CH2 region with alanine substitutions at L235 and N297 (SEQ ID NO:344 of US 2013/0129723, said sequence incorporated by reference herein), human IgG4 CH2 region with alanine substitutions at G236 and N297 (SEQ ID NO:345 of US 2013/0129723, said

sequence incorporated by reference herein), and human IgG4 CH2 region with alanine substitutions at G237 and N297 (SEQ ID NO:346 of US 2013/0129723, said sequence incorporated by reference herein).

5 [00160] In certain embodiments, in addition to the amino acid substitutions described above, an altered CH2 region (e.g., an altered human IgG1 CH2 domain) can contain one or more additional amino acid substitutions at one or more positions other than the above-noted positions. Such amino acid substitutions can be conservative or non-conservative amino acid substitutions. For example, in certain embodiments, P233 can be changed to E233 in an altered IgG2 CH2 region (see, e.g., SEQ ID NO:326 of US 2013/0129723, said sequence
10 incorporated by reference herein). In addition or alternatively, in certain embodiments, the altered CH2 region can contain one or more amino acid insertions, deletions, or both. The insertion(s), deletion(s) or substitution(s) can be anywhere in an immunoglobulin CH2 region, such as at the N- or C-terminus of a wild type immunoglobulin CH2 region resulting from linking the CH2 region with another region (e.g., a binding domain or an immunoglobulin
15 heterodimerization domain) via a hinge.

[00161] In certain embodiments, an altered CH2 region in a polypeptide of the present disclosure comprises or is a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to a wild type immunoglobulin CH2 region, such as the CH2 region of wild type human IgG1,
20 IgG2, or IgG4, or mouse IgG2a (e.g., IGHG2c).

[00162] An altered immunoglobulin CH2 region in a CD3-binding polypeptide of the present disclosure can be derived from a CH2 region of various immunoglobulin isotypes, such as IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, and IgD, from various species (including human, mouse, rat, and other mammals). In certain embodiments, an altered immunoglobulin CH2 region in a fusion
25 protein of the present disclosure can be derived from a CH2 region of human IgG1, IgG2 or IgG4, or mouse IgG2a (e.g., IGHG2c), whose sequences are set forth in SEQ ID NOS:115, 199, 201, and 320 of US 2013/0129723 (said sequences incorporated by reference herein).

[00163] In certain embodiments, an altered CH2 domain is a human IgG1 CH2 domain with alanine substitutions at positions 235, 318, 320, and 322 (i.e., a human IgG1 CH2 domain with
30 L235A, E318A, K320A and K322A substitutions) (SEQ ID NO:595 of US 2013/0129723, said sequence incorporated by reference herein), and optionally an N297 mutation (e.g., to alanine). In certain other embodiments, an altered CH2 domain is a human IgG1 CH2 domain with alanine substitutions at positions 234, 235, 237, 318, 320 and 322 (i.e., a human IgG1 CH2

domain with L234A, L235A, G237A, E318A, K320A and K322A substitutions) (SEQ ID NO:596 of US 2013/0129723, said sequence incorporated by reference herein), and optionally an N297 mutation (e.g., to alanine).

5 [00164] In certain embodiments, an altered CH2 domain is an altered human IgG1 CH2 domain with mutations known in the art that enhance immunological activities such as ADCC, ADCP, CDC, complement fixation, Fc receptor binding, or any combination thereof.

[00165] The CH3 domain that can form an immunoglobulin constant region of a CD3-binding polypeptide of the present disclosure can be a wild type immunoglobulin CH3 domain or an altered immunoglobulin CH3 domain thereof from certain immunoglobulin classes or subclasses 10 (e.g., IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, IgM) of various species (including human, mouse, rat, and other mammals). In certain embodiments, a CH3 domain is a wild type human immunoglobulin CH3 domain, such as wild type CH3 domains of human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, or IgM as set forth in SEQ ID NOS:116, 208-210, 204-207, and 212, respectively of US 2013/0129723 (said sequences incorporated by reference herein). In certain 15 embodiments, the CH3 domain is a wild type human IgG1 CH3 domain as set forth in SEQ ID NO:116 of US 2013/0129723 (said sequence incorporated by reference herein). In certain embodiments, a CH3 domain is an altered human immunoglobulin CH3 domain, such as an altered CH3 domain based on or derived from a wild-type CH3 domain of human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, or IgM antibodies. For example, an altered CH3 domain can 20 be a human IgG1 CH3 domain with one or two mutations at positions H433 and N434 (positions are numbered according to EU numbering). The mutations in such positions can be involved in complement fixation. In certain other embodiments, an altered CH3 domain can be a human IgG1 CH3 domain but with one or two amino acid substitutions at position F405 or Y407. The amino acids at such positions are involved in interacting with another CH3 domain. In certain 25 embodiments, an altered CH3 domain can be an altered human IgG1 CH3 domain with its last lysine deleted. The sequence of this altered CH3 domain is set forth in SEQ ID NO:761 of US 2013/0129723 (said sequence incorporated by reference herein).

[00166] In certain embodiments, CD3-binding polypeptides forming a polypeptide heterodimer 30 comprise a CH3 pair that comprises so called "knobs-into-holes" mutations (see, Marvin and Zhu, *Acta Pharmacologica Sinica* 26:649-58, 2005; Ridgway *et al.*, *Protein Engineering* 9:617-21, 1966). More specifically, mutations can be introduced into each of the two CH3 domains of each polypeptide chain so that the steric complementarity required for CH3/CH3 association obligates these two CH3 domains to pair with each other. For example, a CH3 domain in one

single chain polypeptide of a polypeptide heterodimer can contain a T366W mutation (a "knob" mutation, which substitutes a small amino acid with a larger one), and a CH3 domain in the other single chain polypeptide of the polypeptide heterodimer can contain a Y407A mutation (a "hole" mutation, which substitutes a large amino acid with a smaller one). Other exemplary
5 knobs-into-holes mutations include (1) a T366Y mutation in one CH3 domain and a Y407T in the other CH3 domain, and (2) a T366W mutation in one CH3 domain and T366S, L368A and Y407V mutations in the other CH3 domain.

[00167] The CH4 domain that can form an immunoglobulin constant region of CD3-binding polypeptides of the present disclosure can be a wild type immunoglobulin CH4 domain or an
10 altered immunoglobulin CH4 domain thereof from IgE or IgM molecules. In certain embodiments, the CH4 domain is a wild type human immunoglobulin CH4 domain, such as wild type CH4 domains of human IgE and IgM molecules as set forth in SEQ ID NOS:213 and 214, respectively, of US 2013/0129723 (said sequences incorporated by reference herein). In certain embodiments, a CH4 domain is an altered human immunoglobulin CH4 domain, such as
15 an altered CH4 domain based on or derived from a CH4 domain of human IgE or IgM molecules, which have mutations that increase or decrease an immunological activity known to be associated with an IgE or IgM Fc region.

[00168] In certain embodiments, an immunoglobulin constant region of CD3-binding polypeptides of the present disclosure comprises a combination of CH2, CH3 or CH4 domains
20 (*i.e.*, more than one constant region domain selected from CH2, CH3 and CH4). For example, the immunoglobulin constant region can comprise CH2 and CH3 domains or CH3 and CH4 domains. In certain other embodiments, the immunoglobulin constant region can comprise two CH3 domains and no CH2 or CH4 domains (*i.e.*, only two or more CH3). The multiple constant region domains that form an immunoglobulin constant region can be based on or derived from
25 the same immunoglobulin molecule, or the same class or subclass immunoglobulin molecules. In certain embodiments, the immunoglobulin constant region is an IgG CH2CH3 (*e.g.*, IgG1 CH2CH3, IgG2 CH2CH3, and IgG4 CH2CH3) and can be a human (*e.g.*, human IgG1, IgG2, and IgG4) CH2CH3. For example, in certain embodiments, the immunoglobulin constant region comprises (1) wild type human IgG1 CH2 and CH3 domains, (2) human IgG1 CH2 with N297A
30 substitution (*i.e.*, CH2(N297A)) and wild type human IgG1 CH3, or (3) human IgG1 CH2(N297A) and an altered human IgG1 CH3 with the last lysine deleted.

[00169] Alternatively, the multiple constant region domains can be based on or derived from different immunoglobulin molecules, or different classes or subclasses immunoglobulin

molecules. For example, in certain embodiments, an immunoglobulin constant region comprises both human IgM CH3 domain and human IgG1 CH3 domain. The multiple constant region domains that form an immunoglobulin constant region can be directly linked together or can be linked to each other via one or more (e.g., about 2-10) amino acids.

5 **[00170]** Exemplary immunoglobulin constant regions are set forth in SEQ ID NOS:305-309, 321, 323, 341, 342, and 762 of US 2013/0129723 (said sequences incorporated by reference herein).

10 **[00171]** In certain embodiments, the immunoglobulin constant regions of both CD3-binding polypeptides of a polypeptide homodimer or heterodimer are identical to each other. In certain other embodiments, the immunoglobulin constant region of one polypeptide chain of a heterodimeric protein is different from the immunoglobulin constant region of the other polypeptide chain of the heterodimer. For example, one immunoglobulin constant region of a heterodimeric protein can contain a CH3 domain with a "knob" mutation, whereas the other immunoglobulin constant region of the heterodimeric protein can contain a CH3 domain with a
15 "hole" mutation.

20 **[00172]** The disclosure relates to CD3-binding proteins and polypeptides that may comprise any of the sequences shown in Table 14. Amino acid sequences for polypeptide constructs may or may not include signal sequences. CD3-binding proteins may comprise any of the CD3-binding domains described above. In some aspects, CD3-binding proteins comprise humanized V_H or V_L amino acid sequences, or both.

25 **[00173]** Examples of bispecific CD3-binding polypeptides are provided in Tables 12 and 13. Such examples include anti-PSMA x anti-CD3 binding molecules (SEQ ID NOS:62, 64, 66, and 68), anti-CD37 x anti-CD3 binding molecules (SEQ ID NOS:72, 74, 76, 78, 80, and 82), anti-ROR1 x anti-CD3 binding molecules (SEQ ID NOS:100, 104, 108, 112, 116, and 120), and anti-CD123 x anti-CD3 binding molecules (SEQ ID NOS:197 and 198).

30 **[00174]** CD3-binding molecules may be made using scaffolding as generally disclosed in US 2013/0129723 and US 2013/0095097, which are each incorporated herein by reference in their entirety. The CD3-binding proteins may comprise two non-identical polypeptide chains, each polypeptide chain comprising an immunoglobulin heterodimerization domain. The interfacing immunoglobulin heterodimerization domains are different. In one embodiment, the immunoglobulin heterodimerization domain comprises a CH1 domain or a derivative thereof. In another embodiment, the immunoglobulin heterodimerization domain comprises a CL domain or

a derivative thereof. In one embodiment, the CL domain is a C κ or C λ isotype or a derivative thereof.

[00175] The disclosure also includes nucleic acids (e.g., DNA or RNA) encoding CD3-binding domains, proteins and polypeptides described herein, or one or more polypeptide chains of a homodimeric or heterodimeric CD3-binding protein as described herein. Nucleic acids of the disclosure include nucleic acids having a region that is substantially identical to a polynucleotide as listed in Table 14, *infra*. In certain embodiments, a nucleic acid in accordance with the present disclosure has at least 80%, typically at least about 90%, and more typically at least about 95% or at least about 98% identity to a polypeptide-encoding polynucleotide as listed in Table 14. Nucleic acids of the disclosure also include complementary nucleic acids. In some instances, the sequences will be fully complementary (no mismatches) when aligned. In other instances, there can be up to about a 20% mismatch in the sequences. In some embodiments of the disclosure are provided nucleic acids encoding both first and second polypeptide chains of a heterodimeric CD3-binding protein of the disclosure. The nucleic acid sequences provided herein can be exploited using codon optimization, degenerate sequence, silent mutations, and other DNA techniques to optimize expression in a particular host, and the present disclosure encompasses such sequence modifications.

[00176] The disclosure relates to an isolated nucleic acid molecule encoding CD3-binding domains, proteins and polypeptides (or portions thereof) described herein, wherein said nucleic acid molecule comprises a nucleotide sequence set forth in SEQ ID NO: 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, or 59.

[00177] Polynucleotide molecules comprising a desired polynucleotide sequence are propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination *in vivo*. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of

oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

[00178] For expression, an expression cassette or system may be employed. To express a nucleic acid encoding a polypeptide disclosed herein, a nucleic acid molecule encoding the polypeptide, operably linked to regulatory sequences that control transcriptional expression in an expression vector, is introduced into a host cell. In addition to transcriptional regulatory sequences, such as promoters and enhancers, expression vectors can include translational regulatory sequences and a marker gene which is suitable for selection of cells that carry the expression vector. The gene product encoded by a polynucleotide of the disclosure is expressed in any convenient expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. In the expression vector, the polypeptide-encoding polynucleotide is linked to a regulatory sequence as appropriate to obtain the desired expression properties. These can include promoters, enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated (e.g., the promoter from the steroid inducible pIND vector (Invitrogen)) or constitutive (e.g., promoters from CMV, SV40, Elongation Factor, or LTR sequences). These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used. Accordingly, the expression vector will generally provide a transcriptional and translational initiation region, which can be inducible or constitutive, where the coding region is operably linked under the transcriptional control of the transcriptional initiation region, and a transcriptional and translational termination region.

[00179] An expression cassette ("expression unit") can be introduced into a variety of vectors, e.g., plasmid, BAC, YAC, bacteriophage such as lambda, P1, M13, etc., plant or animal viral vectors (e.g., retroviral-based vectors, adenovirus vectors), and the like, where the vectors are normally characterized by the ability to provide selection of cells comprising the expression vectors. The vectors can provide for extrachromosomal maintenance, particularly as plasmids or viruses, or for integration into the host chromosome. Where extrachromosomal maintenance is desired, an origin sequence is provided for the replication of the plasmid, which can be low- or high copy-number. A wide variety of markers are available for selection, particularly those which protect against toxins, more particularly against antibiotics. The particular marker that is chosen is selected in accordance with the nature of the host, where, in some cases, complementation can be employed with auxotrophic hosts. Introduction of the DNA construct can use any convenient method, including, e.g., conjugation, bacterial transformation, calcium-

precipitated DNA, electroporation, fusion, transfection, infection with viral vectors, biolistics, and the like. The disclosure relates to an expression vector comprising a nucleic acid segment, wherein said nucleic acid segment may comprise a nucleotide sequence set forth in SEQ ID NO: 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, or 59.

[00180] Accordingly, proteins for use within the present disclosure can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells (including cultured cells of multicellular organisms), particularly cultured mammalian cells. Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook and Russell, *Molecular Cloning: A Laboratory Manual* (3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001), and Ausubel *et al.*, *Short Protocols in Molecular Biology* (4th ed., John Wiley & Sons, 1999).

[00181] For example, for recombinant expression of a homodimeric CD3-binding protein comprising two identical CD3-binding polypeptides as described herein, an expression vector will generally include a nucleic acid segment encoding the CD3-binding polypeptide, operably linked to a promoter. For recombinant expression of a heterodimeric CD3-binding protein, comprising different first and second polypeptide chains, the first and second polypeptide chains can be co-expressed from separate vectors in the host cell for expression of the entire heterodimeric protein. Alternatively, for the expression of heterodimeric CD3-binding proteins, the first and second polypeptide chains are co-expressed from separate expression units in the same vector in the host cell for expression of the entire heterodimeric protein. The expression vector(s) are transferred to a host cell by conventional techniques, and the transfected cells are then cultured by conventional techniques to produce the encoded polypeptide(s) to produce the corresponding CD3-binding protein.

[00182] To direct a recombinant protein into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence) is provided in the expression vector. The secretory signal sequence can be that of the native form of the recombinant protein, or can be derived from another secreted protein or synthesized *de novo*. The secretory signal sequence is operably linked to the polypeptide-encoding DNA 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 DNA sequence encoding the polypeptide of interest, although certain signal sequences can be positioned elsewhere in the DNA 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 certain variations, a secretory signal sequence for use in accordance with the present disclosure has the amino acid sequence MEAPAQLLFLLLLWLPDTTG (SEQ ID NO:195).

[00183] Cultured mammalian cells are suitable hosts for production of recombinant proteins for use within the present disclosure. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler *et al.*, *Cell* 14:725, 1978; Corsaro and Pearson, *Somatic Cell Genetics* 7:603, 1981; Graham and Van der Eb, *Virology* 52:456, 1973), electroporation (Neumann *et al.*, *EMBO J.* 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel *et al.*, *supra*), and liposome-mediated transfection (Hawley-Nelson *et al.*, *Focus* 15:73, 1993; Ciccarone *et al.*, *Focus* 15:80, 1993). The production of recombinant polypeptides in cultured mammalian cells is disclosed by, for example, Levinson *et al.*, U.S. Patent No. 4,713,339; Hagen *et al.*, U.S. Patent No. 4,784,950; Palmiter *et al.*, U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134. Examples of suitable mammalian host cells include African green monkey kidney cells (Vero; ATCC CRL 1587), human embryonic kidney cells (293-HEK; ATCC CRL 1573), baby hamster kidney cells (BHK-21, BHK-570; ATCC CRL 8544, ATCC CRL 10314), canine kidney cells (MDCK; ATCC CCL 34), Chinese hamster ovary cells (CHO-K1; ATCC CCL61; CHO DG44; CHO DXB11 (Hyclone, Logan, UT); see *also*, e.g., Chasin *et al.*, *Som. Cell. Molec. Genet.* 12:555, 1986)), rat pituitary cells (GH1; ATCC CCL82), HeLa S3 cells (ATCC CCL2.2), rat hepatoma cells (H-4-II-E; ATCC CRL 1548) SV40-transformed monkey kidney cells (COS-1; ATCC CRL 1650) and murine embryonic cells (NIH-3T3; ATCC CRL 1658). Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Manassas, Virginia. Strong transcription promoters can be used, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patents Nos. 4,579,821 and 4,601,978) and the adenovirus major late promoter.

[00184] Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants." Cells that have been cultured in the presence of the selective agent and are able to pass the gene of interest to their progeny are referred to as "stable transfectants." Exemplary selectable markers include a gene encoding resistance to the antibiotic neomycin, which allows selection to be

carried out in the presence of a neomycin-type drug, such as G-418 or the like; the gpt gene for xanthine-guanine phosphoribosyl transferase, which permits host cell growth in the presence of mycophenolic acid/xanthine; and markers that provide resistance to zeocin, bleomycin, blastocidin, and hygromycin (see, e.g., Gatignol *et al.*, *Mol. Gen. Genet.* 207:342, 1987; Drocourt *et al.*, *Nucl. Acids Res.* 18:4009, 1990). Selection systems can also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. An exemplary amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g., hygromycin resistance, multi-drug resistance, puromycin acetyltransferase) can also be used.

[00185] Other higher eukaryotic cells can also be used as hosts, including insect cells, plant cells and avian cells. The use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar *et al.*, *J. Biosci. (Bangalore)* 11:47-58, 1987. Transformation of insect cells and production of foreign polypeptides therein is disclosed by Guarino *et al.*, US 5,162,222 and WO 94/06463.

[00186] Insect cells can be infected with recombinant baculovirus, commonly derived from *Autographa californica* nuclear polyhedrosis virus (AcNPV). See King and Possee, *The Baculovirus Expression System: A Laboratory Guide* (Chapman & Hall, London); O'Reilly *et al.*, *Baculovirus Expression Vectors: A Laboratory Manual* (Oxford University Press., New York 1994); and *Baculovirus Expression Protocols. Methods in Molecular Biology* (Richardson ed., Humana Press, Totowa, NJ, 1995). Recombinant baculovirus can also be produced through the use of a transposon-based system described by Luckow *et al.* (*J. Virol.* 67:4566-4579, 1993). This system, which utilizes transfer vectors, is commercially available in kit form (BAC-TO-BAC kit; Life Technologies, Gaithersburg, MD). The transfer vector (e.g., PFASTBAC1; Life Technologies) contains a Tn7 transposon to move the DNA encoding the protein of interest into a baculovirus genome maintained in *E. coli* as a large plasmid called a "bacmid." See Hill-Perkins and Possee, *J. Gen. Virol.* 71:971-976, 1990; Bonning *et al.*, *J. Gen. Virol.* 75:1551-1556, 1994; and Chazenbalk and Rapoport, *J. Biol. Chem.* 270:1543-1549, 1995. In addition, transfer vectors can include an in-frame fusion with DNA encoding a polypeptide extension or affinity tag as disclosed above. Using techniques known in the art, a transfer vector containing a protein-encoding DNA sequence is transformed into *E. coli* host cells, and the cells are

screened for bacmids which contain an interrupted lacZ gene indicative of recombinant baculovirus. The bacmid DNA containing the recombinant baculovirus genome is isolated, using common techniques, and used to transfect *Spodoptera frugiperda* cells, such as Sf9 cells. Recombinant virus that expresses the protein of interest is subsequently produced.

5 Recombinant viral stocks are made by methods commonly used in the art.

[00187] For protein production, the recombinant virus is used to infect host cells, typically a cell line derived from the fall armyworm, *Spodoptera frugiperda* (e.g., Sf9 or Sf21 cells) or *Trichoplusia ni* (e.g., HIGH FIVE cells; Invitrogen, Carlsbad, CA). See generally Glick and Pasternak, *Molecular Biotechnology, Principles & Applications of Recombinant DNA* (ASM Press, Washington, D.C., 1994). See also U.S. Patent No. 5,300,435. Serum-free media are used to grow and maintain the cells. Suitable media formulations are known in the art and can be obtained from commercial suppliers. The cells are grown up from an inoculation density of approximately $2-5 \times 10^5$ cells to a density of $1-2 \times 10^6$ cells, at which time a recombinant viral stock is added at a multiplicity of infection (MOI) of 0.1 to 10, more typically near 3. Procedures used are generally described in available laboratory manuals (see, e.g., King and Possee, *supra*; O'Reilly *et al.*, *supra*; Richardson, *supra*).

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[00188] Fungal cells, including yeast cells, can also be used within the present disclosure. Yeast species of in this regard include, e.g., *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Pichia methanolica*. Methods for transforming *S. cerevisiae* cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki *et al.*, U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch *et al.*, U.S. Patent No. 5,037,743; and Murray *et al.*, U.S. Patent No. 4,845,075. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). An exemplary vector system for use in *Saccharomyces cerevisiae* is the POT1 vector system disclosed by Kawasaki *et al.* (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman *et al.*, U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936; and 4,661,454. Transformation systems for other yeasts, including *Hansenula polymorpha*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Kluyveromyces fragilis*, *Ustilago maydis*, *Pichia pastoris*, *Pichia methanolica*, *Pichia guilliermondii*, and *Candida*

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maltosa are known in the art. See, e.g., Gleeson *et al.*, *J. Gen. Microbiol.* 132:3459-3465, 1986; Cregg, U.S. Patent No. 4,882,279; and Raymond *et al.*, *Yeast* 14:11-23, 1998. *Aspergillus* cells can be utilized according to the methods of McKnight *et al.*, U.S. Patent No. 4,935,349.

Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino *et al.*, U.S.

5 Patent No. 5,162,228. Methods for transforming *Neurospora* are disclosed by Lambowitz, U.S. Patent No. 4,486,533. Production of recombinant proteins in *Pichia methanolica* is disclosed in U.S. Patents Nos. 5,716,808; 5,736,383; 5,854,039; and 5,888,768.

[00189] Prokaryotic host cells, including strains of the bacteria *Escherichia coli*, *Bacillus*, and other genera are also useful host cells within the present disclosure. Techniques for

10 transforming these hosts and expressing foreign DNA sequences cloned therein are well-known in the art (see, e.g., Sambrook and Russell, *supra*). When expressing a recombinant protein in bacteria such as *E. coli*, the protein can be retained in the cytoplasm, typically as insoluble granules, or can be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed, and the granules are recovered and denatured using, for
15 example, guanidine isothiocyanate or urea. The denatured protein can then be refolded and dimerized by diluting the denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. In the alternative, the protein can be recovered from the cytoplasm in soluble form and isolated without the use of denaturants. The protein is recovered from the cell as an aqueous
20 extract in, for example, phosphate buffered saline. To capture the protein of interest, the extract is applied directly to a chromatographic medium, such as an immobilized antibody or heparin-Sepharose column. Secreted proteins can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (by, for example, sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein, thereby obviating
25 the need for denaturation and refolding. Antibodies, including single-chain antibodies, can be produced in bacterial host cells according to known methods. See, e.g., Bird *et al.*, *Science* 242:423-426, 1988; Huston *et al.*, *Proc. Natl. Acad. Sci. USA* 85:5879-5883, 1988; and Pantoliano *et al.*, *Biochem.* 30:10117-10125, 1991.

[00190] Transformed or transfected host cells are cultured according to conventional
30 procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media can also contain such components as

growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

5 **[00191]** CD3-binding proteins may be purified by conventional protein purification methods, typically by a combination of chromatographic techniques. See *generally Affinity Chromatography: Principles & Methods* (Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988); Scopes, *Protein Purification: Principles and Practice* (Springer-Verlag, New York 1994). Proteins comprising an immunoglobulin Fc region can be purified by affinity chromatography on
10 immobilized protein A or protein G. Additional purification steps, such as gel filtration, can be used to obtain the desired level of purity or to provide for desalting, buffer exchange, and the like.

[00192] CD3-binding molecules disclosed herein may be used in a method for treating a subject (for example, a human or a non-human primate) or for manufacture of a medicament for treating
15 a subject. Generally, such methods include administering to a subject in need of such treatment a CD3-binding protein as described herein.

[00193] CD3-binding molecules disclosed herein may be used in a method for treating a subject (for example, a human or a non-human primate) or for manufacture of a medicament for treating a subject. Generally, such methods include administering to a subject in need of such treatment
20 a CD3-binding protein as described herein. In some embodiments, a CD3-binding protein comprises at least one effector function selected from antibody-dependent cell-mediated cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC), such that the CD3-binding protein induces ADCC and/or CDC against CD3-expressing cells in the subject.

[00194] In some aspects, the present disclosure provides methods for treating a subject with a
25 disorder characterized by over-expression of CD3. In one case, a monospecific CD3 binding polypeptide is administered to a patient suffering from an autoimmune disease (e.g., rheumatoid arthritis). In certain variations, a CD3-binding protein provided herein could be used for the modulation of T-cell function and fate, thereby providing therapeutic treatment of T cell mediated disease, including autoimmune or inflammatory diseases in which T-cells are significant
30 contributors. Because some CD3-binding proteins of the present disclosure do not activate T-cells and/or do not induce cytokine release, they are advantageous over other molecules directed against the TCR complex (e.g., anti-CD3 antibodies) for having no or reduced side

effects such as cytokine release syndrome and acute toxicity. In another case, a CD3-binding polypeptide is administered to a subject about to undergo an organ transplant.

[00195] In another aspect, the present disclosure provides a method for treating a disorder characterized by overexpression of a tumor antigen, such as cancer. Examples of tumor antigens that may be recognized by bispecific CD3-binding proteins include PSMA, CD19, CD20, CD37, CD38, CD123, Her2, ROR1, RON, glycoprotein A33 antigen (gpA33) and CEA. Generally, such methods include administering to a subject in need of such treatment a therapeutically effective amount of a CD3-binding protein comprising a second binding domain that binds a tumor antigen as described herein. In some embodiments, the CD3 binding protein induces redirected T-cell cytotoxicity (RTCC) against tumor antigen-expressing cells in the subject. Exemplary cancers amenable to treatment in accordance with the present disclosure include, for example, prostate cancer, colorectal cancer, renal cell carcinoma, bladder cancer, salivary gland cancer, pancreatic cancer, ovarian cancer, non-small cell lung cancer, melanoma, breast cancer (e.g., triple negative breast cancer), adrenal cancer, mantle cell lymphoma, acute lymphoblastic leukemia, chronic lymphocytic leukemia, Non-Hodgkin's lymphoma, acute myeloid leukemia (AML), B-lymphoid leukemia, blastic plasmacytoid dendritic neoplasm (BPDCN), and hairy cell leukemia.

[00196] The disclosure also provides methods for treating cancer or an autoimmune disorder comprising administering a therapeutically effective amount of the compositions or CD3-binding polypeptides described herein to a patient in need thereof.

[00197] In some embodiments, the disclosure provides a method of treating a patient with a cancer, comprising administering to the patient a CD3-binding polypeptide comprising a CD3-binding domain that binds specifically to human CD3 and that comprises an immunoglobulin light chain variable region and an immunoglobulin heavy chain variable region; wherein the immunoglobulin light chain variable region comprises an amino acid sequence that is (a) at least about 93% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:88; or (b) at least about 94% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:89; and wherein the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least about 82% identical, at least about 85% identical, at least about 87% identical, at least about 90% identical, at least about 92% identical, at least about 95% identical, at least about 97% identical, at least about 98% identical or at least about 99% identical to the amino acid sequence in SEQ ID NO:86.

[00198] In some embodiments, for treatment methods and uses described herein, a CD3-binding protein is delivered in a manner consistent with conventional methodologies associated with management of the disease or disorder for which treatment is sought. In accordance with the disclosure herein, a therapeutically effective amount of the CD3-binding protein is
5 administered to a subject in need of such treatment for a time and under conditions sufficient to prevent or treat the disease or disorder.

[00199] Subjects for administration of CD3-binding proteins as described herein include patients at high risk for developing a particular disorder as well as patients presenting with an existing such disorder. Typically, the subject has been diagnosed as having the disorder for which
10 treatment is sought. Further, subjects can be monitored during the course of treatment for any change in the disorder (e.g., for an increase or decrease in clinical symptoms of the disorder). Also, in some variations, the subject does not suffer from another disorder requiring treatment that involves targeting CD3-expressing cells.

[00200] In prophylactic applications, pharmaceutical compositions or medicants are
15 administered to a patient susceptible to, or otherwise at risk of, a particular disorder in an amount sufficient to eliminate or reduce the risk or delay the onset of the disorder. In therapeutic applications, compositions or medicants are administered to a patient suspected of, or already suffering from such a disorder in an amount sufficient to cure, or at least partially arrest, the symptoms of the disorder and its complications. An amount adequate to accomplish
20 this is referred to as a therapeutically effective dose or amount. In both prophylactic and therapeutic regimes, agents are usually administered in several dosages until a sufficient response has been achieved. Typically, the response is monitored and repeated dosages are given if the desired response starts to fade.

[00201] To identify subject patients for treatment according to the methods of the disclosure,
25 accepted screening methods can be employed to determine risk factors associated with specific disorders or to determine the status of an existing disorder identified in a subject. Such methods can include, for example, determining whether an individual has relatives who have been diagnosed with a particular disorder. Screening methods can also include, for example, conventional work-ups to determine familial status for a particular disorder known to have a
30 heritable component. For example, various cancers are also known to have certain inheritable components. Inheritable components of cancers include, for example, mutations in multiple genes that are transforming (e.g., Ras, Raf, EGFR, cMet, and others), the presence or absence of certain HLA and killer inhibitory receptor (KIR) molecules, or mechanisms by which cancer

cells are able to modulate immune suppression of cells like NK cells and T-cells, either directly or indirectly (see, e.g., Ljunggren and Malmberg, *Nature Rev. Immunol.* 7:329-339, 2007; Boyton and Altmann, *Clin. Exp. Immunol.* 149:1-8, 2007). Toward this end, nucleotide probes can be routinely employed to identify individuals carrying genetic markers associated with a particular disorder of interest. In addition, a wide variety of immunological methods are known in the art that are useful to identify markers for specific disorder. For example, various ELISA immunoassay methods are available and well-known in the art that employ monoclonal antibody probes to detect antigens associated with specific tumors. Screening can be implemented as indicated by known patient symptomology, age factors, related risk factors, etc. These methods allow the clinician to routinely select patients in need of the methods described herein for treatment. In accordance with these methods, targeting pathological, tumor antigen-expressing cells can be implemented as an independent treatment program or as a follow-up, adjunct, or coordinate treatment regimen to other treatments.

[00202] For administration, a CD3-binding protein may be formulated as a pharmaceutical composition. A pharmaceutical composition may comprise: (i) a CD3-binding polypeptide; and (ii) a pharmaceutically acceptable carrier, diluent or excipient. A pharmaceutical composition comprising a CD3-binding protein can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the therapeutic molecule is combined in a mixture with a pharmaceutically acceptable carrier, diluent or excipient. A carrier is said to be a "pharmaceutically acceptable carrier" if its administration can be tolerated by a recipient patient. Sterile phosphate-buffered saline is one example of a pharmaceutically acceptable carrier. Other suitable carriers, diluents or excipients are well-known to those in the art. (See, e.g., Gennaro (ed.), *Remington's Pharmaceutical Sciences* (Mack Publishing Company, 19th ed. 1995).) Formulations can further include one or more excipients, preservatives, solubilizers, buffering agents, albumin to prevent protein loss on vial surfaces, etc.

[00203] A pharmaceutical composition may be formulated in a dosage form selected from the group consisting of: an oral unit dosage form, an intravenous unit dosage form, an intranasal unit dosage form, a suppository unit dosage form, an intradermal unit dosage form, an intramuscular unit dosage form, an intraperitoneal unit dosage form, a subcutaneous unit dosage form, an epidural unit dosage form, a sublingual unit dosage form, and an intracerebral unit dosage form. The oral unit dosage form may be selected from the group consisting of: tablets, pills, pellets, capsules, powders, lozenges, granules, solutions, suspensions, emulsions, syrups, elixirs, sustained-release formulations, aerosols, and sprays.

[00204] A pharmaceutical composition comprising a CD3-binding protein therapeutic may be administered to a subject in a therapeutically effective amount. According to the methods of the present disclosure, a CD3-binding protein can be administered to subjects by a variety of administration modes, including, for example, by intramuscular, subcutaneous, intravenous, intra-atrial, intra-articular, parenteral, intranasal, intrapulmonary, transdermal, intrapleural, intrathecal, and oral routes of administration. For prevention and treatment purposes, an antagonist can be administered to a subject in a single bolus delivery, via continuous delivery (e.g., continuous transdermal delivery) over an extended time period, or in a repeated administration protocol (e.g., on an hourly, daily, weekly, or monthly basis).

[00205] Determination of effective dosages in this context is typically based on animal model studies followed up by human clinical trials and is guided by determining effective dosages and administration protocols that significantly reduce the occurrence or severity of the subject disorder in model subjects. Effective doses of the compositions of the present disclosure vary depending upon many different factors, including means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, whether treatment is prophylactic or therapeutic, as well as the specific activity of the composition itself and its ability to elicit the desired response in the individual. Usually, the patient is a human, but in some diseases, the patient can be a nonhuman mammal. Typically, dosage regimens are adjusted to provide an optimum therapeutic response, *i.e.*, to optimize safety and efficacy. Accordingly, a therapeutically effective amount is also one in which any undesired collateral effects are outweighed by the beneficial effects of administering a CD3-binding protein as described herein. For administration of a CD3-binding protein, a dosage may range from about 0.1 μg to 100 mg/kg or 1 $\mu\text{g/kg}$ to about 50 mg/kg, and more usually 10 μg to 5 mg/kg of the subject's body weight. In more specific embodiments, an effective amount of the agent is between about 1 $\mu\text{g/kg}$ and about 20 mg/kg, between about 10 $\mu\text{g/kg}$ and about 10 mg/kg, or between about 0.1 mg/kg and about 5 mg/kg. Dosages within this range can be achieved by single or multiple administrations, including, *e.g.*, multiple administrations per day or daily, weekly, bi-weekly, or monthly administrations. For example, in certain variations, a regimen consists of an initial administration followed by multiple, subsequent administrations at weekly or bi-weekly intervals. Another regimen consists of an initial administration followed by multiple, subsequent administrations at monthly or bi-monthly intervals. Alternatively, administrations can be on an irregular basis as indicated by monitoring clinical symptoms of the disorder.

[00206] Dosage of the pharmaceutical composition can be varied by the attending clinician to maintain a desired concentration at a target site. For example, if an intravenous mode of delivery is selected, local concentration of the agent in the bloodstream at the target tissue can be between about 0.01-50 nanomoles of the composition per liter, sometimes between about 1.0 nanomole per liter and 10, 15, or 25 nanomoles per liter depending on the subject's status and projected measured response. Higher or lower concentrations can be selected based on the mode of delivery, e.g., trans-epidermal delivery versus delivery to a mucosal surface. Dosage should also be adjusted based on the release rate of the administered formulation, e.g., nasal spray versus powder, sustained release oral or injected particles, transdermal formulations, etc. To achieve the same serum concentration level, for example, slow-release particles with a release rate of 5 nanomolar (under standard conditions) would be administered at about twice the dosage of particles with a release rate of 10 nanomolar.

[00207] The anti-CD3 therapeutic (e.g., CD3-binding protein) may also be administered at a daily dosage of from about 0.001 to about 10 milligrams (mg) per kilogram (mpk) of body weight, preferably given as a single daily dose or in divided doses about two to six times a day. For administration to a human adult patient, the therapeutically effective amount may be administered in doses in the range of 0.2 mg to 800 mg per dose, including but not limited to 0.2 mg per dose, 0.5 mg per dose, 1 mg per dose, 5 mg per dose, 10 mg per dose, 25 mg per dose, 100 mg per dose, 200 mg per dose, and 400 mg per dose, and multiple, usually consecutive daily doses may be administered in a course of treatment. The anti-CD3 therapeutic can be administered at different times of the day. In one embodiment the optimal therapeutic dose can be administered in the evening. In another embodiment the optimal therapeutic dose can be administered in the morning. The total daily dosage of the anti-CD3 therapeutic thus can in one embodiment range from about 1 mg to about 2 g, and often ranges from about 100 mg to about 1.5 g, and most often ranges from about 200 mg to about 1200 mg. In the case of a typical 70 kg adult human, the total daily dose of the anti-CD3 therapeutic can range from about 2 mg to about 1200 mg and will often range, as noted above, from about 0.2 mg to about 800 mg.

[00208] With particular regard to treatment of solid tumors, protocols for assessing endpoints and anti-tumor activity are well-known in the art. While each protocol may define tumor response assessments differently, the RECIST (Response evaluation Criteria in solid tumors) criteria is currently considered to be the recommended guidelines for assessment of tumor response by the National Cancer Institute (see Therasse *et al.*, *J. Natl. Cancer Inst.* 92:205-216, 2000). According to the RECIST criteria tumor response means a reduction or elimination of all

measurable lesions or metastases. Disease is generally considered measurable if it comprises lesions that can be accurately measured in at least one dimension as ≥ 20 mm with conventional techniques or ≥ 10 mm with spiral CT scan with clearly defined margins by medical photograph or X-ray, computerized axial tomography (CT), magnetic resonance imaging (MRI), or clinical examination (if lesions are superficial). Non-measurable disease means the disease comprises of lesions < 20 mm with conventional techniques or < 10 mm with spiral CT scan, and truly non-measurable lesions (too small to accurately measure). Non-measurable disease includes pleural effusions, ascites, and disease documented by indirect evidence.

[00209] The criteria for objective status are required for protocols to assess solid tumor response. Representative criteria include the following: (1) Complete Response (CR), defined as complete disappearance of all measurable disease; no new lesions; no disease related symptoms; no evidence of non-measurable disease; (2) Partial Response (PR) defined as 30% decrease in the sum of the longest diameter of target lesions (3) Progressive Disease (PD), defined as 20% increase in the sum of the longest diameter of target lesions or appearance of any new lesion; (4) Stable or No Response, defined as not qualifying for CR, PR, or Progressive Disease. (See Therasse *et al.*, *supra*.)

[00210] Additional endpoints that are accepted within the oncology art include overall survival (OS), disease-free survival (DFS), objective response rate (ORR), time to progression (TTP), and progression-free survival (PFS) (see *Guidance for Industry: Clinical Trial Endpoints for the Approval of Cancer Drugs and Biologics*, April 2005, Center for Drug Evaluation and Research, FDA, Rockville, MD.)

[00211] Pharmaceutical compositions can be supplied as a kit comprising a container that comprises the pharmaceutical composition as described herein. A pharmaceutical composition can be provided, for example, in the form of an injectable solution for single or multiple doses, or as a sterile powder that will be reconstituted before injection. Alternatively, such a kit can include a dry-powder disperser, liquid aerosol generator, or nebulizer for administration of a pharmaceutical composition. Such a kit can further comprise written information on indications and usage of the pharmaceutical composition.

[00212] The disclosure will be further clarified by the following examples, which are intended to be purely exemplary of the disclosure and in no way limiting.

EXAMPLES

Example 1. Generation of stabilized CD3-binding molecules

[00213] To improve thermal stability of the CD3-binding molecule DRA222, an engineered variant of the humanized Cris7 antibody, the Cris7 variable domains were re-humanized using alternate human germline framework sequences. The DRA222 variable heavy chain domain is SEQ ID NO:87, and the DRA222 variable light chain domain is SEQ ID NO:90. Fc DRA222 is sometimes referred to as TSC311 or TSC312 (amino acid sequence is SEQ ID NO:2; nucleic acid sequence is SEQ ID NO:1). See, Reinherz, E. L. et al. (eds.), Leukocyte typing II., Springer Verlag, New York, (1986) for description of parent Cris7 antibody. Additional changes were also made to improve affinity and thermal stability.

Methods

[00214] The following methods were used to obtain results shown in this example:

[00215] **Differential Scanning Calorimetry (DSC).** Thermograms for recombinant proteins purified by standard purification techniques were obtained on a GE VP-Capillary DSC instrument equipped with an autosampler. Approximately 550 μ L of each sample (typically 0.5 mg/mL) in PBS was injected into the sample capillary, using PBS as a control in the second capillary. Analysis was conducted at temperatures from 25°C to 130°C, with a heating rate of 1°C per min. Feedback was set to low, and a sampling time of 8 ms was used. Data analysis was conducted using Origin. Sample thermogram was corrected for heat capacity of the buffer by subtracting a previous buffer/buffer scan using formulation vehicle, and normalized based on sample concentration and baseline corrected.

[00216] **Differential Scanning Fluorimetry (DSF).** In a high throughput format, thermograms for recombinant proteins purified by standard purification techniques were also obtained by DSF assay run on a Real Time PCR machine (Bio-Rad iCycler iQ5). Approximately 40 μ L of each sample in a concentration of 0.8 mg/mL in PBS was mixed with 5 μ L of pre-diluted SYPRO Orange Dye (Catalogue # S-6650, Life Technologies). A melting curve protocol was set up as ramping the temperature up from 25°C to 90°C, 0.2°C per step. Fluorescent signals were collected through the TexasRed Fluorescent Dye filter set, which is 575/30X Excitation Filter and 620/30M Emission Filter. The collected fluorescent intensity data was exported to data analysis software Prism 6 (GraphPad Software, Inc.). Protein thermal T_m value was calculated as the temperature when second derivatives of fluorescent intensity against temperature – $d(RUF)/dT^2=0$.

[00217] **Flow cytometry on human Jurkat T-cells.** Binding studies were performed by standard flow cytometry-based staining procedures using the CD3⁺ Jurkat T-cell line. All

labeling and washes were performed in U-bottom 96-well plates in saline buffer with 3% BSA and 2mM EDTA. Jurkat cells were plated at 200,000 cells per well and incubated with a range of 0.1 nM to 200 nM concentrations of test molecules in 50 μ L volume/well, for 30 minutes on ice. Cells were washed three times then incubated for another 30 minutes on ice with fluorescently-labeled minimum cross reactive secondary polyclonal antibody, F(ab')² goat anti-human IgG, (Jackson ImmunoResearch Laboratories) and the viability dye 7-AAD. The cells were then washed twice, and the samples acquired in a BD LSRII flow cytometer. The sample files were analyzed using FlowJo software; the mean fluorescence intensity (MFI) of the live population of Jurkat cells in each well was calculated after gating on live cells (forward vs. side scatter, then 7-AAD⁻ cells).

[00218] Homology modeling, Spatial Aggregation Propensity analysis. Homology models were constructed within Accelrys Discovery Studio 4.0 for variable domains using the Annotate Antibody Sequence, Identify Framework Templates, Model Antibody Framework, and Model Antibody Loops protocols. Spatial Aggregation Propensity analysis was also conducted within Accelrys Discovery Studio 4.0 using the Calculate Aggregation Scores protocol.

[00219] Chromium release assays with Human T-cells. Target positive tumor cell lines (MDA-MB-231, Kasumi-2, C4-2B and Ramos cell lines) were all cultured according to the provided protocols. Peripheral blood mononuclear cells (PBMC) were isolated from human blood using standard ficoll gradients. The isolated cells were washed in saline buffer. T-cells were additionally isolated using a Pan T-cell Isolation Kit (catalogue#130-096-535, Miltenyi Biotec, Bergisch Gladbach, Germany) using the manufacturer's protocol. Isolated T-cells were aliquoted and stored long term in Liquid Nitrogen. The pre-prepared T-cells were thawed one day before the assay into warm RPMI media with 10% human serum. During the assay, concentrations of bispecific molecules with final concentration ranging from 200 pM to 0.01 pM were added to the pre-prepared T-cells (approximately 100,000 per well). A total lysis control was generated by including 0.04% NP-40 as the treatment.

[00220] Approximately 2.5×10^6 target cells were treated with 0.125 mCi of ⁵¹Cr and incubated for 90 minutes in a 37°C, 5% CO₂ humidified incubator. After incubation, cells were washed 4 times with diluted assay media (RPMI with 1% human serum) and re-suspended in 12.5 mL of the complete assay media (RPMI with 10% human serum). From this suspension, 50 μ L was dispensed per well into 96 well U-bottom plates (approximately 10,000 cells per well) to bring the total volume to 200 μ L per well, and the T-cell to target cell ratio to 10:1. A zero lysis control was generated by target cells only, omitting the T-cells.

[00221] Plates were incubated for 4 hours (and occasionally also for 24 hours) at 37°C, 5% CO₂ in a humidified incubator, after which they were centrifuged at 1000 rpm for 3 minutes, and 25 µL of supernatant was transferred from each well to the corresponding well of a 96-well Luma sample plate. Sample plates were allowed to air dry in a chemical safety hood for 18 hours, and
5 then radioactivity was read on a TopCount microplate scintillation counter (PerkinElmer) using a standard protocol.

[00222] Percent specific lysis was calculated using the formula: ((signal in drug treated sample – background signal from samples with Target Cell only)/(signal in total lysis wells - background signal from samples with Target Cell only))×100.

10 [00223] **Flow Cytometry on Cynomolgus T-cells.** Cynomolgus macaque peripheral blood collected in heparin tubes was shipped overnight from a vendor (Charles River laboratories). When received, peripheral blood cells (PBMC) were isolated using density separation tubes (CPT tubes, Beckton Dickinson). Blood was diluted 1 to 1.5 in saline buffer prior to transfer into CPT tubes. CPT tubes were centrifuged and the separated PBMC population was collected and
15 washed with saline buffer containing 0.2% BSA and 5nM EDTA. Remaining red blood cells in the preparation were lysed using Ammonium-Chloride-Potassium red blood lysis buffer. Cells were washed an additional time to remove remaining platelets.

[00224] PBMC labeling and washing steps were performed in U-bottom 96-well plates in saline buffer with 0.2% BSA and 2mM EDTA. PBMC were plated at 200,000 cells per well and
20 incubated with a range of 0.1 nM to 300 nM concentrations of test molecules in 50 µL volume/well, for 30 minutes on ice. Cells were washed three times, then incubated for another 30 min on ice with fluorescently-labeled antibodies to non-human primate CD2 and CD16 (Biolegend), anti-idiotypic antibodies to either anti-PSMA or anti-CD37 binding domains, and the viability dye 7-AAD. The samples were washed twice, fixed for 20 minutes on ice with 1%
25 formaldehyde solution in saline, washed again, and acquired in a BD LSRII flow cytometer. The sample files were analyzed using FlowJo software; the mean fluorescence intensity (MFI) of test molecule binding on T-cells in each well was calculated after gating on live T-cells (forward vs. side scatter, 7-AAD⁻, CD2⁺ CD16⁻ cells).

[00225] **Chromium Release assays with Cynomolgus PBMC.** C4-2B and Ramos cell lines
30 were both cultured according to the provided protocols. Peripheral blood mononuclear cells (PBMC) were isolated from cynomolgus macaque peripheral blood using BD VACUTAINER® CPT™ Cell Preparation Tube with Sodium Heparin (Cat#362753). The isolated cells were washed in saline buffer. Concentrations of bispecific molecules with final concentration ranging

from 10000 pM to 0.0128 pM were added to isolated PBMC (approximately 100,000). A total lysis control was generated by including 0.04% NP-40 as the treatment.

[00226] Approximately 5×10^6 target C4-2B or Ramos cells were treated with 0.25 mCi of ^{51}Cr and incubated for 75 minutes at 37°C. After incubation, cells were washed 4 times with the cell culture media (RPMI with 10% FBS, 1% NEAA, 1% sodium pyruvate, Na Glutamine and 20 mM HEPES) and re-suspended in 25 mL of media. From this suspension, 50 μL was dispensed per well into 96 well U-bottom plates (approximately 10,000 cells/well) to bring the T-cell to target cell ratio to 10:1.

[00227] Plates were incubated for 4 hours at 37°C, 5% CO_2 in a humidified incubator, after which they were centrifuged at 225 x G for 3 minutes, and 25 μL of supernatant was transferred from each well to the corresponding well of a 96-well Luma sample plate. Sample plates were allowed to air dry in a chemical safety hood for 18 hours, and then radioactivity was read on a Topcount scintillation counter using a standard protocol.

Results

[00228] Step 1: Generation of Initial Humanized CD3-Binding Constructs

[00229] The Cris7 variable domains were re-humanized using four human variable heavy germline sequences (IGHV1-2*02 (H7), IGHV1-46*02 (H8), IGHV1-3*01 (H9) and IGHV1-69*02 (H10)) and 2 human variable light chain germline sequences (IGKV3-11*01 (L4) and IGKV1-33*01 (L5)) based on sequence homology. A total of 12 single chain variable fragment (scFv) constructs were generated in the Fc anti-CD3 scFv format using the H75 linker (QRHNNSSLNTGTQMAGHSPNS; SEQ ID NO:148) (Table 3). Sequences of the 12 constructs and the control molecule Fc DRA222 (TSC311 or TSC312) are provided in Table 14.

Table 3. Variable Domain Composition of Initial Constructs

Heavy chain	Light chain		
	L1 (original light chain)	L4	L5
H7	H7L1 (TSC313)	H7L4 (TSC314)	H7L5 (TSC315)
H8	H8L1 (TSC316)	H8L4 (TSC317)	H8L5 (TSC318)
H9	H9L1 (TSC319)	H9L4 (TSC320)	H9L5 (TSC321)
H10	H10L1 (TSC322)	H10L4 (TSC323)	H10L5 (TSC324)

[00230] All 12 constructs were expressed transiently in HEK293 cells, purified and tested for binding to Jurkat T-cells and evaluated for thermal stability. Constructs containing the L4 light chain or H9 heavy chain had lower levels of protein expression (see final yield column in Table 4) and/or higher levels of high molecular weight aggregates (see analytical SEC column in Table 4) and were eliminated in the subsequent optimization step. While most of the other

constructs had some improvement in thermal stability of the scFv over the original humanized domains (TSC312) as measured by the midpoint of thermal denaturation (T_m) using Differential Scanning Calorimetry (DSC) (Table 5), the level of binding saturation observed on Jurkat T-cells was reduced by varying levels (Figure 1). The most stable construct, TSC324, had a nearly 50% reduction in observed median fluorescence intensity at saturation and an two-fold increase in the EC_{50} of binding (3.6 nM) when compared to the original humanized construct (TSC312, also known as DRA222).

Table 4. Expression and Purity of Transiently Expressed Material

Molecule	Database Name	1st step titer (μ g/ml)	Final yield (mg)	Analytical SEC - Main Peak (%)	Analytical SEC - Recovery %
Fc DRA222	TSC312	43.8	4.12	92.6	100.3
Fc H7L1	TSC313	35.2	2.66	95.3	90.2
Fc H7L4	TSC314	57.8	5.78	58.8	96.0
Fc H7L5	TSC315	52.6	6.99	90.6	93.3
Fc H8L1	TSC316	39.9	3.73	93.4	99.5
Fc H8L4	TSC317	52.9	4.95	66.5	97.6
Fc H8L5	TSC318	48.1	4.83	92.1	96.2
Fc DRA222	TSC312	16.1	1.41	95.4	97.8
Fc H9L1	TSC319	8.0	0.71	80.0	85.8
Fc H9L4	TSC320	43.1	3.60	69.3	102.5
Fc H9L5	TSC321	31.1	2.66	92.6	98.6
Fc H10L1	TSC322	45.6	3.94	73.2	56.7
Fc H10L4	TSC323	50.6	4.58	67.3	106.7
Fc H10L5	TSC324	33.1	2.85	90.7	104.0

Table 5. Thermal Stability as Measured by Differential Scanning Calorimetry

Molecules	T_m of anti-CD3 scFv ($^{\circ}$ C)	Improvement in T_m (over DRA222)
TSC312 (DRA222)	53.02	
TSC313 (H7L1)	54.47	1.45
TSC315 (H7L5)	54.99	1.97
TSC316 (H8L1)	53.70	0.68

TSC318 (H8L5)	55.16	2.14
TSC312 (H7L1)	52.88	-0.14
TSC321 (H9L5)	53.10	0.08
TSC324 (H10L5)	55.83	2.81

[00231] Step 2: Initial optimization to restore binding to CD3

[00232] The goal of the next step was to improve binding to CD3 while maintaining improved thermal stability over DRA222. Three additional light chain sequences were introduced at this step. The first light chain was based on the L5 sequence containing two amino acid reverted to the parental murine residues at positions 52 and 53 (LL to RW), and this light chain was named L6. Two additional germline light chains were also used (IGKV1-39*01 (L7) and IGKV3D-20*1 (L8) containing the same two amino acids reverted at position 52 and 53. The 3 new light chains (L6, L7 and L8) were combined with 3 heavy chains (H7, H8 and H10) in the Fc anti-CD3 scFv format to give the following scFv combinations (Table 6):

Table 6. Variable Domain Composition of Second Round Constructs

Heavy chain	Light chain		
	L6	L7	L8
H7	H7L6 (TSC334)	H7L7 (TSC335)	H7L8 (TSC336)
H8	H8L6 (TSC337)	H8L7 (TSC338)	H8L8 (TSC339)
H10	H10L6 (TSC340)	H10L7 (TSC341)	H10L8 (TSC342)

[00233] These 9 constructs were expressed transiently in HEK293 cells and examined for protein quality, expression, binding and thermal stability. The sequences of these 9 constructs are found in Table 14. The H10 series of molecules (TSC340, TSC341, TSC342) had the best binding of all the new constructs (Figure 2), and achieved comparable levels of binding saturation on Jurkat T-cells as TSC312. However, the EC50 measured for binding was still two-fold higher than the original molecule, TSC312. The H10 series of molecules also had significant improvement in thermal stability as measured by increase in T_m over TSC312 using Differential Scanning Fluorimetry (DSF) (Figure 3). Of these three molecules, TSC342 was picked as the lead molecule for further optimization due to its improvement in thermal stability.

[00234] The parent murine sequence was then examined for potential hotspots to mutate to improve binding. Three residues were chosen for reversion and back-mutated independently: G27Y(TSC370), M53I(TSC371) and I21M(TSC372). Binding studies of these three constructs on Jurkat T-cells revealed that the G27Y mutation on the heavy chain restored binding to CD3 to comparable levels as the original construct TSC312 (Figure 4). The stability of these three constructs was also evaluated by DSC. While the G27Y mutation did not improve T_m, surprisingly, both of the remaining mutations, M53I on the heavy chain and I21M on the light chain independently improved T_m by 3-4°C (Table 7).

Table 7. Thermal Stability of Mutants Designed to Improve Binding

Mutations	Constructs	T _m (°C)	ΔT _m (°C)
No mutation	TSC312	52.8	-
TSC342 G27Y	TSC370	53.6	0.8
TSC342 M53I	TSC371	55.97	3.17
TSC342 I21M	TSC372	56.55	3.75

[00235] Step 3: Final optimization step to improve thermal stability

[00236] The homology model of TSC370 was examined using Spatial Aggregation Propensity to identify hotspots for potential aggregation. One mutation, A9P on the heavy chain, was identified to reduce a potential aggregation hotspot in the homology model. This mutation was introduced into the TSC370 backbone to produce TSC390. This mutation alone had a mild effect on improving T_m (0.25°C). A9P mutation was combined with the M53I and I21M mutations described above to generate the following Fc anti-CD3 constructs (Table 8):

Table 8. Rationale behind Mutation Set of Fourth Round Constructs

Constructs	G27Y (improved affinity)	A9P (improved stability)	M53I (improved stability)	I21M (improved stability)
TSC390	X	X		
TSC391	X	X	X	
TSC392	X	X		X
TSC393	X		X	X
TSC394	X	X	X	X

Table 9. Thermal Stability of Fourth Round Constructs Assessed by DSC

Mutations	Name	T _m	ΔT _m
No mutation	TSC312	52.8	-
TSC370_A9P	TSC390	53.05	0.25
TSC370_A9P_M53I	TSC391	56.57	3.77
TSC370_A9P_I21M	TSC392	59.15	6.35
TSC370_M53I_I21M	TSC393	58.29	5.49
TSC370_A9P_M53I_I21M	TSC394	59.3	6.5

[00237] Combining two or more of these mutations seemed to have beneficial effect on thermal stability as shown by a substantial increase in T_m from DSC analysis (Table 9). Surprisingly, the A9P mutation was also synergistic with the other mutations, providing anywhere from a 1 to 2.6 C increase in stability compared to the matched constructs not featuring the A9P mutation. More importantly, the stabilizing mutations did not affect the binding to CD3 (Figure 5).

[00238] Bispecific molecules targeting PSMA and CD3 were also built using these new anti-CD3 scFv molecules to study the effect, if any, of the changes to the anti-CD3 scFv on redirected T-cell cytotoxicity (RTCC) activity. The original humanized construct (DRA222) is highly efficient at redirecting T-cell cytotoxicity (see, e.g., US 2014/0161800). The new constructs were tested for their ability to show similar activity. Four different anti-PSMA x anti-CD3 constructs were made using TSC391, TSC392, TSC393 and TSC394 and these were named as TSC408, TSC409, TSC410 and TSC411 respectively. All the four constructs had similar RTCC activity as a molecule built with the parental DRA222 scFv (TSC249) (Figure 6), verifying that cytotoxic activity as well as binding was comparable with human T-cells.

[00239] Step 4: Optimization step to restore Cynomolgus cross-reactivity and activity

[00240] The original humanized construct (DRA222) was previously shown to also bind cynomolgus monkey T-cells and redirect their cytotoxic activity towards target cells when used in a bispecific format. TSC408, TSC409, TSC410 and TSC411 were all evaluated for binding and cytotoxic activity with cynomolgus T-cells. Unexpectedly, TSC408, TSC409, TSC410 and TSC411 all had reduced binding to cynomolgus monkey T-cells (Figures 7A and 7B) and significant reduction in RTCC activity using cynomolgus T-cells as effector cells when compared to an anti-PSMA x anti-CD3 bispecific molecule containing DRA222 (Figures 8A and 8B). This

was not anticipated as the binding and activity with human T-cells was directly comparable to constructs containing DRA222.

[00241] Two approaches were used to attempt to restore binding to cynomolgus CD3. One approach was to combine the light chain from TSC394 with the heavy chain from DRA222 or to combine the heavy chain from TSC394 with the light chain from DRA222 to see if framework residues specific to one framework were contributing to binding. The second approach was to back mutate residues at positions 86 and 87 on the light chain of TSC394. Residues at these two positions interact with light chain CDRs that could influence binding to cynomolgus CD3. These variants were incorporated into anti-CD37 x anti-CD3 bispecific molecules (Table 10).

Some of the variants, especially TSC455, TSC456 and TSC452 displayed improved binding to cynomolgus T-cells when compared to anti-CD37 x TSC394 (TSC445), as reflected by higher levels of binding at saturating concentrations (Figure 9). A cynomolgus RTCC assay was also performed that showed TSC456 and TSC452 had comparable activity to CAS105 (Figure 10). In addition, these molecules had superior thermal stability compared to CAS105 (Table 11) as shown by a higher T_{m1} when analyzed by DSC. Alignments of the DRA222 scFv, TSC455 scFv, and TSC456 scFv are shown in Figure 13.

Table 10. Fifth Round of Optimized Constructs

Anti-CD3 Constructs	Description of anti-CD37 X anti-CD3 bispecific molecules
CAS105	anti-CD37 x DRA222
TSC445	anti-CD37 x TSC394
TSC452	anti-CD37 x (TSC394VL+ DRA222 VH)
TSC453	anti-CD37 x (TSC394VH + DRA222 VL)
TSC454	anti-CD37 x TSC394 E86D
TSC455	anti-CD37 x TSC394 F87Y
TSC456	anti-CD37 x TSC394 E86D F87Y

Table 11. Stability of Bispecific Constructs

Anti-CD3 Constructs	Description of anti-CD37 X anti-CD3 bispecific molecules	T _m 1
CAS105	Anti-CD37 x DRA222	53.04
TSC445	anti-CD37 x TSC394	55.45

TSC452	anti-CD37 x (TSC394VL+ DRA222 VH)	55.37
TSC453	Anti-CD37 x (TSC394VH + DRA222 VL)	56.54
TSC454	Anti-CD37 x TSC394 E86D	57.94
TSC455	Anti-CD37 x TSC394 F87Y	56.73
TSC456	Anti-CD37x TSC394 E86D F87Y	55.45

Example 2. Impacts of Improved Thermal Stability on Storage Stability

[00242] In principle, proteins with improved thermodynamic stability should also be more resistant to aggregation upon storage, and should have enhanced storage stability compared to less stable proteins. To determine whether or not the increases seen in T_m correlated with improved storage stability, the proteins listed in Table 10 were evaluated for storage stability in PBS at 25°C over two weeks.

[00243] Each protein was buffer exchanged into PBS using preparative size exclusion chromatography and the protein concentration was adjusted to 1 mg/mL. For every protein to be assessed, four vials each containing approximately 120 μ L were prepared. One vial was used at each stability time point. Purity was determined by analyzing 25 μ L (or 25 μ g) on an analytical size exclusion HPLC column equilibrated in PBS and measuring the absorbance at 280 nm. Triplicate injections were performed for each construct at each time point. Following completion of the SEC method, the chromatograph was integrated using the Agilent ChemStation software. The percent purity of each protein was calculated by dividing the peak area of the intact molecule by the total peak area, then multiplying by 100.

$$(\text{peak area of intact molecule}) / (\text{total peak area}) \times 100 = \% \text{Purity}$$

[00244] The reported purity was an average of the values obtained from three injections from the same vial. Purity was typically determined at T=0, 3, 7 and 14 days. Purity values were plotted on a graph as a function of time and a linear regression analysis was performed. The slope of the regression line represented the rate at purity was decreasing for each protein. The rate of purity decline was used to estimate the number of days of storage that would cause a 2% decrease in purity. The stability of different variants was compared by ranking them by the highest to lowest number of days estimated to cause a 2% decline. To mitigate inter-assay variability, storage stability values were not compared across different experiments, constructs within the same experimental group were only ranked against each other.

[00245] All new molecules displayed superior solution stability in PBS at 25°C compared to CAS105 (Figure 11). The time to the formation of aggregate was also calculated for each construct (Table 12).

Table 12. Relative Storage Stability at 25°C

Anti-CD3 Construct	Description of anti-CD37 X anti-CD3 bispecific molecules	# of days to drop 2%
CAS105	Anti-CD37 x DRA222	4
TSC445	Anti-CD37 x TSC394	8
TSC450	Anti-CD37 x TSC313	12
TSC451	Anti-CD37 x TSC316	12
TSC452	Anti-CD37 x (TSC394VL+H4)	7
TSC453	Anti-CD37 x (TSC394VH+L1)	8
TSC454	Anti-CD37 x TSC394 E462D	7
TSC455	Anti-CD37 x TSC394 F463Y	10
TSC456	Anti-CD37 x TSC394 DY	10

[00246] This data showed that almost all constructs had a two-fold or greater increase in storage stability at 25°C when compared to the construct containing the original anti-CD3 scFv (DRA222).

Example 3. Impacts of Improved Thermal Stability on Serum Stability

[00247] Similar to storage stability, molecules with higher thermodynamic stability are also frequently more resistant to proteolysis, which can improve stability in human serum. This can in turn improve overall serum pharmacokinetics and the overall exposure of a therapeutic.

[00248] To test if the improvements in thermodynamic stability impacted the overall serum stability, one of the stabilized anti-CD3 scFv molecules (TSC394 F463Y) was evaluated for serum stability in the context of an anti-ROR1 x anti-CD3 bispecific molecule (ROR193). A similar bispecific molecule was also evaluated simultaneously which contained the original anti-CD3 scFv, DRA222 (ROR133). The parent rabbit anti-ROR1 antibody R11 used to generate the ROR1-binding domains is described in, for example, U.S. Patent Application Publication No. 2013/0251642 and Yang et al., PLoS ONE 6(6): e21018 (2011).

[00249] Human serum donated by a random healthy donor was collected in a Red/Grey Vacutanor (BD# 367988), and was prepared according to vendor suggested protocol. Test articles were spiked into 50 µL serum at a concentration of 1 µM in sterile PCR tubes, and were incubated in a humidified 37°C tissue culture incubator for up to 21 days. Specific time points were 21, 14, 7, 3 and 0 days. Samples were incubated in a reverse chronological order starting as "assay day 21", and all samples were assessed simultaneously using a chromium release

RTCC assay at the end of incubation on “experiment day 0” following the protocol listed above in Example 1. EC50 values were fit from titration curves conducted with samples at each time points and were normalized against the EC50 value measured for each construct at day 0.

[00250] Plotting the EC50 values over time showed a dramatic difference for the observed serum stability of ROR133 vs ROR193 (Figure 12), with a 2.5 fold loss in observed EC50 over 21 days for ROR133 but minimal change in EC50 for ROR193. This demonstrates that a moderate change in thermodynamic stability can have a noticeable impact on serum stability.

Example 4. Impacts of Improved Thermodynamic Stability on Protein Expression and Quality

[00251] Previously, it has also been shown that improvements in thermodynamic stability can result in improvements in protein expression and overall protein quality, as measured by the production of high molecular weight aggregates during protein production.

[00252] To test whether or not the improved thermodynamic stability of the new anti-CD3 scFv regions translated into improved protein expression or protein quality, one of the anti-CD3 domains (TSC394DY) was compared to DRA222 in the context of five different pairs of anti-ROR1 x anti-CD3 bispecific molecules, each featuring the same anti-ROR1 scFv (Table 13).

Table 13. Relative Expression and Protein Quality

BD pair	Construct ID	CD3 binding domain	Expression (ug/mL)	% improvement	SEC (post-ProA)	% HMW aggregate	% reduction aggregate
A	ROR134	DRA222	26		78	22	
	ROR189	TSC394DY	37	42%	89	11	50%
B	ROR154	DRA222	16		91	9	
	ROR185	TSC394DY	26	63%	94	6	33%
C	ROR179	DRA222	14		83	17	
	ROR186	TSC394DY	27	93%	88	12	29%
D	ROR181	DRA222	25		81	19	
	ROR191	TSC394DY	33	32%	90	10	47%
E	ROR182	DRA222	16		90	10	
	ROR192	TSC394DY	21	31%	92	8	20%

[00253] With each molecule pair, a higher titer of overall protein expression was seen – from 31% to 93% higher – with the construct featuring the stabilized anti-CD3 scFv (TSC394DY). Also, within each molecule pair, the construct featuring the stabilized anti-CD3 scFv had a lower level of high molecular weight aggregates after protein A purification (anywhere from a 20% to 50% reduction in aggregate levels). This confirms that inclusion of a stabilized anti-CD3 scFv

can result in improved protein expression and improved protein quality when compared to the original anti-CD3 scFv.

Example 5. Effects of Stabilized Anti-CD3 Binding Domains on Stability and Pharmacokinetics of Anti-PSMA X Anti-CD3 Binding Molecules

5 [00254] To test the effects of a stabilized anti-CD3 scFv on stability and pharmacokinetics of a bispecific binding molecule, the PSMA-binding domain of TSC266 (an anti-PSMA X anti-CD3 bispecific molecule comprising the DRA222 CD3 binding domain) was transferred into a bispecific molecule utilizing the TSC456 anti-CD3 scFv. This new bispecific molecule is referred to as TSC471. BALB/c mice were dosed intravenously with TSC266 and TSC471 at
10 approximately 10 mg/kg. TSC266 was diluted into PBS, while TSC471 was diluted into formulation buffer, which was used for all dilutions (5mM succinate, 6.5% sucrose, 0.02% Tween80, pH 4.8). Serum was collected from 3 animals at 10 time points (n = 30 total). The time points were 15 min and 2, 6, 24, 48, 72, 96, 168, 336, and 504 hr post-administration of the bispecific molecules. Terminal bleeds were used to collect larger volumes. Serum
15 concentrations were determined using ELISA methods capturing the anti-PSMA binding domain and detecting the anti-CD3 binding domain. Serum concentrations over time were used to determine pharmacokinetic (PK) parameter estimates by non-compartmental analysis (NCA) and compartmental analysis. Serum samples from late time points were also tested for anti-drug antibodies using a standard bridging ELISA with the respective bispecific molecules +/-
20 biotin.

[00255] More specifically, the following ELISA methods were used. Concentrations of anti-PSMA X anti-CD3 bispecifics were determined using 96-well plates coated with a mouse monoclonal antibody (mAb 1H5) to capture the anti-PSMA portion of each construct. The other ends of constructs were detected using a biotin conjugated mouse monoclonal antibody
25 targeting the anti-CD3-binding domain (mAb 5H5), so only intact protein would be measured with this ELISA method. To quantify bound immune complexes from serum samples and assay controls, polymerized horseradish peroxidase (poly HRP) and a fluorogenic peroxidase substrate were used, with results measured on a fluorescent plate reader. Standard curves used to calculate serum concentrations consisted of various known concentrations of the
30 appropriate PSMA bispecific construct spiked into ELISA diluent. SOFTMAX® Pro software was used to calculate serum concentrations using a 4-parameter logistic equation, as well as precision and accuracy for standards and test samples.

[00256] Results of these studies are shown in Figures 14 and 15. By non compartmental analysis (NCA) using Phoenix-64 WinNonLin Software, TSC471 had about a 2-fold

improvement in half-life, with a 3-4 fold reduction in clearance parameter, over TSC266. The Fc of TSC471 maintained functional characteristics of TSC266 (no ADCC or CDC activity, equivalent FcRn binding) with improved stability. The Fc of TSC471 comprises a stability improved version of the CH2 domain. The mutations are the same in the '234-236' region of the molecule as in the TSC266 Fc, but the TSC471 Fc has a reduced number of mutations in the CDC region, maintaining only the K322A mutation, rather than all three found in the null Fc CH2. The anti-CD3 scFv of TSC471 maintained binding and activity on human and cynomolgus T-cells. The linker used in TSC471 had enhanced resistance to CHO proteases and other PTMs and does not contain an N-linked glycosylation site.

Example 6. Effects of Stabilized Anti-CD3 Binding Domains on Pharmacokinetics of Anti-ROR1 X Anti-CD3 Binding Molecules

[00257] The pharmacokinetics of anti-ROR1 x anti-CD3 bispecific molecules containing either the less stable DRA222 CD3 binding domain or the more stable TSC456 CD3 binding domain were compared. The following constructs were evaluated. The sequences of the constructs are provided in Table 14.

Construct	Anti-ROR1	Anti-CD3
ROR206 (CHO line: ROR206a)	Binding domain A	DRA222
ROR207 (CHO line: ROR207a)	Binding domain A	TSC456
ROR208 (CHO line: ROR208a)	Binding domain B	DRA222
ROR209 (CHO line: ROR209a)	Binding domain B	TSC456

[00258] NSG mice were dosed intravenously with the anti-ROR1 X anti-CD3 bispecifics at approximately 10 mg/kg. All bispecifics were diluted into PBS. Serum was collected from 3 animals at 10 time points (n = 30 for each construct) post-administration as well as at one time point pre-dose. The time points were 15 min and 2, 6, 24, 48, 72, 96, 168, 336, and 504 hr post-administration of the bispecific molecules. Terminal bleeds were used to collect larger volumes. Serum concentrations were determined using ELISA methods to detect the intact molecule. Serum concentrations over time were used to determine PK parameter estimates by non-compartmental analysis (NCA) and compartmental analysis.

[00259] More specifically, the following ELISA methods were used. Concentrations of anti-ROR1 X anti-CD3 bispecifics were determined using 96-well plates coated with ROR1 ECD-AFH (ROR177) to capture the anti-ROR1 portion of each construct. The other end of ROR constructs was detected using a biotin conjugated mouse monoclonal antibody targeting the anti-CD3-binding-domain (mAb 5H5), so only intact protein would be measured with this ELISA method. To quantify bound immune complexes from serum samples and assay controls, polymerized horseradish peroxidase (poly HRP) and a fluorogenic peroxidase substrate were used, with results measured on a fluorescent plate reader. Standard curves used to calculate serum concentrations consisted of various known concentrations of the appropriate ROR construct spiked into ELISA diluent. SOFTMAX[®] Pro software was used to calculate serum concentrations using a 4-parameter logistic equation, as well as precision and accuracy for standards and test samples.

[00260] Results of these studies are shown in Figures 16, 17A and 17B. By NCA and compartmental analysis, ROR209a had the longest half-life. ROR207a had the lowest clearance and volume estimates by both analysis methods. Both anti-ROR1 bispecifics with the DRA222 CD3 binding domain had shorter half-life and faster clearance parameters. Notably, constructs with the improved anti-CD3 binding domain (TSC456) had better pharmacokinetics than those with the less stable anti-CD3 binding domain (DRA222).

Example 7. Effects of Stabilized Anti-CD3 Binding Domains on *In Vivo* Efficacy of Anti-ROR1 X Anti-CD3 Binding Molecules

[00261] MDA-MB-231 cells were co-mixed with donor T-cells and matrigel and implanted into the flank of NOD/SCID mice on day 0 of the study. Each group contained N=5 animals, with T-cells from one donor. Figure 18 shows an example graph which shows minimal impact of T-cells on tumor growth by the donor T-cells. Animals were treated with PBS or with 30 µg or 3 µg of ROR208 (DRA222 anti-CD3 binding domain) or ROR209 (TSC456 anti-CD3 binding domain). The dose was administered on day 0, 4, and 8. Tumor growth was measured with calipers over time of study.

[00262] Significant inhibition of tumor growth was seen after treatment with both ROR bispecifics. No significant difference of tumor growth was seen with T-cells from the donor (Figure 18) compared to tumor only. There were no significant differences between animals treated with ROR208 compared to ROR209 at any dose level, indicating the stability improved anti-CD3 binding domain had the same potency as the non-stable anti-CD3 binding domain.

Example 8. Effects of Stabilized Anti-CD3 Binding Domains on *In Vivo* Efficacy of Anti-ROR1 X Anti-CD3 Binding Molecules

[00263] Kasumi-2 cells were co-mixed with donor T-cells and matrigel and implanted into the flank of NOD/SCID mice on day 0 of the study. Each group contained N=10 animals, with T-cells from one donor. Animals were treated with PBS or with 30 µg, 3 µg or 0.3 µg of ROR243 (TSC456 anti-CD3 binding domain) as shown in Figure 19. The dose was administered on day 0, 4, and 8. The route for administration was intravenous (IV), with exception of one group, where the dose was administered subcutaneously (SC). Figure 19 shows results of the assay. Tumor growth was measured with calipers over time of study.

[00264] No inhibition of tumor growth was seen in the presence of T-cells in the absence of ROR243 or with ROR243 treatment in the absence of T-cells. Significant inhibition of tumor growth was seen at 0.3 µg per dose, with dose dependent titration. No difference in route of administration was seen.

Table 14. Binding Domain and Polypeptide Sequences and Components

DNA sequence of Fc DRA222 (TSC311 or TSC312):

15	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccacccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcacogt	cagtcttctc	cttcccccca	aaacccaagg	acacccctcat	gatctcccg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcacogtcc	tgcaaccagga	ctggctgaat	360
20	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acacccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacogt	ggacaagagc	660
25	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tccagctggg	ggagtctggg	840
	ggcggagtgg	tgacgcctgg	gcggtcactg	aggctgtcct	gcaaggcttc	tggtctacacc	900
	tttactagat	ctacgatgca	ctgggttaagg	caggccctcg	gacaaggctc	ggaatggatt	960
30	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacaggttc	1020
	acaatcagcg	cagacaaatc	caagagcaca	gccttctctg	agatggacag	cctgaggccc	1080
	gaggacacog	gcgtctatct	ctgtgcacgg	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggac	tcccgtcact	gtctctagcg	gtggcggagg	gtctgggggt	1200
	ggcggatccg	gaggtggtgg	ctctgcacaa	gacatccaga	tgaccacagtc	tccaagcagc	1260
35	ctgtctgcaa	gcgtggggga	cagggtcacc	atgacctgca	gtgccagctc	aagtgttaagt	1320
	tacatgaact	ggtaccagca	gaagccgggc	aaggccccc	aaagatggat	ttatgactca	1380
	tccaaactgg	cttctggagt	ccctgctcgc	ttcagtgcca	gtgggtctgg	gaccgactat	1440
	accctcacaa	tcagcagcct	gcagcccga	gatttcgcca	cttattactg	ccagcagtg	1500
40	agtcgtaacc	caccacgctt	cggagggggg	accaagctac	aaattacatc	ctccagctaa	1560

(SEQ ID NO:1)

Signal sequence is residue 1 to 60. Fc region is residue 61 - 753. Linker is 754 to 816. Anti-CD3 scFv is 817 to 1560.

45 Mature protein sequence of Fc DRA222 (TSC311 or TSC312)

45	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	QGRHNSSSLN	240
50	TGTQMAGHSP	NSQVQLVESG	GGVVQPGRSL	RLSCKASGYT	FTRSTMHWVR	QAPGQGLEWI	300
	GYINPSSAYT	NYNQKFKDRF	TISADKSKST	AFLQMSLRP	EDTGVYFCAR	PQVHYDNGF	360

PYWGGQGPVT	VSSGGGGSGG	GGSGGGGSAQ	DIQMTQSPSS	LSASVGDRVT	MTCSSASSSVS	420
YMNWYQQKPG	KAPKRWIYDS	SKLASGVPAR	FSGSGSGTDY	TLTISSLQPE	DFATYYCQQW	480
SRNPPTFGGG	TKLQITSSS					499

(SEQ ID NO:2)

5

DNA sequence of Fc H7L1 (TSC313):

	atggaagcac	cagcgagcgt	tctcttcttc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccggg	120
	ggtgcacogt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
10	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccggg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggctgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
15	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcctgtagtc	atgaggtctt	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
20	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgagctgggt	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggettc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtgggat	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
25	gacgacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	cccttactggg	gccaagggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gaccagctct	1260
	ccaagcagcc	tgtctgcaag	cgtgggggac	agggtcacca	tgacctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccagcag	aagccgggca	aggcccccaa	aagatggatt	1380
30	tatgactcat	ccaaactggc	ttctggagtc	cctgctcgct	tcagtggcag	tgggtctggg	1440
	accgactata	cctccacaat	cagcagcctg	cagccogaag	atttcgccac	ttattactgc	1500
	cagcagtggg	gtcgtaaccc	acccacgttc	ggagggggga	ccaagctaca	aattacatcc	1560
	tccagctaa						1569

(SEQ ID NO:3)

35 Signal sequence is residue 1 to 60. Fc region is residue 61 - 753. Linker is 754 to 816. Anti-CD3 scFv is 817 to 1569.

Mature protein sequence of Fc H7L1 (TSC313):

	EPKSSDKTHT	CPFCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
45	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCAKSGYT	FTRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TMTRDTSIST	AYMELSLRLS	DDTAVYYCAR	PQVHYDNGF	360
	PYWGGQGLVT	VSSGGGGSGG	GGSGGGGSGG	GGSDIQMTQS	PSSLSASVGD	RVTMTCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLASGV	PARFSGSGSG	TDYTLTISSL	QPEDFATYYC	480
	QQWSRNPTTF	GGGTKLQITS	SS				502

(SEQ ID NO:4)**DNA sequence of Fc H7L4 (TSC314):**

	atggaagcac	cagcgagcgt	tctcttcttc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccggg	120
	ggtgcacogt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
55	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccggg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggctgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
60	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600

	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggetct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggg	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggg	gcagctctggg	840
5	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggettc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgettatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
10	gacgacacgg	cogtgtatta	ctgtgcgaga	ccccaagtec	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	gggtgatccg	gcggtggcgg	atcggtgggc	ggcggatctg	aaattgtgtt	gacacagtct	1260
	ccagccaccc	tgtctttgtc	tccaggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccaacag	aaacctggcc	aggtcccag	gctcctcatc	1380
	tatgactcat	ccaaactggc	ttctggcatc	ccagccaggt	tcagtggcag	tgggtctggg	1440
15	acagacttca	ctctcaccat	cagcagccta	gagcctgaag	atthtgcagt	ttattactgt	1500
	cagcagtggg	gtcgtaaccc	accacatttc	ggcggaggga	ccaagtgga	gatcaaaccg	1560
	tcctccagct	aa					1572

(SEQ ID NO:5)

Signal sequence is residue 1 to 60

20 Mature protein sequence of Fc H7L4 (TSC314):

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NATKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
25	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALANH	YTQKSLSLSP	QGRHNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TMTRDTSIST	AYMELSRRLS	DDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTILVT	VSSGGGGSGG	GGSGGGSGGG	GGSEIVLTQS	PATLSLSPGE	RATLSCSASS	420
30	SVSYMNWYQQ	KPGQAPRLLI	YDSSKLAGSI	PARFSGSGSG	TDFLTITSSL	EPEDFAVYYC	480
	QQWSRNPPTF	GGGTKVEIKR	SSS				503

(SEQ ID NO:6)**35 DNA sequence of Fc H7L5 (TSC315):**

	atggaagcac	cagcgcagct	tctcttcttc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacagt	gcccagcacc	tgaagccggc	120
	gggtgcacgt	cagtcttctc	cttcccccca	aaacccaagg	acacctcat	gatctccggg	180
	acccctgagg	tcacatgcgt	gggtggtggc	gtgagccacg	aagacctga	ggtcaagttc	240
40	aactggtaag	tggacggcgt	ggaggtgcat	aatgccaaga	caaaagccgg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgccaccagga	ctggctgaat	360
	ggcaagggcat	acgggtgcgc	gggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccagaaa	ccacaggtgt	acacctgtcc	cccatccggg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
45	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggetct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggg	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggg	gcagctctggg	840
50	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggettc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgettatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
	gacgacacgg	cogtgtatta	ctgtgcgaga	ccccaagtec	actatgatta	caacgggttt	1140
55	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	gggtgatccg	gcggtggcgg	atcggtgggc	ggcggatctg	acatccagat	gaccacagtct	1260
	ccatcctccc	tgtctgcctc	tgtaggagac	agagtcacca	tcacttgccg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccttaa	gctcctgatc	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagtggcag	tggatctggg	1440
60	acagatttca	ctctcaccat	cagcagctctg	caacctgaag	atthtgcac	ttactactgt	1500
	caacagtggg	gtcgtaaccc	accacatttc	ggcggaggga	ccaagtgga	gatcaaaccg	1560
	tcctccagct	aa					1572

(SEQ ID NO:7)

Signal sequence is residue 1 to 60

Mature protein sequence of Fc H7L5 (TSC315):

5 EPKSSDKTHT CPPCPAPEAA GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF 60
 NWYVDGVEVH NARTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
 ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTFP 180
 10 PVLDSGSEFF LYSKLTVDKS RWQGGNVFSC SVMHEALHNH YTKSLSLSP GQRHNNSSLN 240
 TGTQMAGHSP NSQVQLVQSG AEVKKPGASV KVSCKASGYT FTRSTMHWVR QAPGGGLEWM 300
 GYINPSSAYT NYNQKFKDRV TMTRDTSIST AYMELSLRLS DDTAVYYCAR PQVHYDYNF 360
 PYWGGTTLVT VSSGGGGSGG GSGGGGGSGG GGSIDIQMTQS PSSLSASVGD RVTITCSASS 420
 SVSYMNWYQQ KPGKAPKLLI YDSSKLAGSV PSRFGSGSGG TDFTLTISSL QPEDFATYYC 480
 QQWSRNPPTF GGGTKVEIKR SSS 503
 15 (SEQ ID NO:8)

DNA sequence of Fc H8L1 (TSC316):

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggg 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccggc 120
 20 ggtgcaccgt cagtcttctc cttcccccca aaacccaagg acacctcat gatctcccgg 180
 acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagacctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaga caaagccggc ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaaac 420
 25 atctccaaag ccaaaggcca gccccgagaa ccacaggtgt acacctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatgcgcg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 30 tacacgcaga agagcctctc cctgtctcgg ggtcagaggg acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctcgg aattctcagg tgcagctggg gcagctctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aagggttctc gcaaggcacc tggatacacc 900
 ttcaccagat ctacgatgca ctgggtgcca caggccctcg gacaagggtt tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
 35 accatgacca ggacacgctc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgctaga cccaagtcac actatgatta caacgggttt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcgatctg acatccagat gaccagctct 1260
 ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgag tgcagctca 1320
 40 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggccccaa aagatggatt 1380
 tatgactcat ccaaaactgc ttctggagtc cctgctcgct tcagtgccag tgggtctggg 1440
 accgactata cctcacaat cagcagcctg cagcccgagg atttcgccac ttattactgc 1500
 cagcagtgga gtcgtaaccc acccacgttc ggagggggga ccaagctaca aattacatcc 1560
 tccagctaa 1569

(SEQ ID NO:9)

Signal sequence is residue 1 to 60

Mature protein sequence of Fc H8L1 (TSC316):

50 EPKSSDKTHT CPPCPAPEAA GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF 60
 NWYVDGVEVH NARTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
 ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTFP 180
 55 PVLDSGSEFF LYSKLTVDKS RWQGGNVFSC SVMHEALHNH YTKSLSLSP GQRHNNSSLN 240
 TGTQMAGHSP NSQVQLVQSG AEVKKPGASV KVSCKASGYT FTRSTMHWVR QAPGGGLEWM 300
 GYINPSSAYT NYNQKFKDRV TMTRDTSIST AYMELSLRLS DDTAVYYCAR PQVHYDYNF 360
 PYWGGTTLVT VSSGGGGSGG GSGGGGGSGG GGSIDIQMTQS PSSLSASVGD RVTMTCSASS 420
 SVSYMNWYQQ KPGKAPKRWI YDSSKLAGSV PARFSGSGSG TDTLTITSSL QPEDFATYYC 480
 60 QQWSRNPPTF GGGTKLQITS SS 502

(SEQ ID NO:10)

DNA sequence of Fc H8L4 (TSC317):

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	gggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
5	acccctgagg	tcacatgcgt	gggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaa	ccaaaggcca	gccccagaaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
10	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctgctg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcctgtgatg	atgaggtctc	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
15	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggg	gcagctctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtttcct	gcaaggcatc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	accatgacca	gggacacgtc	cacgagcaca	gtctacatgg	agctgagcag	cctgagatct	1080
20	gaggacacgg	ccgtgtatta	ctgtgctaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctgggtcacc	gtctctcag	gtggaggcgg	ttcaggcggga	1200
	gggtggatcg	ggcgtggcgg	atcgggtggc	ggcggatctg	aaattgtgtt	gacacagtct	1260
	ccagccaccc	tgtctttgtc	tccaggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccaacag	aaacctggcc	aggctcccag	gctcctcatc	1380
25	tatgactcat	ccaaactggc	ttctggcatc	ccagccaggt	tcagtggcag	tgggtctggg	1440
	acagacttca	ctctcaccat	cagcagccta	gagcctgaag	atcttgagct	ttattactgt	1500
	cagcagtgga	gtcgttaacc	accacttttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
	tctccagct	aa					1572

(SEQ ID NO:11)

Signal sequence is residue 1 to 60

Mature protein sequence of Fc H8L4 (TSC317):

35	EPKSSDKRHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCAKSGYT	FTRSTMHWVR	QAPGGGLEWM	300
40	GYINPSSAYT	NYNQKFKDRV	TMTRDTSTST	VYMESSSLRS	EDTAVYYCAR	PQVHYDYNF	360
	PYWGGTLVT	VSSGGGSGG	GGSGGGSGG	GGSEIVLTQS	PATLSLSPGE	RATLSLSCASS	420
	SVSYMNWYQQ	KPGQAPRLLI	YDSSKLAGSI	PARFSGSGSG	TDFTLTISL	EPEDFAVYYC	480
	QQWSRNPFTF	GGGTVKVEIKR	SSS				503

(SEQ ID NO:12)

DNA sequence of Fc H8L5 (TSC318):

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	gggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
50	acccctgagg	tcacatgcgt	gggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaa	ccaaaggcca	gccccagaaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
55	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctgctg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcctgtgatg	atgaggtctc	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
60	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggg	gcagctctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtttcct	gcaaggcatc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960

5 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
 accatgacca gggacacgtc cagcagcaca gtctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgctaga ccccaagtc actatgatta caacggggtt 1140
 ccttactggg gccaaaggaa cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcgggtggcg atcgggtggc ggaggatctg acatccagat gaccagctct 1260
 ccctctccc tgtctgcatc tgtaggagac agagtcacca tcacttgagc tgcagctca 1320
 agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagccctaa gctcctgac 1380
 tatgactcat ccaaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440
 10 acagatttoa ctctcaccat cagcagctct caacctgaag attttgcaac ttactactgt 1500
 caacagtga gtcgtaaccc acccactttc ggaggaggga ccaaggtgga gatcaaacgg 1560
 tctccagct aa 1572

(SEQ ID NO:13)

Signal sequence is residue 1 to 60

15

Mature protein sequence of Fc H8L5 (TSC318):

EPKSSDKTHT CPPCPAPEAA GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF 60
 NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
 20 ISKAKQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTFP 180
 PVLDSGSGFF LYSKLTVDKS RWQGGNVFSC SVMHEALHNH YTQKSLSLSP QQRHNNSSLN 240
 TGTQMAGHSP NSQVQLVQSG AEVKKPGASV KVSCKASGYT FTRSTMHWVR QAPGQGLEWM 300
 GYINPSSAYT NYNQKFKDRV TMTRDTSTST VYMEISSLR EDVAVYYCAR PQVHYDINGF 360
 PYWGQGTILVT VSSGGGGSGG GSGGGGGSGG GGSIDIQMTQS PSSLSASVGD RVTITCSASS 420
 25 SVSYMNWYQQ KPGKAPKLLI YDSSKSLASGV PSRFSGSGSG TDFTLTISSL QPEDFATYYC 480
 QQWSRNPPTF GGGTKVEIKR SSS 503

(SEQ ID NO:14)

30

DNA sequence of Fc H9L1 (TSC319):

atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggg 60
 gagcccaaatt cttctgacaa aactcacaca tgcccacggt gccacgacc tgaagccggc 120
 35 ggtgcaacgt cagtcttctc ctcccccca aaacccaagg acacctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtgggtggc gtgagccacg aagacctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcccgctcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcgtggc ggtctccaac aaagccctcc cagcccccac cgagaaaacc 420
 40 atctccaaag ccaaaggcca gccccgagaa ccacaggtgt acacctgcc ccatccccg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggc cagccggaga acaactacaa gaccacgct 600
 cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggtctt gcacaaccac 720
 45 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840
 gctgaggtga agaagcctgg ggccctcagtg aaggtttctt gcaaggcttc tggctacacc 900
 ttactagat ctacgatgca ttgggtggc caggcccccg gacaaaggct tgagtggatg 960
 50 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020
 accattacca gggacacatc cgcgagcaca gctacatgg agctgagcag cctgagatct 1080
 gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtc actatgatta caacggggtt 1140
 ccttactggg gccaaaggaa cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcgggtggcg atcgggtggc ggaggatctg acatccagat gaccagctct 1260
 ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgcagctca 1320
 55 agtgtaagtt acatgaactg gtaccagcag aagccgggca aggccccaa aagatggatt 1380
 tatgactcat ccaaaactggc ttctggagtc cctgctcgtc tcagtggcag tgggtctggg 1440
 accgactata cctcacaat cagcagcctg cagccogaag atttcgcac ttattactgt 1500
 cagcagtga gtcgtaaccc acccagttc ggagggggga ccaagctaca aattacatcc 1560
 tccagctaa 1569

(SEQ ID NO:15)

Signal sequence is residue 1 to 60

60

Mature protein sequence of Fc H9L1 (TSC319):

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDITLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
5	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGQRLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITRDTSAST	AYMELSSLRS	EDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTIVT	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSSLSASVGD	RVTMTCSASS	420
10	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PARFSGSGSG	TDYTLTISSL	QPEDFATYYC	480
	QQWSRNPTTF	GGGTKLQITS	SS				502

(SEQ ID NO:16)

DNA sequence of Fc H9L4 (TSC320):

15	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccgag	120
	gggtgcacgt	cagtcttctt	cttcccccca	aaacccaagg	acaccctcat	gatctcccg	180
	acccctgagg	tcacatgcgt	gggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgag	ggaggagcag	300
20	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctgggtgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgag	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
25	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggtctt	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaact	agatggcagg	tcattctccg	aattctcagg	tccagcttgt	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtttctt	gcaaggcttc	tggtacacc	900
30	tttactagat	ctacgatgca	ttgggtgcgc	caggcccccg	gacaaaggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accattacca	gggacacatc	cgcgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaagacacgg	ctgtgtatta	ctgtgcgaga	ccccaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaagggaac	cctggtcacc	gtctcttcag	gtggaggcgg	ttcaggcgga	1200
35	gggtgatccg	gcgggtggcg	atcgggtggc	ggcggatctg	aaattgtgtt	gacacagtct	1260
	ccagccaccc	tgtctttgtc	tccaggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccaacag	aaacctggcc	aggctcccag	gctcctcatc	1380
	tatgactcat	ccaaaactggc	ttctggcatc	ccagccaggt	tcagtggcag	tgggtctggg	1440
	acagacttca	ctctcaccat	cagcagccta	gagcctgaag	atthtgcagt	ttattactgt	1500
40	cagcagtggg	gtcgttaacc	accacatttc	ggcggaggga	ccaagggtga	gatcaaacgg	1560
	tctccagct	aa					1572

(SEQ ID NO:17)

Signal sequence is residue 1 to 60

45							
	Mature protein sequence of Fc H9L4 (TSC320):						
	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDITLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
50	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGQRLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITRDTSAST	AYMELSSLRS	EDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTIVT	VSSGGGGSGG	GGSGGGGGSG	GGSEIVLTQS	PATLSLSPGE	RATLSCSASS	420
55	SVSYMNWYQQ	KPGQAPRLLI	YDSSKLAGSI	PARFSGSGSG	TDFTLTISL	EPEDFAVYYC	480
	QQWSRNPTTF	GGGKVEIKR	SSS				503

(SEQ ID NO:18)

60							
	DNA sequence of Fc H9L5 (TSC321):						
	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccgag	120

	gggtgcacggt	cagtcttctct	cttcccccca	aaacccaagg	acacccctcat	gatctccccg	180
	acccctgagg	tcacatgcgt	gggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtagc	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcacccgtcc	tgacccagga	ctggctgaat	360
5	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acacccctgcc	cccatccccg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
10	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
	aggtggcagc	agggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tccagcttgt	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtttctc	gcaaggcttc	tggctacacc	900
	tttactagat	ctacgatgca	ttgggtgcgc	caggcccccg	gacaaaggct	tgagtggatg	960
15	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accattacca	gggacacatc	cgcgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaagacacgg	ctgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	gggtgatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gaccacgtct	1260
20	ccatcctccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgcag	tgccagctca	1320
	agtgtaagtt	acatgaactg	gtatcagcag	aaaccaggga	aagccctcaa	gctcctgato	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagtggcag	tggatctggg	1440
	acagatttca	ctctcaccat	cagcagctctg	caacctgaag	attttgcaac	ttactactgt	1500
25	caacagtggg	gtcgtaaccc	acccactttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:19)

Signal sequence is residue 1 to 60

30	Mature protein sequence of Fc H9L5 (TSC321):						
	EPKSSDKTHT	CPPCFAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAREWESNG	QPENNYKTFP	180
	PVLDSGDSFF	LYSKLTVDKS	RWQGGNVFSC	SVMHEALHNN	YTQKSLSLSP	QQRHNNSSLN	240
35	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGQRLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITRDTAST	AYMELSSLR	EDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTIVT	VSSGGGSGG	GGSGGGSGG	GGSDIQMTQS	PSSLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPGKAPKLLI	YDSSKLAGSV	PSRFSGSGSG	TDFTLTISSL	QPEDFATYYC	480
	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:20)**DNA sequence of Fc H10L1 (TSC322):**

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggg	60
45	gagcccaaat	cttctgacaa	aactcacaca	tgcccacccg	gcccagcacc	tgaagccgcg	120
	gggtgcacggt	cagtcttctct	cttcccccca	aaacccaagg	acacccctcat	gatctccccg	180
	acccctgagg	tcacatgcgt	gggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtagc	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcacccgtcc	tgacccagga	ctggctgaat	360
50	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acacccctgcc	cccatccccg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
55	aggtggcagc	agggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tccagcttgt	gcaatctggg	840
	gctgaggtga	agaagcctgg	gtcctcggtg	aaggctctct	gcaaggcttc	tggaggcacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggcccccg	gacaaaggct	tgagtggatg	960
60	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaaac	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200

	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	acatccagat	gaccagctct	1260
	ccaagcagcc	tgtctgcaag	cgtgggggac	agggtcacca	tgacctgcag	tgccagctca	1320
	agtgttaagtt	acatgaactg	gtaccagcag	aagccgggca	aggcccccac	aagatggatt	1380
	tatgactcat	ccaaactggc	ttctggagtc	cctgctcgt	tcagtggcag	tgggtctggg	1440
5	accgactata	ccctcacaat	cagcagcctg	cagcccgaag	atttcgccac	ttattactgc	1500
	cagcagtggg	gtcgttaacc	acccacgttc	ggagggggga	ccaagctaca	aattacatcc	1560
	tccagctaa						1569

(SEQ ID NO:21)

Signal sequence is residue 1 to 60

10

Mature protein sequence of Fc H10L1 (TSC322):

15	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQFRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFS	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGGT	FSRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLSR	EDTAVYYCAR	PQVHYDNGF	360
20	PYWGQGTLLV	VSSGGGSGG	GGSGGGSGG	GGSDIQMTQS	PSSLSASVGD	RVTMTCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PARFSGSGSG	TDYTLTISSL	QPEDFATYYC	480
	QQWSRNPPTF	GGGTKLQITS	SS				502

(SEQ ID NO:22)

25

DNA sequence of Fc H10L4 (TSC323):

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccggg	120
30	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtgggtggc	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccggg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggctgaat	360
	ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
35	atctccaaag	ccaaggggca	gccccagaaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctgctg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcgctgatgc	atgaggctct	gcacaaccac	720
40	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaact	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
	gctgaggtga	agaagcctgg	gtcctcgggt	aaggtctcct	gcaaggcttc	tggaggcacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggtc	tgagtggatg	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
45	acgattaccg	cggacaaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaaggaac	cctgggtcacc	gtctctcag	gtggaggcgg	ttcaggcggg	1200
	gggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	aaattgtgtt	gacacagtct	1260
	ccagccaccc	tgtctttgtc	tccaggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
50	agtgttaagtt	acatgaactg	gtaccaacag	aaacctggcc	aggtcccag	gctcctcatc	1380
	tatgactcat	ccaaactggc	ttctggcatc	ccagccaggt	tcagtggcag	tgggtctggg	1440
	acagacttca	ctctcaccat	cagcagccta	gagcctgaag	attttgcagt	ttattactgt	1500
	cagcagtggg	gtcgttaacc	acccactttc	ggcggaggga	ccaagggtga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:23)

Signal sequence is residue 1 to 60

60

Mature protein sequence of Fc H10L4 (TSC323):

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120

ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTFP	180
PVLDSDGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSKASGGT	FSRSTMHWVR	QAPGQGLEWM	300
GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSSLRS	EDTAVYYCAR	PQVHYDYNGF	360
PYWGGTGLVT	VSSGGGGSGG	GGSGGGGGSGG	GGSEIVLTQS	PATLSLSLSPGE	RATLSCSASS	420
SVSYMNWYQQ	KPGQAPRLLI	YDSSKSLASGI	PARFSGSGSGG	TDFTLTISL	EPEDFAVYYC	480
QQWSRNPPTF	GGGTKVEIKR	SSS				503

(SEQ ID NO:24)

DNA sequence of Fc H10L5 (TSC324):

atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
ggtgcaccgt	cagtcttcc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcccagga	ctggctgaat	360
ggcaaggcat	acgcgtgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggtctc	gcacaaccac	720
tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccttgaat	780
acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tccagctggg	gcaatctggg	840
gctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggaggcacc	900
ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggtc	tgagtggatg	960
ggatacatta	atcctagcag	tgettatact	aattacaatc	agaaattcaa	ggacagagtc	1020
acgattaccg	cggacaaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
ccttactggg	gccaaggaac	cctgggtcacc	gtctcctcag	gtggaggcgg	ttcaggcggg	1200
ggtggatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gaccacgtct	1260
ccatccctcc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgcag	tgccagctca	1320
agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccctaa	gctcctgac	1380
tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagtggcag	tggatctggg	1440
acagatttca	ctctcaccat	cagcagctctg	caacctgaag	atcttgcaac	ttactactgt	1500
caacagtggg	gtcgtaaacc	accacatttc	ggcggaggga	ccaagggtga	gatcaaaccg	1560
tctccagct aa						1572

(SEQ ID NO:25)

Signal sequence is residue 1 to 60

Mature protein sequence of Fc H10L5 (TSC324):

EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
NWYVDGVEVH	NAKTKPREEQ	YNSTYRVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTFP	180
PVLDSDGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSKASGGT	FSRSTMHWVR	QAPGQGLEWM	300
GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSSLRS	EDTAVYYCAR	PQVHYDYNGF	360
PYWGGTGLVT	VSSGGGGSGG	GGSGGGGGSGG	GGSDIQMTQS	PSSLSASVGD	RVTITCSASS	420
SVSYMNWYQQ	KPGKAPKLLI	YDSSKSLASGV	PSRFSGSGSG	TDFTLTISL	QPEDFATYYC	480
QQWSRNPPTF	GGGTKVEIKR	SSS				503

(SEQ ID NO:26)

DNA sequence of Fc H7L6 (TSC334):

atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
ggtgcaccgt	cagtcttcc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcccagga	ctggctgaat	360

	ggcaaggcat	acgcatgccc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaggggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgag	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
5	cccggtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacccg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggt	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggcttc	tggatacacc	900
10	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgettatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
	gacgacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacggggtt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
15	gggtggatccg	atcggtggcg	atcggtggcg	ggcggtctcg	acatccagat	gaccagctct	1260
	ccatcctccc	tgctctgcatc	tgtaggagac	agagtcacca	tcacttgcat	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagccctcaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagtggcag	tggatctggg	1440
	acagatttca	ctctcaccat	cagcagctcg	caacctgaag	atthttgcaac	ttactactgt	1500
20	caacagtggg	gtcgtaaccc	accacttttc	ggcggaaggga	ccaagggtgga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:27)

Signal sequence is residue 1 to 60

25

Mature protein sequence of Fc H7L6 (TSC334):

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGPQRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTFP	180
	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	QGRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TMTRDTSIST	AYMELSLRLS	DDTAVYYCAR	PQVHYDYNGF	360
35	PYWGQGTIVT	VSSGGGSGG	GGSGGGSGG	GGSDIQMTQS	PSSLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPKGAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TDFTLTISSL	QPEDFATYYC	480
	QQWSRNPPTF	GGGTKVEIKR	SSS*				504

(SEQ ID NO:28)

40

DNA sequence of Fc H7L7 (TSC335):

	atggaagcac	cagcgcagct	tctcttcttc	ctgctactct	ggctcccaga	taccacccgg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgccccacgt	gcccagcacc	tgaagccgag	120
	ggtgcacccg	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
45	acccttgagg	tcacatgcgt	ggtgggtggc	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactgggtacg	tggacggcgt	ggaggtgcat	aatgccaaag	caaagccgag	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcacccgtc	tgcaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgccc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaggggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
50	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgag	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccggtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacccg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
55	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tgcagctggt	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggcttc	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgettatact	aattacaatc	agaaattcaa	ggacagggtc	1020
	accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
60	gacgacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacggggtt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	gggtgatccg	gcgggtggcg	atcggtggcg	ggcggtatcg	aaattgtgtt	gacgcagctc	1260
	ccagccaccc	tgctcttctg	tccaggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccagcag	aaacctggcc	tggcgcccag	gagatggatt	1380

tatgactcat	ccaaactggc	ttctggcatc	ccagacaggt	tcagtggcag	tgggtctggg	1440
acagacttca	ctctcaccat	cagcagactg	gagcctgaag	atthttgcagt	gtattactgt	1500
cagcagtgga	gtcgttaacc	accacttttc	ggcggaggga	ccaaggtgga	gatcaaaccg	1560
tcctccagct	aa					1572

5 (SEQ ID NO:29)

Signal sequence is residue 1 to 60

10 Mature protein sequence of Fc H7L7 (TSC335):

EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
NWYVDGVEVE	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTTT	180
PVLDSGDSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGGGLEWM	300
GYINPSSAYT	NYNQKFKDRV	TMTRDTSIST	AYMELSLRLS	DDTAVYYCAR	PQVHYDYNF	360
PYWGGQTLVT	VSSGGGSGSG	GGSGGGGSGG	GGSEIVLTQS	PATLSLSPGE	RATLSCSASS	420
SVSYMNWYQQ	KPGLAPRRWI	YDSSKLAGSI	PDRFSGSGSG	TDFTLTISRL	EPEDFAVYYC	480
QQWSRNPPTF	GGGTKVEIKR	SSS				504

20 (SEQ ID NO:30)**DNA sequence of Fc H7L8 (TSC336):**

atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggg	60
gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccggg	120
ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctccggg	180
acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccggg	ggaggagcag	300
tacaacagca	cgtaccgtgt	ggtcagcgct	ctcaccgtcc	tgcccaggga	ctggctgaat	360
ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatccggg	480
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
cccggtgctg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
agggtggcag	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggg	acaacaattc	ttccctgaat	780
acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcaagctgt	gcagtctggg	840
gctgaggtga	agaagcctgg	ggcctcagtg	aaggtctcct	gcaaggcttc	tggatacacc	900
ttcaccagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagggtc	1020
accatgacca	gggacacgtc	catcagcaca	gcctacatgg	agctgagcag	gctgagatct	1080
gacgacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
ccttactggg	gccaagggaac	cctgggtcacc	gtctctcag	gtggaggcgg	ttcaggcggg	1200
ggtggatccg	gcggtggcgg	atcggtgggc	ggcggatctg	acatccagat	gacccagttc	1260
ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgacg	tgccagctca	1320
agtgttaagtt	acatgaactg	gtatcagcag	aaaccaggga	aagccctcaa	gagatggatt	1380
tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
acagaattca	ctctcaccat	cagcagcctg	cagcctgatg	atthttgcaac	ttattactgc	1500
caacagtgga	gtcgttaacc	accacttttc	ggcggaggga	ccaaggtgga	gatcaaaccg	1560
tcctccagct	aa					1572

(SEQ ID NO:31)

Signal sequence is residue 1 to 60

55 Mature protein sequence of Fc H7L8 (TSC336):

EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
NWYVDGVEVE	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTTT	180
PVLDSGDSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGGGLEWM	300
GYINPSSAYT	NYNQKFKDRV	TMTRDTSIST	AYMELSLRLS	DDTAVYYCAR	PQVHYDYNF	360
PYWGGQTLVT	VSSGGGSGSG	GGSGGGGSGG	GGSDIQTQS	PSTLSASVGD	RVTITCSASS	420

SVSYMNWYQQ KPGKAPKRWI YDSSKSLASGV PSRFSGSGSG TEFTLTISL QPDDFATYYC 480
 QQWSRNPPTF GGGTKVEIKR SSS* 504

(SEQ ID NO:32)

5

DNA sequence of Fc H8L6 (TSC337):

	atggaagcac	cagcgcagct	tctcttcttc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccgcg	120
10	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaag	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
15	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggtctt	gcacaaccac	720
20	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tgcaagctgg	gcagtctggg	840
	gctgaggtga	agaagcctgg	ggcctcagtg	aaggtttctt	gcaaggcatt	tggatacacc	900
	ttcaccagat	ctacgatgca	ctgggtgcga	caggcccttg	gacaagggct	tgagtgggat	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
25	accatgacca	gggacacgtc	cacgagcaca	gtctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgctaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	cccaagggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gaccagctct	1260
	ccatcctccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgag	tgccagctca	1320
30	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccttaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagtggcag	tggatctggg	1440
	acagatttca	ctctcaccat	cagcagctct	caacctgaag	atcttgcaac	ttactactgt	1500
	caacagtggg	gtcgtaaccc	acccactttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
	tctccagct	aa					1572

(SEQ ID NO:33)

Signal sequence is residue 1 to 60

40 Mature protein sequence of Fc H8L6 (TSC337):

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKE	60
	NWYVDGVEVE	NARKTPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
45	ISKAKQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQSLSLSP	GORHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGASV	KVSCKASGYT	FTRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TMTRDTSTST	VYMESSLRS	EDTAVYYCAR	PQVHYDNGF	360
	PYWGGQTLVT	VSSGGGSGSG	GGSGGGSGSG	GGSDIQMTQS	PSSLSASVGD	RVTITCSASS	420
50	SVSYMNWYQQ	KPGKAPKRWI	YDSSKSLASGV	PSRFSGSGSG	TEFTLTISL	QPEDFATYYC	480
	QQWSRNPPTF	GGGTKVEIKR	SSS*				504

(SEQ ID NO:34)**DNA sequence of Fc H8L7 (TSC338):**

55	atggaagcac	cagcgcagct	tctcttcttc	ctgctactct	ggctcccaga	taccaccggg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaag	caaagccgcg	ggaggagcag	300
60	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540

5 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt ctctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900
 ttaccagat ctacgatgca ctgggtgcga caggccctcg gacaagggct tgagtggatg 960
 ggatacatta atcctagcag tgettatact aattacaatc agaaattcaa ggacagagtc 1020
 accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080
 10 gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcg atcgggtggc ggcgatctg aaattgtgtt gacgcagtct 1260
 ccagccacc tgtctttgtc tccaggggaa agagccacc tctcctgcag tgccagctca 1320
 agtgaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380
 15 tatgactcat ccaaaactgc tcttgcatc ccagacaggt tcagtggcag tgggtctggg 1440
 acagacttca ctctcaccat cagcagactg gagcctgaag attttgaggt gtattactgt 1500
 cagcagtgga gtgcgtaacc acccacttcc ggcgagggga ccaaggtgga gatcaaacgg 1560
 tcctccagct aa 1572

(SEQ ID NO:35)

20 Signal sequence is residue 1 to 60

Mature protein sequence of Fc H8L7 (TSC338):

25 EPKSSDKTHT CPFCFAPEAA GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF 60
 NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
 ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVRGFPYS DIAVEWESNG QPENNYKTFP 180
 PVLDSGSEFF LYSKLTVDKS RWQGGNVFSC SVMHEALHNH YTQKSLSLSP GQRHNNSSLN 240
 30 TGTQMAHGSP NSQVQLVQSG AEVKKPGASV KVSCKASGYT FTRSTMHWVR QAPGGGLEWM 300
 GYINPSSAYT NYNQKFKDRV TMTRDTSTST VYMELSSLSR EDTAVYYCAR PQVHYDYNF 360
 PYWGGTGLVT VSSGGGGSGG GSGGGGGSGG GGSEIVLTQS PATLSLSPGE RATLSCSASS 420
 SVSYMNWYQQ KPLAPRRWI YDSGKLASGI PDRFSGSGSG TDFTLTISRL EPEDFAVYYC 480
 QQWSRNPPTF GGGTKVEIKR SSS 503

(SEQ ID NO:36)**DNA sequence of Fc H8L8 (TSC339):**

40 atggaagcac cagcgcagct tctcttcttc ctgctactct ggctcccaga taccaccggg 60
 gagcccaaat ctctcgacaa aactcacaca tgcccaccgt gccagcacc tgaagccggc 120
 ggtgcaccgt cagtcttctc ctcccccca aaacccaagg acaccctcat gatctcccgg 180
 accctgagg tcacatgcgt ggtgggtggc gtgagccacg aagaccctga ggtcaagttc 240
 aactggtaag tggacggcgt ggaggtgcat aatgccaaag caaagccggc ggaggagcag 300
 45 tacaacagca cgtacogtgt ggtcagcgtc ctacacgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccac cgagaaaaac 420
 atctccaaag ccaaagggca gcccagagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 660
 aggtgctcagc aggggaacgt ctctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900
 55 ttaccagat ctacgatgca ctgggtgcga caggccctcg gacaagggct tgagtggatg 960
 ggatacatta atcctagcag tgettatact aattacaatc agaaattcaa ggacagagtc 1020
 accatgacca gggacacgtc cagagcaca gtctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctctcag gtggaggcgg ttcaggcgga 1200
 60 ggtggatccg gcggtggcg atcgggtggc ggcgatctg acatccagat gaccaggtct 1260
 ccttccacc tgtctgcac tgtaggagac agagtcacca tcaattgcag tgccagctca 1320
 agtgaagtt acatgaactg gtatcagcag aaaccggga aagccctaa gagatggatt 1380
 tatgactcat ccaaaactgc tcttggtgtc ccatcaaggt tcagcggcag tggatctggg 1440
 acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcgaggga ccaaggtgga gatcaaacgg 1560
tctccagct aa 1572

(SEQ ID NO:37)

Signal sequence is residue 1 to 60

5

Mature protein sequence of Fc H8L8 (TSC339):

10 EPKSSDKTHT CPPCPAPEAA GAPSVFLFPP KPKDTLMISR TFEVTCVVVD VSHEDPEVKE 60
NWYVDGVEVE NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFPYS DIAVEWESNG QPENNYKTFP 180
PVLDSGSEFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTKSLSLSP GQRHNNSSLN 240
TGTQMAGHSP NSQVQLVQSG AEVVKPGASV KVSCKASGYT FTRSTMHWVR QAPGGGLEWM 300
15 GYINPSSAYT NYNQKFKDRV TMTTRDTSTST VYMESSLRS EDTAVYYCAR PQVHYDNGF 360
PYWQGTLVT VSSGGGSGG GSGGGGSGG GSGDIQMTQS PSTLSASVGD RVTITCSASS 420
SVSYMNWYQQ KPGKAPKRWI YDSSKLAGSV PSRFSGSGSG TEFTLTISSL QPDDFATYYC 480
QQWSRNPPTF GGGTKVEIKR SSS 504

(SEQ ID NO:38)

20

DNA sequence of Fc H10L6 (TSC340):

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggg 60
gagcccaaat ctcttgacaa aactcacaca tgcccaccgt gccagcacc tgaagccggc 120
25 ggtgcaccgt cagtcttctc ctccccccaa aaacccaagg acaccctcat gatctcccg 180
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccggc ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccac cgagaaaaac 420
30 atctccaaag ccaaggggca gcccagagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatgcgcg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgctgctg actccgacgg ctctcttctc ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt ctctctatgc tccgtgatgc atgaggtctc gcacaaccac 720
35 tacacgcaga agagcctctc cctgtctccg ggtcagagcc acaacaattc ttccctgaat 780
acaggaaactc agatggcagg tcattctccg aattctcagg tcagctggt gcaatctggg 840
gctgaggtga agaagcctgg gtctctcggt aaggtctcct gcaaggcttc tggaggcacc 900
ttcagcagat ctacgatgca ctgggtgcga caggccctcg gacaagggtc tgagtggatg 960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
40 acgattaccg cggacaaatc cagcagcaca gcctagatgg agctgagcag cctgagatct ctgagatct 1080
gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtc actatgatta caacgggttt 1140
ccttactggg gccaaaggaa cctgggtcacc gtctctcag gtggaggcgg ttcaggcggg 1200
ggtggatccg gcgggtggcg atcgggtggc ggcgatctg acatccagat gaccagtcct 1260
ccatcctccc tgtctgcacg tgtaggagac agagtcacca tcaattgcag tgccagctca 1320
45 agtgaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440
acagatttca ctctaccat cagcagctcg caacctgaag attttgcaac ttactactgt 1500
caacagtgga gtcgtaaccc acccactttc ggcgaggga ccaaggtgga gatcaaacgg 1560
tctccagct aa 1572

(SEQ ID NO:39)

Signal sequence is residue 1 to 60

50

Mature protein sequence of Fc H10L6 (TSC340):

55 EPKSSDKTHT CPPCPAPEAA GAPSVFLFPP KPKDTLMISR TFEVTCVVVD VSHEDPEVKE 60
NWYVDGVEVE NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKAYACAVSN KALPAPIEKT 120
ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFPYS DIAVEWESNG QPENNYKTFP 180
60 PVLDSGSEFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTKSLSLSP GQRHNNSSLN 240
TGTQMAGHSP NSQVQLVQSG AEVVKPGSSV KVSCKASGGT FSRSTMHWVR QAPGGGLEWM 300
GYINPSSAYT NYNQKFKDRV TITADKSTST AYMESSLRS EDTAVYYCAR PQVHYDNGF 360
PYWQGTLVT VSSGGGSGG GSGGGGSGG GSGDIQMTQS PSSLSASVGD RVTITCSASS 420
SVSYMNWYQQ KPGKAPKRWI YDSSKLAGSV PSRFSGSGSG TDFTLTISSL QPEDFATYYC 480
QQWSRNPPTF GGGTKVEIKR SSS 503

(SEQ ID NO:40)

DNA sequence of Fc H10L7 (TSC341):

5	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acacctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagacctga	ggtcaagtgc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
10	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaaac	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acacctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
15	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcctgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
	gctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggaggcacc	900
20	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctgggtcacc	gtctctcag	gtggaggcgg	ttcaggcggg	1200
25	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	aaattgtgtt	gacgcagtct	1260
	ccagccaccc	tgtctttgtc	tcacggggaa	agagccaccc	tctcctgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtaccagcag	aaacctggcc	tggcgcaccg	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggcatc	ccagacaggt	tcagtggcag	tgggtctggg	1440
	acagacttca	ctctcaccat	cagcagactg	gagcctgaag	atcttgagct	gtattactgt	1500
30	cagcagtgga	gtcgtaaccc	acccactttc	ggcggaggga	ccaagggtga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:41)

Signal sequence is residue 1 to 60

35

Mature protein sequence of Fc H10L7 (TSC341):

40	ERKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTTT	180
45	PVLDSGGSFF	LYSKLTVDKS	RWQQGNVFS	SVMHEALAHN	YTQKSLSLSP	QGRHNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGGT	FSRSTMHWVR	QAPGQGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TTTADKSTST	AYMELSSLSR	EDTAVYYCAR	PQVHYDYNFG	360
	PYWGGTLVLT	VSSGGGSGSG	GGSGGGSGSG	GGSEIVLTQS	PATLSLSPGE	RATLSCSASS	420
	SVSYMNWYQQ	KPGLAPRRWI	YDSSKSLASGI	PDRFSGSGSG	TDFTLTISRL	EPEDFAVYYC	480
50	QQWSRNPPTF	GGGTKVEIKR	SSS				503

(SEQ ID NO:42)

DNA sequence of Fc H10L8 (TSC342):

55	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acacctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagacctga	ggtcaagtgc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
60	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaaac	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acacctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600

	cccggtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	agggtggcagc	aggggaacgt	cttctcatgc	tcggtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggg	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tcacagctgg	gcaatctggg	840
5	gctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggaggcacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccccctg	gacaagggtc	tgagtggatg	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	cogtgtatta	ctgtgcgaga	ccccaagtc	actatgatta	caacgggttt	1140
10	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcggg	1200
	gggtgatccg	gcggtggcgg	atcggtgggc	ggcggatctg	acatccagat	gacccagtct	1260
	ccttcacccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgacg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagccccctaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
15	acagaattca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
	caacagtggg	gtcgtaaccc	accacatttc	ggcggaggga	ccaaggtgga	gatcaaaccg	1560
	tcctccagct	aa					1572

(SEQ ID NO:43)

Signal sequence is residue 1 to 60

20

Mature protein sequence of Fc H10L8 (TSC342):

25	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPF	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALFAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QFENNYKTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGGT	FSRSTMHWVR	QAPGQGLEWM	300
30	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLRS	EDTAVYYCAR	PQVHYDYNFG	360
	PYWGQGTTLV	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSTLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISSL	QPDFFATYYC	480
	QQWSRNPPTF	GGGTVKEIKR	SSS				503

(SEQ ID NO:44)

35

DNA sequence of TSC370:

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggg	60
40	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccggc	120
	gggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccg	180
	acccctgagg	tcacatgcgt	gggtggtggc	gtgagccaag	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcac	aatgccaaag	caaagccggc	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccaggga	ctggctgaat	360
45	ggcaaggcat	acgcatggcg	gggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccggtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
50	agggtggcagc	aggggaacgt	cttctcatgc	tcggtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggg	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tcacagctgg	gcaatctggg	840
	gctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccccctg	gacaagggtc	tgagtggatg	960
55	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	cogtgtatta	ctgtgcgaga	ccccaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcggg	1200
	gggtgatccg	gcggtggcgg	atcggtgggc	ggcggatctg	acatccagat	gacccagtct	1260
60	ccttcacccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgacg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagccccctaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
	acagaattca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
	caacagtggg	gtcgtaaccc	accacatttc	ggcggaggga	ccaaggtgga	gatcaaaccg	1560

tcctccagct aa

1572

(SEQ ID NO:45)

Signal sequence is residue 1 to 60

5

Mature protein sequence of TSC370:

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
10	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGYT	FSRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLR	EDTAVYYCAR	PQVHYDNGF	360
	PYWGGTGLVT	VSSGGGSGG	GGSGGGSGG	GGSDIQMTQS	PSTLSASVGD	RVTITCSASS	420
15	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISL	QPDDEFATYYC	480
	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:46)

20

DNA sequence of TSC371:

	atggaagcac	cagcgcagct	tctcttccct	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gccagcacc	tgaagccg	120
25	ggtgcaccgt	cagtcttccct	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtagc	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccg	ggaggagcag	300
	tacaacagca	cgtagccgtg	ggtcagcgtc	ctcaccgtcc	tgacccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
30	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagccctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtgagg	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccggtgctg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tcctgtgatgc	atgaggctct	gcacaaccac	720
35	tacacgcaga	agagccctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tccagctggg	gcaatctggg	840
	gctgaggtga	agaagccctg	gtcctcgggtg	aaggtctcct	gcaaggcttc	tggaggcacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggtc	tgagtggata	960
	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
40	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaaggaac	cctgggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gacccagctc	1260
	ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgcag	tgccagctca	1320
45	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccttaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
	acagaattca	ctctcaccat	cagcagcctg	cagcctgatg	attttgcaac	ttattactgc	1500
	caacagtggg	gtcgttaacc	accacatttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:47)

Signal sequence is residue 1 to 60

55

Mature protein sequence of TSC371:

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
60	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGGT	FSRSTMHWVR	QAPGGGLEWI	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLR	EDTAVYYCAR	PQVHYDNGF	360
	PYWGGTGLVT	VSSGGGSGG	GGSGGGSGG	GGSDIQMTQS	PSTLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISL	QPDDEFATYYC	480
65	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:48)

DNA sequence of TSC372:

5	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccacccgt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagtct	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
10	tacaacagca	cgtacogtgt	ggtcagcgtc	ctcacogtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
15	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacogt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
	gctgagtgga	agaagcctgg	gtcctcgggt	aaggtctcct	gcaaggcttc	tggaggcacc	900
20	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctgggtcacc	gtctctcag	gtggaggcgg	ttcaggcggga	1200
25	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	acatccagat	gaccacagtc	1260
	ccttccaccc	tgtctgcac	tgtaggagac	agagtaccca	tgacttgacg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccagggg	aagcccttaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
	acagaattca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
30	caacagtgga	gtcgtaaccc	accacatttc	ggcggaggga	ccaagggtga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:49)

Signal sequence is residue 1 to 60

35

Mature protein sequence of TSC372:

40	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLFPPR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTF	180
	PVLDSGSGFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	QQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSCKASGGT	FSRSTMHWVR	QAPGGGLEWM	300
45	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLSR	EDTAVYYCAR	PQVHYDYNFG	360
	PYWGGTTLVT	VSSGGGSGSG	GGSGGGGSGG	GGSDIQMTQS	PSTLSASVGD	RVTMTCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLASGV	PSRFSGSGSG	TEFTLTISSL	QPDDEFATYYC	480
	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:50)

50

DNA sequence of TSC390:

55	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccacccgt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagtct	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtacogtgt	ggtcagcgtc	ctcacogtcc	tgcaaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
60	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacogt	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720

	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
	cctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggatg	960
5	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacggggtt	1140
	ccttactggg	gccaaggaac	cctgggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	acatccagat	gacccagtct	1260
10	ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgacg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccttaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
	acagagtcca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
	caacagtggg	gtcgtaaacc	accacttttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
15	tcctccagct	aa					1572

(SEQ ID NO:51)

Signal sequence is residue 1 to 60

20 Mature protein sequence of TSC390:

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKRTT	180
25	PVLDSGGSFF	LYSKLTVDKS	RWQOGNVFSC	SVMHEALHNN	YTQKSLSLSP	QGRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	PEVVKPGSSV	KVSCKASGYT	FSRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLRS	EDTAVYYCAR	PQVHYDYNF	360
	PYWGQGTILVT	VSSGGGSGSG	GGSGGGSGSG	GGSDIQMTQS	PSTLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISL	QPDFFATYYC	480
30	QQWSRNPTTF	GGGTRKVEIKR	SSS				503

(SEQ ID NO:52)**35 DNA sequence of TSC391:**

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccacccgg	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccacogt	gcccagcacc	tgaagccggc	120
	ggtgcacogt	cagtcttctc	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccttgagg	tcacatgcgt	ggtgggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
40	aaactggtag	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccggc	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcacccgtc	tgcccaggga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaaggcca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
45	gacatgcggc	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	660
	aggtggcagc	aggggaaagt	cttctcatgc	tccgtgatgc	atgaggtctc	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
50	cctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggata	960
	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacggggtt	1140
55	ccttactggg	gccaaggaac	cctgggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	acatccagat	gacccagtct	1260
	ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tcacttgacg	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccttaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
60	acagagtcca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
	caacagtggg	gtcgtaaacc	accacttttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:53)

Signal sequence is residue 1 to 60

Mature protein sequence of TSC391:

5	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGDSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	PEVKKPGSSV	KVSCKASGYT	FSRSTMHWVR	QAPGGGLEWI	300
10	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLR	EDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTIVT	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSTLSASVGD	RVTITCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFGSGSGG	TEFTLTISL	QPDDEFATYYC	480
	QQWSRNPPTF	GGGTVKEIKR	SSS				503

(SEQ ID NO:54)

15

DNA sequence of TSC392:

20	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgog	120
	ggtgcaccgt	cagtcttctt	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgog	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggttgaat	360
25	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccac	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccagaaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccggtctgg	actccgacgg	ctccttcttc	ctctacagca	agctcacctg	ggacaagagc	660
30	aggtggcagc	aggggaaagt	cttctcatgc	tcctgtatgc	atgaggtctt	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaaactc	agatggcagg	tcattctccg	aattctcagg	tcagctgggt	gcaatctggg	840
	cctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctaccgatgc	ctgggtgcga	caggccctcg	gacaagggtc	tgagtggatg	960
35	ggatacatta	atcctagcag	tgcttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaaggaac	cctggtcacc	gtctctcag	gtggaggcgg	ttcaggcgga	1200
	ggtggatccg	gcggtggcgg	atcgggtggc	ggcggatctg	acatccagat	gaccagctct	1260
40	ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tgacttgag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagccctcaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaagggt	tcagcggcag	tggatctggg	1440
	acagagtcca	ctctcaccat	cagcagcctg	cagcctgatg	atcttgcaac	ttattactgc	1500
	caacagtggg	gtcgttaacc	accacatttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
45	tcctccagct	aa					1572

(SEQ ID NO:55)

Signal sequence is residue 1 to 60

Mature protein sequence of TSC392:

55	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKARGQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTTT	180
	PVLDSGDSFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNN	YTQKSLSLSP	GQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	PEVKKPGSSV	KVSCKASGYT	FSRSTMHWVR	QAPGGGLEWM	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLR	EDTAVYYCAR	PQVHYDNGF	360
	PYWGQGTIVT	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSTLSASVGD	RVTMTCSASS	420
60	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFGSGSGG	TEFTLTISL	QPDDEFATYYC	480
	QQWSRNPPTF	GGGTVKEIKR	SSS				503

(SEQ ID NO:56)

DNA sequence of TSC393:

65

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
	ggtgcaccgt	cagtcttctt	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
5	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
10	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctgtgg	actccgacgg	ctccttcttc	ctctacagca	agctcacccg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tccagctggg	gcaatctggg	840
15	gctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggata	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020
	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
20	gaggacacgg	ccgtgtatta	ctgtgcgaga	ccccaaagtc	actatgatta	caacggggtt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	ggttgatccg	gcggtggcgg	atcggtgggc	ggcggatctg	acatccagat	gaccagctct	1260
	ccttccaccc	tgtctgcctc	tgtaggagac	agagtcacca	tgacttgacg	tgccagctca	1320
	agtgttaagt	acatgaactg	gtatcagcag	aaaccaggga	aagccctcaa	gagatggatt	1380
25	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggatctggg	1440
	acagagtcca	ctctcaccat	cagcagcctg	cagcctgatg	atthtgcaac	ttattactgc	1500
	caacagtggg	gtcgtaacct	acccactttc	ggcggaggga	ccaagggtgga	gatcaaacgg	1560
	tcctccagct	aa					1572

(SEQ ID NO:57)

Signal sequence is residue 1 to 60

30

Mature protein sequence of TSC393:

35	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKE	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
	ISKAKQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFYPS	DIAVEWESNG	QPENNYKTFP	180
	PVLDSGSGFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	QQRHNNSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	AEVKKPGSSV	KVSKKASGYT	FSRSTMHWVR	QAPGQGLEWI	300
40	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLSR	EDTAVYYCAR	PQVHYDYNGF	360
	PYWQQGTILT	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSTLSASVGD	RVTMTCSASS	420
	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISSL	QPDFFATYYC	480
	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:58)

45

DNA sequence of TSC394:

	atggaagcac	cagcgcagct	tctcttctct	ctgctactct	ggctcccaga	taccaccggt	60
	gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgcg	120
50	ggtgcaccgt	cagtcttctt	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	180
	acccctgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	240
	aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	300
	tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	360
	ggcaaggcat	acgcatgcgc	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	420
55	atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	480
	gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatccaagc	540
	gacatgcgcg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	600
	cccgctgtgg	actccgacgg	ctccttcttc	ctctacagca	agctcacccg	ggacaagagc	660
	aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	720
	tacacgcaga	agagcctctc	cctgtctccg	ggtcagaggc	acaacaattc	ttccctgaat	780
	acaggaactc	agatggcagg	tcattctccg	aattctcagg	tccagctggg	gcaatctggg	840
60	cctgaggtga	agaagcctgg	gtcctcggtg	aaggtctcct	gcaaggcttc	tggatatacc	900
	ttcagcagat	ctacgatgca	ctgggtgcga	caggccctcg	gacaagggct	tgagtggata	960
	ggatacatta	atcctagcag	tgtttatact	aattacaatc	agaaattcaa	ggacagagtc	1020

	acgattaccg	cggacaaatc	cacgagcaca	gcctacatgg	agctgagcag	cctgagatct	1080
	gaggacacgg	cctgtgatta	ctgtgcgaga	ccccaagtc	actatgatta	caacgggttt	1140
	ccttactggg	gccaaggaac	cctggtcacc	gtctcctcag	gtggaggcgg	ttcaggcgga	1200
	gggtggatccg	gcgggtggcg	atcgggtggc	ggcggatctg	acatccagat	gacccagtct	1260
5	ccttccaccc	tgtctgcac	tgtaggagac	agagtcacca	tgacttgcag	tgccagctca	1320
	agtgtaaagt	acatgaactg	gtatcagcag	aaaccaggga	aagcccctaa	gagatggatt	1380
	tatgactcat	ccaaactggc	ttctggggtc	ccatcaaggt	tcagcggcag	tggtatctggg	1440
	acagagtcca	ctctcaccat	cagcagcctg	cagcctgatg	attttgcaac	ttattactgc	1500
	caacagtggg	gtcgtaaccc	acccactttc	ggcggaggga	ccaaggtgga	gatcaaacgg	1560
10	tcctccagct	aa					1572

(SEQ ID NO:59)

Signal sequence is residue 1 to 60

15 Mature protein sequence of TSC394:

	EPKSSDKTHT	CPPCPAPEAA	GAPSVFLFPP	KPKDITLMISR	TPEVTCVVVD	VSHEDPEVKF	60
	NWYVDGVEVH	NAKTKPREEQ	YNSTYRVVSV	LTVLHQDWLN	GKAYACAVSN	KALPAPIEKT	120
20	ISKAKQPRE	PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTTP	180
	PVLDSGSEFF	LYSKLTVDKS	RWQQGNVFSC	SVMHEALHNH	YTQKSLSLSP	QGRHNSSSLN	240
	TGTQMAGHSP	NSQVQLVQSG	PEVKKPGSSV	KVSKKASGYT	FSRSTMHWVR	QAPGQGLEWI	300
	GYINPSSAYT	NYNQKFKDRV	TITADKSTST	AYMELSSLR	EDTAVYYCAR	PQVHYDYNF	360
	PYWQQTLVT	VSSGGGGSGG	GGSGGGGGSG	GGSDIQMTQS	PSTLSASVGD	RVTMTCSASS	420
25	SVSYMNWYQQ	KPGKAPKRWI	YDSSKLAGSV	PSRFSGSGSG	TEFTLTISSL	QPDFFATYYC	480
	QQWSRNPPTF	GGGKVEIKR	SSS				503

(SEQ ID NO:60)**30 DNA sequence of TSC408:**

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggg	60
	gatatccaga	tgaccagtc	tccatccgcc	atgtctgcac	ctgtaggaga	cagagtcacc	120
	atcacttgcc	ggcgagtaga	gagcattagc	aaatatctag	cctgggttca	gcagaaacca	180
	gggaagttc	ctaagctccg	catccattct	ggatctactt	tgcaatcagg	ggteccatct	240
35	cggttcagtg	gcagtggatc	tgggacagaa	tttactctca	ccatcagcag	cctgcagcct	300
	gaagattttg	caacttatta	ctgtcaacag	catattgaat	acccgtggac	gttcggccaa	360
	gggaccaagg	tggaaatcaa	acgaggtggc	ggagggtctg	gggtggcg	atccggaggt	420
	ggtggctctc	aggtccagct	ggtacagctc	ggggctgagg	tgaagaagcc	tggggcttca	480
	gtgaaggctc	cctgcaaggc	ttctggatac	acattcactg	actactacat	gcactgggtg	540
40	cgacaggccc	ctggacaagg	gcttgagtg	atgggatatt	ttaatcctta	taatgattat	600
	actagatacg	cacagaagtt	ccagggcaga	gtcaccatga	ccaggggcac	gtctatcagc	660
	acagcctaca	tggagctgag	cagcctgaga	tctgacgaca	cggccgtgta	ttactgtgca	720
	agatcggatg	gttactacga	tgtatggac	tactgggtgc	aaggaaaccac	agtcaccgtc	780
	tcctcgagtg	agcccaaatc	ttctgacaaa	actcacacat	gcccaccgtg	cccagcacct	840
45	gaagccggcg	gtgcaaccgtc	agtcttctct	ttcccccaa	aaccaagga	cacctcatg	900
	atctcccgga	ccctgaggt	cacatgcgtg	gtgggtgacg	tgagccacga	agaccctgag	960
	gtcaagttca	actggtacgt	ggacggcggtg	gaggtgcata	atgccaagac	aaagccggcg	1020
	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	1080
	tggctgaatg	gcaaggcgta	cgcgtgcgcg	gtctccaaaca	aagccctccc	agcccccatc	1140
50	gagaaaacca	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	cacctgtccc	1200
	ccatcccggg	atgagctgac	caagaaccag	gtcagcctga	cctgctgtgt	caaaggcttc	1260
	tatccaagcg	acatgcgcgt	ggagtgggag	agcaatgggc	agccggagaa	caactacaag	1320
	accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	1380
	gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1440
55	cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtcagaggca	caacaattct	1500
	tcctgaata	caggaaactca	gatggcaggt	cattctccga	attctcaggt	ccagctgggtg	1560
	caatctgggc	ctgaggtgaa	gaagctggg	tcctcggtga	aggtctcctg	caaggcttct	1620
	ggatatactc	tcagcagatc	tacgatgcac	tgggtgcgac	aggccctgg	acaaggcctt	1680
	gagtggatag	gatacattaa	tcctagcagt	gcttatacta	attacaatca	gaaattcaag	1740
60	gacagagtoa	cgattaccgc	ggacaaatcc	acgagcacag	cctacatgga	gctgagcagc	1800
	ctgagatctg	aggacacggc	cgtgtattac	tgtgcgagac	cccaagtcca	ctatgattac	1860
	aacgggtttc	cttactgggg	ccaaggaacc	ctggctcaccg	tctcctcagg	tggaggcggt	1920
	tcaggcggag	gtggatccgg	cggtggcgga	tcgggtggcg	gcggatctga	catccagatg	1980
	accagctctc	cttccaccct	gtctgcattc	gtaggagaca	gagtcaccat	cacttgcatg	2040

	gccagctcaa	gtgtaagtta	catgaactgg	tatcagcaga	aaccagggaa	agccccctaag	2100
	agatggattt	atgactcacc	caaactgggt	tctgggggtc	catcaagggt	cagcgggcagt	2160
	ggatctggga	cagagttcac	tctcaccatc	agcagcctgc	agcctgatga	ttttgcaact	2220
	tattactgcc	aacagtggag	tcgtaaccca	cccactttcg	gcggaggggac	caagggtggag	2280
5	atcaaacggt	cctccagcta	a				2301

(SEQ ID NO:61)

Signal sequence is residue 1 to 60

10

Mature protein sequence of TSC408:

15	DIQMTQSPSA	MSASVGDRV	ITCRASKSIS	KYLAWFQQKP	GKVPKLRIHS	GSTLQSGVPS	60
	RFSGSGSGTE	FTLTISLQP	EDFATYYCQ	HIEYPWTFGQ	GTKVEIKRGG	GGSGGGGSGG	120
	GGSQVQLVQS	GAEVKKGAS	VKVSCKASGY	TFTDYYMHV	RQAPGGGLEW	MGYFNPYNDY	180
	TRYAQKFQGR	VTMTRDTSIS	TAYMELSSLR	SDDTAVYYCA	RSDGYDAMD	YWGQGTITVTV	240
	SSSEPKSSDK	THTCPPCPAP	EAAGAPSVFL	FPPKPKDTLM	ISRTEVTCV	VVDVSHEDPE	300
20	VKFNWYVDGV	EVHNARTKPR	EEQYNSTYRV	VSVLTVLHQD	WLNGKAYACA	VSNKALPAPI	360
	EKTISKAKGQ	PREPQVYTLF	PSRDELTKNQ	VSLTCLVKGF	YPSDIAVEWE	SNGQPENNYK	420
	TTTPVLDSDG	SFFLYSKLTV	DKSRWQQGNV	FSCSVMEAL	HNHYTQKSL	LSPGQRHNS	480
	SLNTGTQMG	HSPNSQVQLV	QSGPEVKKPG	SSVKVSKAS	GYTFSRSTMH	WVRQAPGQGL	540
	EWIGYINPSS	AYTNYNQKFK	DRVITITADKS	TSTAYMELSS	LRSEDYAVYY	CARPQVHYDY	600
	NGFPYWGQGT	LVTVSSGGGG	SGGGGSGGGG	SGGGGSDIQM	TQSPSTLSAS	VGDRVITITCS	660
25	ASSSVSYMNW	YQKPKGKAPK	RWIYDSSKLA	SGVPSRFSGS	GGTEFTLTI	SSLQPDDEFAT	720
	YYCQQWSRNP	PTFGGQTKVE	IKRSSS				746

(SEQ ID NO:62)**30 DNA sequence of TSC409:**

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
	gatatccaga	tgaccagtc	tccatccgcc	atgtctgcat	ctgtaggaga	cagagtcacc	120
	atcacttgcc	ggcgagtaga	gagcattagc	aaatatctag	cctgggttca	gcagaaaacca	180
	gggaaagtcc	ctaagctccg	catccattct	ggatctactt	tgcaatcagg	ggteccatct	240
35	cggttcagtg	gcagtggatc	tgggacagaa	tttactctca	ccatcagcag	cctgcagcct	300
	gaagattttg	caacttatta	ctgtcaacag	catattgaat	acccgtggac	gttcggccaa	360
	gggaccaagg	tggaaatcaa	acgaggtggc	ggagggtctg	gggtgggcgg	atccggaggt	420
	ggtggtcttc	aggtccagct	ggtacagtct	ggggctgagg	tgaagaagcc	tggggcttca	480
	gtgaaggctc	cctgcaaggc	ttctggatac	acattcactg	actactacat	gcactgggtg	540
40	cgacaggccc	ctggacaagg	gcttgagtgg	atgggatatt	ttaatcotta	taatgattat	600
	actagatacg	cacagaagtt	ccagggcaga	gtcaccatga	ccagggcac	gtctatcagc	660
	acagcctaca	tggagctgag	cagcctgaga	tctgacgaca	cggccgtgta	ttactgtgca	720
	agatcgatg	gttactacga	tgttatggac	tactgggtgc	aaggaaaccac	agtcaccgtc	780
	tcctcgagtg	agcccaaatc	ttctgacaaa	actcacacat	gcccaccgtg	cccagcacct	840
45	gaagccggcg	gtgcaaccgtc	agtcttcttc	ttcccccaa	aaccaagga	cacctcatg	900
	atctcccgga	ccctgaggt	cacatgcgtg	gtggtggacg	tgagccacga	agaccctgag	960
	gtcaagttca	actggtacgt	ggacggcggtg	gaggtgcata	atgccaagac	aaagccgcgg	1020
	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	1080
	tggctgaatg	gcaaggcgta	cgcgtgcgcg	gtctccaaac	aagccctccc	agcccccatc	1140
50	gagaaaacca	tctccaaagc	caaagggcag	ccccgagaa	cacaggtgta	cacctgtccc	1200
	ccatcccggtg	atgagctgac	caagaaccag	gtcagcctga	cctgctgtgt	caaaggcttc	1260
	tatccaagcg	acatgcgcgt	ggagtgggag	agcaatgggc	agccggagaa	caactacaag	1320
	accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	1380
	gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1440
55	cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtcagaggca	caacaattct	1500
	tcctgaata	caggaaactca	gatggcaggt	cattctccga	attctcaggt	ccagctgggtg	1560
	caatctgggc	ctgaggtgaa	gaagctggg	tcctcggtga	aggtctcctg	caaggcttct	1620
	ggatatact	tcagcagatc	tacgctgcac	tgggtgcgac	aggccctgg	acaaggcctt	1680
	gagtggatgg	gatacattaa	tcctagcagt	gcttatacta	attacaatca	gaaattcaag	1740
60	gacagagtoa	cgattaccgc	ggacaaatcc	acgagcacag	cctacatgga	gctgagcagc	1800
	ctgagatctg	aggacacggc	cgtgtattac	tgtgcgagac	cccaagtcca	ctatgattac	1860
	aacgggtttc	cttactgggg	ccaaggaacc	ctggctcaccg	tctcctcagg	tggaggcgggt	1920
	tcaggcggag	gtggatccgg	cggtggcgga	tcgggtggcg	gcggatctga	catccagatg	1980
	accagctctc	cttccaccct	gtctgcatct	gtaggagaca	gagtcaccat	gacttgcatg	2040

	gccagctcaa	gtgtaagtta	catgaactgg	tatcagcaga	aaccagggaa	agccccctaag	2100
	agatggattt	atgactcadc	caaactgggt	tctgggggtcc	catcaagggtt	cagcgggcagt	2160
	ggatctggga	cagagttcac	tctcaccatc	agcagcctgc	agcctgatga	ttttgcaact	2220
	tattactgcc	aacagtggag	tcgtaaccca	cccactttcg	gcggagggac	caagggtggag	2280
5	atcaaacggt	cctccagcta	a				2301

(SEQ ID NO:63)

Signal sequence is residue 1 to 60

10 Mature protein sequence of TSC409:

	DIQMTQSPSA	MSASVGDVRT	ITCRASKSIS	KYLAWFQQKP	GKVPKLRIHS	GSTLQSGVPS	60
	RFSGSGSGTE	FTLTISLQF	EDFATYYCQQ	HIEYPWTFGQ	GTKVEIKRGG	GGSGGGGSGG	120
	GGSQVQLVQS	GAEVKKPGAS	VKVSCKASGY	TFTDYYMHVW	RQAPGQGLEW	MGYFNPYNDY	180
15	TRYAQKFQGR	VTMTRDTSIS	TAYMELSSLR	SDDTAVYYCA	RSDDGYDAMD	YWGQGTITVTV	240
	SSSEPKSSDK	THTCPPCPAP	EAAGAPSVFL	FPPKPKDTLM	ISRTEVTCV	VVDVSHEDPE	300
	VKFNWYVDGV	EVHNAKTKPR	EEQYNSTYRV	VSVLTVLHQD	WLNGKAYACA	VSNKALPAPI	360
	EKTISKAKGQ	PREPQVYTLF	PSRDELTKNQ	VSLTCLVKGF	YPSDIAVEWE	SNGQPENNYK	420
	TTPPVLDSDG	SFFLYSKLTV	DKSRWQQGNV	FSCSVMEAL	HNHYTQKSLS	LSPGQRHNS	480
20	SLNTGTQMAS	HSPNSQVQLV	QSGPEVKKPG	SSVKVSKAS	GYTFSRSTMH	WVRQAPGQGL	540
	EWMGYINPSS	AYTNYNQKFK	DRVTITADKS	TSTAYMELSS	LRSEDTAVYY	CARFQVHYDY	600
	NGFFPYWQGT	LVTVSSGGGG	SGGGSGGGGG	SGGGSGDIQM	TQSPSTLSAS	VGDRVMTTCS	660
	ASSSVSYMNW	YQQKPKGAPK	RWIYDSSKLA	SGVPSRPSGS	SGSTEFTLTI	SSLQPDDEFAT	720
	YYCQQWSRNP	PTFGGGTKVE	IKRSSS				746

25 (SEQ ID NO:64)**DNA sequence of TSC410:**

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
30	gatatccaga	tgacccagtc	tccatccgcc	atgtctgcat	ctgtaggaga	cagagtcacc	120
	atcacttgcc	ggcgagtaga	gagcattagc	aaatatttag	cctgggttca	gcagaaacca	180
	gggaaagttc	ctaagctccg	catccattct	ggatctactt	tgcaatcagg	ggtcccctct	240
	cggttcagtg	gcagtggatc	tgggacagaa	tttactctca	ccatcagcag	cctgcagcct	300
	gaagattttg	caacttatta	ctgtcaacag	catattgaat	acccgtggac	gttcggccaa	360
35	gggaccaagc	tggaatcaa	acgaggtggc	ggagggtctg	gggtggcgg	atccggaggt	420
	ggtggctctc	aggtccagct	ggtacagtct	ggggctgagg	tgaagaagcc	tggggcttca	480
	gtgaaggctc	cctgcaaggc	ttctggatac	acattcactg	actactacat	gcactgggtg	540
	cgacaggccc	ctggacaagg	gcttgagtgg	atgggatatt	ttaatcotta	taatgattat	600
	actagatacg	cacagaagtt	ccagggcaga	gtcaccatga	ccagggcac	gtctatcagc	660
40	acagcctaca	tggagctgag	cagcctgaga	tctgacgata	cggccgtgta	ttactgtgca	720
	agatcggatg	gttactacga	tgctatggac	tactgggtgc	aaggaaccac	agtcaccgtc	780
	tcctcgagtg	agcccaaatc	ttctgacaaa	actcacacat	gcccaccgtg	cccagcact	840
	gaagccgcgg	gtgcaaccgtc	agtcttcttc	ttcccccaaa	aacccaagga	caccctcatg	900
	atctcccgga	ccctgaggtg	cacatgcgtg	gtgggtggag	tgagccacga	agaccctgag	960
45	gtcaagttca	actggtacgt	ggacggcgtg	gaggtgcata	atgccaagac	aaagccgcgg	1020
	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	1080
	tggctgaatg	gcaaggcgta	cgcgtgcgcg	gtctccaaca	aagccctccc	agccccatc	1140
	gagaaaacca	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	caccctgccc	1200
	ccatcccggg	atgagctgac	caagaaccag	gtcagcctga	cctgcctggg	caaaggcttc	1260
50	tatccaagcg	acatcgccgt	ggagtgagg	agcaatgggc	agccggagaa	caactacaag	1320
	accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	1380
	gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1440
	cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtcagaggca	caacaattct	1500
	tcctgaata	caggaactca	gatggcaggt	cattctccga	attctcaggt	ccagctgggtg	1560
55	caatctgggg	ctgaggtgaa	gaagcctggg	tcctcggtga	aggtctcctg	caaggcttct	1620
	ggatatacct	tcagcagatc	tacgatgcac	tgggtgcgac	aggccctgg	acaagggtct	1680
	gagtgatag	gatacattaa	tcctagcagt	gcttatacta	attacaatca	gaaattcaag	1740
	gacagagtc	cgattaccgc	ggacaaatcc	acgagcacag	cctacatgga	gctgagcagc	1800
	ctgagatctg	aggacacggc	cgtgtattac	tgtgcgagac	cccaagtcca	ctatgattac	1860
60	aacgggtttc	cttactgggg	ccaaggaacc	ctgggtcaccg	tctcctcagg	tggaggcggt	1920
	tcaggcggag	gtggatccgg	cgggtggcga	tgggtggcg	gcggatctga	catccagatg	1980
	accagctctc	cttccaccct	gtctgcatct	gtaggagaca	gagtcacccat	gacttgcatg	2040
	gccagctcaa	gtgtaagtta	catgaactgg	tatcagcaga	aaccagggaa	agccccctaag	2100
	agatggattt	atgactcadc	caaactgggt	tctgggggtcc	catcaagggtt	cagcgggcagt	2160

ggatctgga	cagagttcac	tctcaccatc	agcagcctgc	agcctgatga	ttttgcaact	2220
tattactgcc	aacagtggag	togtaaccca	cccactttcg	gcggagggac	caaggtggag	2280
atcaaacggt	cctccagcta	a				2301

(SEQ ID NO:65)

5 Signal sequence is residue 1 to 60

Mature protein sequence of TSC410:

10	DIQMTQSFSA	MSASVGDRTV	ITCRASKSIS	KYLAWFQQKP	GKVPKLRIHS	GSTLQSGVPS	60
	RFSGSGSGTE	FTLTISLQP	EDFATYYCQQ	HIEYPWTFGQ	GTRVETKRGG	GGSGGGSGG	120
	GGSQVQLVQS	GAEVKKPGAS	VKVSCKASGY	TFTDYIMHWV	RQAPQGGLW	MGYFNPNYNDY	180
	TRYAQKFQGR	VTMTRDTSIS	TAYMELSSLR	SDDTAVYYCA	RSDGYDAMD	YWGQGTITVTV	240
	SSSEPKSSDK	THTCPPCPAP	EAAGAPSVFL	FPPKPKDTLM	ISRTPEVTCV	VVDVSHEDPE	300
15	VKFNWYVDGV	EVHNAKTKPR	EEQYNSTYRV	VSVLTVLHQD	WLNGKAYACA	VSNKALPAPI	360
	EKTISKAKGQ	PREPQVYTLF	PSRDELTKNQ	VSLTCLVKGF	YPSDIAVEWE	SNGQFENNYK	420
	TTPPVLDSDG	SFFLYSKLTV	DKSRWQQGNV	FSCSVMHEAL	HNHYTQKSLS	LSPGQRHNS	480
	SLNTGTQMG	HSPNSQVQLV	QSGAEVKKPG	SSVKVSCKAS	GYTFSRSTMH	WVRQAPGQGL	540
	EWIGYINPSS	AYTNYNQKFK	DRVTITADKS	TSTAYMELSS	LRSEDVAVYY	CARPOVHYDY	600
20	NGFPYWGQGT	LVTVSSGGGG	SGGGSGGGG	SGGGSGDIQM	TQSPSTLSAS	VGDRVTMTCS	660
	ASSSVSYMNW	YQQKPGKAPK	RWIYDSSKLA	SGVPSRFSGS	GSSTFTLTI	SSLQPDDEFAT	720
	YYCQWSRNP	PTFGGGTKVE	IKRSSS				746

(SEQ ID NO:66)**25 DNA sequence of TSC411:**

	atggaagcac	cagcgcagct	tctcttctct	ctgtctactct	ggctcccaga	taccaccggt	60
	gatattccaga	tgaccacgtc	tccatccgcc	atgtctgcat	ctgtaggaga	cagagtcacc	120
	atcacttgcc	ggcgagtaaa	gagcattagc	aaatatttag	cctggtttca	gcagaaacca	180
	gggaaggttc	ctaagctccg	catccattct	ggatctactt	tgcaatcagg	ggtcccctct	240
30	cgggttcagtg	gcagtgagtc	tgggacagaa	tttactctca	ccatcagcag	cctgcagcct	300
	gaagattttg	caacttatta	ctgtcaacag	catattgaat	accctgggac	gttcggccaa	360
	gggaccaagg	tggaaatcaa	acgaggtggc	ggagggctctg	gggggtggcg	atccggaggt	420
	ggtggctctc	aggtccagct	ggtacagttc	ggggctgagg	tgaagaagcc	tggggcttca	480
	gtgaaggtct	cctgcaaggc	ttctggatac	acattcactg	actactacat	gcactgggtg	540
35	cgacaggccc	ctggacaagg	gcttgagtg	atgggatatt	ttaatcctta	taatgattat	600
	actagatacg	cacagaagtt	ccagggcaga	gtcaccatga	ccaggacac	gtctatcagc	660
	acagctaca	tggagctgag	cagcctgaga	tctgacgaca	cggccgtgta	ttactgtgca	720
	agatcggatg	gttactacga	tgtctatggc	tactgggtgc	aaggaaccac	agtcaccgtc	780
	tcctcgagtg	agcccaaatc	ttctgacaaa	actcacacat	gccacccgtg	cccagcacct	840
40	gaagccggcg	gtgcaccgtc	agtcttctct	ttcccccaa	aaccaaggga	cacctctatg	900
	atctcccga	cccctgaggt	cacatgcgtg	gtgggtggag	tgagccacga	agaccctgag	960
	gtcaaagttc	actgttagct	ggacggcgtg	gaggtgcata	atgccaaagc	aaagccggcg	1020
	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	1080
	tggctgaatg	gcaaggcgta	cgcgtgctgc	gtctccaaca	aagccctccc	agccccatc	1140
45	gagaaaaacca	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	cacctgccc	1200
	ccatcccggg	atgagctgac	caagaaccag	gtcagcctga	cctgcctggt	caaaggcttc	1260
	tatccaagcg	acatcgccgt	ggagtgggag	agcaattggc	agccggagaa	caactacaag	1320
	accacgcctc	cgtgtctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	1380
	gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1440
50	cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtcagaggca	caacaattct	1500
	tccttgaaata	caggaaactca	gatggcaggt	cattctccga	attctcaggt	ccagctggtg	1560
	caatctgggc	ctgaggtgaa	gaagcctggg	tcctcggtga	aggtctctct	caaggcttct	1620
	ggatatacct	tcagcagatc	tacgatgcac	tgggtgcgac	aggccctgg	acaagggtct	1680
	gagtgatag	gatacattaa	tcctagcagt	gcttatacta	attacaatca	gaaattcaag	1740
55	gacagagtca	cgattaccgc	ggacaaatcc	acgagcacag	cctacatgga	gctgagcagc	1800
	ctgagatctg	aggacacggc	cgtgtattac	tgtgcgagac	cccaagtcca	ctatgattac	1860
	aacgggtttc	cttactgggg	ccaaggaacc	ctggtcaccc	tcctcctcagg	tggaggcggt	1920
	tcaggcgagg	gtggatccgg	cgttgccgga	tcgggtggcg	gcggatctga	catccagatg	1980
	accagctctc	cttccaccct	gtctgcatct	gtaggagaca	gagtcaccat	gacttgcaat	2040
60	gccagctcaa	gtgtaagtta	catgaactgg	tatcagcaga	aaccagggaa	agccccaaag	2100
	agatggattt	atgactcatc	caaactggct	tctgggtctc	catcaagggt	cagcggcagc	2160
	ggatctggga	cagagttcac	tctcaccatc	agcagcctgc	agcctgatga	ttttgcaact	2220
	tattactgcc	aacagtggag	togtaaccca	cccactttcg	gcggagggac	caaggtggag	2280

atcaaacgggt cctccagcta a
(SEQ ID NO:67)
 Signal sequence is residue 1 to 60

2301

5

Mature protein sequence of TSC411:

10	DIQMTQSPSA MSASVGDRTV ITCRASKSIS KYLAWFQQKP GKVPKLRIHS GSTLQSGVPS	60
	RFSGSGSGSTE FTLTISSLQP EDFATYYCQQ HIEYFWTFGQ GTKVEIKRGG GSGGGGSGG	120
	GGSQVQLVQS GAENVKPGAS VKVSCRASGY TFTDYIMHWV RQAPQGGLW MGYNFNPYNDY	180
	TRYAQKFQGR VTMRDTSIS TAYMELSSLR SDDTAVYYCA RSDGYDAMD YWGQGTITVTV	240
	SSSEPKSSDK THTCPPCPAP EAAGAPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE	300
	VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNGKAYACA VSNKALPAPI	360
15	EKTISKAKGQ PREPQVYTLF PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK	420
	TTTPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMEAL HNHYTQKSL SLPGRHNS	480
	SLNTGTQMG HSPNSQVQLV QSGPEVKKPG SSVKVSCKAS GYTFSRSTMH WVRQAPGQGL	540
	EWIGYINPSS AYTNYNQKFK DRVITITADKS TSTAYMELSS LRSEDYAVYY CARPQVHYDY	600
	NGFPYWGQT LVTVSSGGGG SGGGGSGGGG SGGGGSDIQM TQSPSTLSAS VGDRVMTMCS	660
20	ASSSVSYMNW YQQKPGKAPK RWIYDSSKLA SGVPSRFSGS GSGTEFTLTI SSLQPDDEFAT	720
	YYCQWSRNP PTFGGGTKEV IKRSSS	746

(SEQ ID NO:68)

DNA sequence of CAS105:

25	atggaagcac cagcgcagct tctcttctct ctgctactct ggctcccaga taccaccggg	60
	gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt	120
	tcctgtlaagg gctccgggta ctcatctact ggctacaata tgaactgggt gcgccagatg	180
	cccgggaaaag gctctggagt gatgggcaat attgatcctt attatgggtg tactacctac	240
	aaccggaaagt tcaagggcca ggtcactatc tccgcgcaga agtccatcag caccgcctac	300
30	ctgcaatgga gcagcctgaa ggccctcgac accgccatgt attactgtgc acgctcagtc	360
	ggcccttttgc actcctgggg ccaggggcacc ctgggtcactg tctcctctgg ggggtggaggc	420
	tctgggtggcg gtggctctgg cggaggtgga tccgggtggcg gcgcatctgg cgggggtggc	480
	tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc	540
	accctctcct gccaggaag tgaaaatggt tacagctact tagcctggta ccaacagaaa	600
35	cctggccagc ctcttaggct cctcatctat ttgcaaaaa ccttagcaga aggtattcca	660
	gccaggttca gtggcagtg ctccgggaca gacttactc tcaccatcag cagcctagag	720
	cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc	780
	caagggaacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac	840
	acatgcccac cgtgccagc acctgaagcc gcgggtgcac cgtcagttt cctcttcccc	900
40	ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtgggtggg	960
	gacgtgagcc acgaagacc tgaggtcaag ttcaactggg acgtggacgg cgtggagggt	1020
	cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
	gtcctcaccg tctgcacca ggactggctg aatggcaagg catacgcgtg cgcgggtctc	1140
	aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1200
45	gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
	ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
	gggcagccgg agaacaacta caagaccacg cctccgtgc tggactccga cggctccttc	1380
	ttcctctaca gcaagctcac cgtggacaag agcagggtgc agcaggggaa cgtcttctca	1440
	tgctccgtga tgcagtaggc tctgcacaa cactacacgc agaagagcct ctccctgtct	1500
50	ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct	1560
	ccgaattctc aggtccagct ggtggagtct gggggcggag tgggtgcagcc tggggcggta	1620
	ctgaggtctc cctgcaaggc ttctggctac accttacta gatctacgat gcaactgggt	1680
	aggcaggccc cctggacaagg tctggaatgg attggataca ttaatcctag cagtgcctat	1740
	actaattaca atcagaaatt caaggacagg ttcaaatca gcgcagacaa atccaagagc	1800
55	acagccttcc tgcagatgga cagcctgagg cccgaggaca ccggcgtcta tttctgtgca	1860
	cggccccaaag tccactatga ttacaacggg ttctcttact ggggccaagg gactcccgtc	1920
	actgtctcta cgggtggcgg agggctctgg ggtggcggat ccggaggtgg tggctctgca	1980
	caagacatcc agatgaccca gtctccaagc agctctctg caagcgtggg ggacagggtc	2040
	accatgacct gcagtgccag ctcaagtgt aattacatga actggtacca gcagaagccg	2100
60	ggcaaggccc ccaaaagatg gatattatgac tcatccaaac tggcttctgg agtccctgct	2160
	cgcttcagtg gcagtggttc tgggaccgac tataccctca caatcagcag cctgcagccc	2220
	gaagatttgc ccacttatta ctgccagcag tggagtctga acccaccac gttcggaggg	2280
	gggaccaagc tacaaattac atcctccagc taa	2313

(SEQ ID NO:69)

Signal sequence is residue 1 to 60

5 Mature protein sequence of CAS105:

	EVQLVQSGAE VKKPGESLKI SCKGSGYSFT GYNMNVWRQM PGKGLEWMGN IDPYYGGTTY	60
	NRKFKGQVTI SADKSISTAY LQWSSLKASD TAMYYCARSV GPFDSWGQGT LVTVSSGGGG	120
10	SGGGGSGGGG SGGGSGGGG SEIVLTQSPA TLSLSPGERA TLSCRAENV YSYLAWYQQK	180
	PGQAPRLLIY FAKTLAEGIP ARFSGSGSGT DFTLTISSE PEDFAVYQC HHSDNPWTFG	240
	QGTKVEIKSS SEPKSSDKTH TCFPCPAPEA AGAPSVFLFP PKPKDTLMIS RTPEVTCVVV	300
	DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKAYACAVS	360
15	NKALPAPIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN	420
	GQFENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL	480
	PGQRHNNSSL NTGTQAGHS PNSQVQLVES GGGVVQPGRS LRLSCKASGY TFRSTMHWV	540
	RQAPGGGLEW IGYINPSSAY TNYNQKFKDR FTISADKSKS TAFLQMDSLR PEDTGVYFCA	600
	RPQVHYDYNP FPYWGQGTPTV TVSSGGGGSG GGGSGGGGSA QDIQMTQSPS SLSASVGDV	660
20	TMTCSASSSV SYMNWYQQKPK GKAPKRWIYD SSKLASGVPA RFGSGSGGTD YTLTISSSLQ	720
	EDFATYYCQQ WSRNPPTFGG GTKLQITSSS	750

(SEQ ID NO:70)**25 DNA sequence of Anti-CD37 X TSC445:**

	atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggg	60
	gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt	120
	tcctgttaagg gctccgggta ctcattcact ggctacaata tgaactgggt gcgccagatg	180
	cccgggaaaag gctcggagtg gatgggcaat attgatcctt attatgggtg tactacctac	240
30	aaccgggaagt tcaagggcca ggtcactatc tccgcgcaca agtccatcag caccgcctac	300
	ctgcaatgga gcagcctgaa ggccctcggac accgccatgt attactgtgc accctcagtc	360
	ggcccttttcg actcctgggg ccagggcacc ctgggtcactg tctcctcttg gggtggaggc	420
	tctgttgggc gtggctcttg cggaggtgga tccggtgccg gcggatctgg cgggggtggc	480
	tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc	540
35	accctctctt gccaggaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa	600
	cctggccagg ctccataggt cctcatctat tttgcaaaaa ccttagcaga aggtattcca	660
	gccaggttca gtggcagtg ctccgggaca gacttcactc tcaccatcag cagcctagag	720
	cctgaagatt ttgcagttta ttactgtcaa catcattccg ataactccgtg gacattcggc	780
40	caagggaaca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac	840
	acatgcccac cgtgccagc acctgaagcc cggggtgcac cgtcagttt cctcttcccc	900
	ccaaaaccca aggacaccct catgatctcc cggaccctcg aggtcacatg cgtgggtggg	960
	gacgtgagcc acgaagaccc tgaggtcaag ttcaactggg acgtggacgg cgtggaggtg	1020
	cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
45	gtcctcaccc tcttcgacca ggactggctg aatggcaagg catacgcgtg cgcgggtctc	1140
	aacaaaagccc tcccagcccc catcgagaaa accatctcca aagccaaaagg gcagcccccga	1200
	gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
	ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
	gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1380
50	ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca	1440
	tgctccgtga tgcagtggc tctgcacaac cactacacgg agaagagcct ctccctgtct	1500
	ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct	1560
	ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg	1620
	gtgaaggtct cctgcaaggg ttctggatat accttcagca gatctacgat gcactgggtg	1680
55	cgacagggcc ctggacaagg gcttgagtg ataggatata ttaactctag cagtgccttat	1740
	actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc	1800
	acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg	1860
	agaccccaag tccactatga ttacaacggg ttctctact ggggccaaagg aacctgtgtc	1920
	accgtctctt caggtggagg cgggttcaggc ggaggtggat ccggcgggtg cggatcgggt	1980
	ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga	2040
60	gacagagtca ccatgacttg cagtgcacgc tcaagtgtaa gttacatgaa ctggtatcag	2100
	cagaaaccag ggaagacccc taagagatgg atttatgact catccaaact ggcttctggg	2160
	gtcccaccaa ggttcagcgg cagtggatct gggacagagt tcaactctac catcagcagc	2220
	ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccaccact	2280
	ttcggcggag ggaccaaggt ggagatcaaa cggctctcca gctaa	2325

(SEQ ID NO:71)

Signal sequence is residue 1 to 60

5 Mature protein sequence of Anti-CD37 X TSC445:

	EVQLVQSGAE	VKKPGESLKI	SCKGSGYSFT	GYNMNWPVQM	PGKGLEWMGN	IDPYYGGTTY	60
	NRKFKGQVTI	SADKSISTAY	LQWSSLKASD	TAMYYCARSV	GPFDSWGQGT	LVTIVSSGGGG	120
	SGGGGSGGGG	SGGGGSGGGG	SEIVLTQSPA	TLSLSPGERA	TLSCRASENV	YSYLAWYQQK	180
10	PGQAPRLLIY	FAKTLAEGIP	ARFSGSGSGT	DFTLTISSE	PEDFAVYYCQ	HHSDNPWTFG	240
	QGTKVEIKSS	SEPKSSDKTH	TCPPCPAPEA	AGAPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	300
	DVSHEDPEVK	FNWYVDGVEV	HNAKTKPREE	QYNSTYRVVS	VLTVLHQDWL	NGKAYACAVS	360
	NKALPAPIEK	TISKAKGQPR	EPQVYTLPPS	RDELTKNQVS	LTCLVKGFYP	SDIAVEWESN	420
	GQFENNYKTT	PPVLDSGGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTQKSLSL	480
15	PGQRHNSSL	NTGTQMAGHS	PNSQVQLVQS	GPEVKKPGSS	VKVCKASGY	TFSRSTMHV	540
	RQAPGQGLEW	IGYINPSSAY	TNYNQKFKDR	VTITADKSTS	TAYMELSSLR	SEDTAVYYCA	600
	RPQVHYDYN	FPVWGQGTIV	TVSSGGGGSG	GGGSDIQMTQ	SPSTLSASVG		660
	DRVMTTCSAS	SSVSVMWYQ	QKPGKAPKRW	IYDSSKLASG	VPSRFGSGGS	GTEFTLTISS	720
	LQPDDEFATYY	CQQWSRNPPT	FGGGTKVEIK	RSSS			754

20 (SEQ ID NO:72)**DNA sequence of Anti-CD37 X TSC452:**

25	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
	gaggtgcagc	tgtgtgcagtc	tggagcagag	gtgaaaaagc	ccggagagtc	tctgaagatt	120
	tcctgtgaag	gctccgggta	ctcattcact	ggctacaata	tgaactgggt	gcgcagatg	180
	cccggaagag	gcctggagtg	gatgggcaat	attgatcctt	attatgggtg	tactacctac	240
	aaccggaagt	tcaagggcca	ggtcactatc	tccgcgcaca	agtccatcag	caccgcctac	300
30	ctgcaatgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	acgctcagtc	360
	ggccctttcg	actcctgggg	ccagggcacc	ctggctactg	tctcctctgg	gggtggaggg	420
	tctgtgtggc	gtggtctctg	cggaggtgga	tccggtggcg	gcggatctgg	cgggggtggc	480
	tctgaaattg	tgttgacaca	gtctccagcc	accctgtctt	tgtctccagg	cgaaagagcc	540
	accctctcct	gcgcagcaag	tgaatatgtt	tacagctact	tagcctggta	ccaacagaaa	600
35	cctgtgcagg	ctcctaggct	ctcctctat	tttgcaaaaa	ccttagcaga	aggtattcca	660
	gccaggttca	gtggcagtg	ctccgggaca	gacttcactc	tcaccatcag	cagcctagag	720
	cctgaagatt	ttgcagttta	ttactgtcaa	catcattccg	ataatccgtg	gacattccgg	780
	caagggacca	aggtggaaat	caaatcctcg	agtgagccca	aatcttctga	caaaactcac	840
	acatgcccac	cgtgccccagc	acctgaagcc	gcggtgtcac	cgtcagttct	cctcttcccc	900
40	ccaaaaacca	aggacaccct	catgatctcc	cggaccctcg	aggtcacatg	cgtgggtggg	960
	gacgtgagcc	ccgaagaccc	tgagggtcaag	ttcaactggg	acgtggacgg	cgtggaggtg	1020
	cataatgcc	agacaaagcc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtgggtcagc	1080
	gtcctcaccc	tctgcacca	ggactggctg	aatggcaagg	catacggctg	cgcgggtctcc	1140
	aacaaagccc	tcccagcccc	catcgagaaa	accatctcca	aagccaaagg	gcagccccga	1200
45	gaaccacagg	tgtacaccct	gcccccatcc	cgggatgagc	tgaccaagaa	ccaggtcagc	1260
	ctgacctgcc	tgtcaaaagg	cttctatcca	agcgacatcg	ccgtggagtg	ggagagcaat	1320
	gggcagccgg	agaacaacta	caagaccacg	cctcccgctg	tggactccga	cggctccttc	1380
	ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcaggggaa	cgtcttctca	1440
	tgctccgtga	tgcatgaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1500
50	ccgggtcaga	ggcacaacaa	ttcttccctg	aatacaggaa	ctcagatggc	aggtcattct	1560
	ccgaattctc	aggtccagct	ggtggagctc	gggggcggag	tgggtgcagc	tgggcgggtc	1620
	ctgaggctgt	cctgcaaggc	ttctggctac	accttacta	gatctacgat	gcactgggta	1680
	aggcaggccc	ctggacaagg	tctggaatgg	attggataca	ttaatcctag	cagtgccttat	1740
	actaattaca	atcagaaatt	caaggacagg	ttcacaatca	gcgcagacaa	atccaagagc	1800
55	acagccttcc	tgcatgagga	cagcctgagg	cccgaggaca	ccggcgtcta	tttctgtgca	1860
	cggcccccaag	tccactatga	ttacaacggg	tttcttact	ggggccaagg	gactcccgct	1920
	actgtctctc	cgggtggcgg	agggctctgg	ggtggcggat	ccggcgggtg	cggatcgggt	1980
	ggcggcggtg	gatgacctca	tctccttcca	ccctgtctgc	atctgtagga		2040
	gacagagtca	ccatgacttg	cagtggccagc	tcaagtgtaa	gttacatgaa	ctggtatcag	2100
60	cagaaaaccag	ggaagacccc	taagagatgg	atcttatgact	catccaaact	ggcttctggg	2160
	gtcccatcaa	ggttcagcgg	cagtggatct	gggacagagt	tcactctcac	catcagcagc	2220
	ctgcagcctg	atgatttttg	aacttattac	tgccaacagt	ggagtcgtaa	cccacccact	2280
	ttcggcggag	ggaccaaggt	ggagatcaaa	cggctctcca	gctaa		2325

(SEQ ID NO:73)

Signal sequence is residue 1 to 60

5 Mature protein sequence of Anti-CD37 X TSC452:

	EVQLVQSGAE	VKKPGESLKI	SCKGSGYSFT	GYNMNVWRQM	PGKGLEWMGN	IDPYYGGTTY	60
	NRKFKGQVTI	SADKSISTAY	LQWSSSLKASD	TAMYYCARSV	GPFDSWGQGT	LVTIVSSGGGG	120
	SGGGGSGGGG	SGGGGSGGGG	SEIVLTQSPA	TLSLSPGERA	TLSCRASENV	YSYLAWYQQK	180
10	PGQAPRLLIY	FAKTLAEGIP	ARFSGSGSGT	DFTLTISSE	PEDFAVYYCQ	HHSDNPWTFG	240
	QGTKVEIKSS	SEPKSSDKTH	TCPPCPAPEA	AGAPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	300
	DVSHEDPEVK	FNWYVDGVEV	HNAKTKPREE	QYNSTYRVVS	VLTVLHQDWL	NGKAYACAVS	360
	NKALPAPIEK	TISKAKGQPR	EPQVYTLPPS	RDELTKNQVS	LTCLVKGFYP	SDIAVEWESN	420
	GQFENNYKTT	PPVLDSGGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTQKSLSLS	480
15	PGQRHNSSL	NTGTQMAGHS	PNSQVQLVES	GGGVVQPGRS	LRLSCKASGY	TFTRSTMHWV	540
	RQAPGGGLEW	IGYINPSSAY	TNYNQKFKDR	FTISADKSKS	TAFLQMDSLR	PEDTGVYFCA	600
	RPQVHYDYN	FPVWGQGT	TVSSGGGGSG	GGGSDIQMTQ	SPSTLSASVG		660
	DRVMTTCSAS	SSVSVMWYQ	QKPGKAPKRW	IYDSSKLASG	VPSRFGSGGS	GTEFTLTISS	720
	LQPDDEFATYY	CQQWSRNPPT	FGGGTKVEIK	RSSS			754

20 (SEQ ID NO:74)**DNA sequence of Anti-CD37 X TSC453:**

25	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggt	60
	gaggtgcagc	tgtgtgcagtc	tggagcagag	gtgaaaaagc	ccggagagtc	tctgaagatt	120
	tcctgtgaagg	gctccgggtta	ctcatttact	ggctacaata	tgaactgggt	gcgcagatg	180
	cccgggaaag	gcctggagtg	gatgggcaat	attgatcctt	attatgggtg	tactacctac	240
	aaccgggaagt	tcaagggcca	ggtcactatc	tccgcccaga	agtccatcag	caccgcctac	300
30	ctgcaatgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	acgctcagtc	360
	ggcccttttcg	actcctgggg	ccagggcacc	ctggctactg	tctcctcttg	gggtggaggg	420
	tctgttggeg	gtggtctctg	cggaggtgga	tccggtggcg	gcggtctctg	cgggggtggc	480
	tctgaaattg	tgttgacaca	gtctccagcc	accctgtctt	tgtctccagg	cgaagagacc	540
	accctctcct	gcgcagcaag	tgaatatgtt	tacagctact	tagcctggta	ccaacagaaa	600
35	cctggccagg	ctcctaggct	ctcctcttat	tttgcaaaaa	ccttagcaga	aggtattcca	660
	gccaggttca	gtggcagtg	ctccgggaca	gacttcactc	tcaccatcag	cagcctagag	720
	cctgaagatt	ttgcagttta	ttactgtcaa	catcattccg	ataatccgtg	gacattccgg	780
	caagggacca	aggtggaaat	caaatcctcg	agtgagccca	aatcttctga	caaaactcac	840
	acatgcccac	cgtgcccagc	acctgaagcc	gcggtgtcac	cgtcagttct	cctcttcccc	900
40	ccaaaaacca	aggacacctc	catgatctcc	cggaccctcg	aggtcacatg	cgtgggtggg	960
	gacgtgagcc	accgaagacc	tgaggtcaag	ttcaactggg	acgtggacgg	cgtggaggtg	1020
	cataatgcc	agacaaagcc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtgggtcagc	1080
	gtcctcaccc	tctgcacca	ggactggctg	aatggcaagg	catacggctg	cgcggtctcc	1140
	aacaaagccc	tcccagcccc	catcgagaaa	accatctcca	aagccaaagg	gcagccccga	1200
45	gaaccacagg	tgtacacctc	gcccccatcc	cgggatgagc	tgaccaagaa	ccaggtcagc	1260
	ctgacctgcc	tggtcaaaagg	cttctatcca	agcgacatcg	ccgtggagtg	ggagagcaat	1320
	gggcagccgg	agaacaacta	caagaccacg	cctcccgctg	tggactccga	cggctccttc	1380
	ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcaggggaa	cgtcttctca	1440
	tgctccgtga	tgcatgaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1500
50	ccgggtcaga	ggcacaacaa	ttcttccctg	aatacaggaa	ctcagatggc	aggtcattct	1560
	ccgaattctc	aggtccagct	ggtgcaatct	gggcctgagg	tgaagaagcc	tgggtcctcg	1620
	gtgaagggtc	cctgcaaggc	ttctggatat	accttcagca	gatctacgat	gcactgggtg	1680
	cgacaggccc	ctggacaagg	gcttgagtg	ataggataca	ttaatcctag	cagtgtctat	1740
	actaattaca	atcagaaatt	caaggacaga	gtcacgatta	ccgcggacaa	atccacgagc	1800
55	acagcctaca	tggagctgag	cagcctgaga	tctgaggaca	cggcctgtga	ttactgtgcg	1860
	agaccccaag	tccactatga	ttacaacggg	tttcttact	ggggccaagg	aacctgtgtc	1920
	accgtctcct	caggtggagg	cgggttcagg	ggaggtggat	ccggaggtgg	tgggtctgtg	1980
	ggcggcggtg	gatgacctca	gatgacctca	tctccaagca	gcctgtctgc	aagcgtgggg	2040
	gacaggggtc	ccatgacctg	cagtggccagc	tcaagtgtaa	gttacatgaa	ctggtaccag	2100
60	cagaagccgg	gcaaggcccc	caaaagatgg	atcttatgact	catccaaact	ggcttctgga	2160
	gtccctgtct	gcttcagtg	cagtgggtct	gggaccgact	ataccctcac	aatcagcagc	2220
	ctgcagcccg	aagattttcg	cacttattac	tgccagcagt	ggagtcgtaa	cccacccacg	2280
	ttcggagggg	ggaccaagct	acaaattaca	tcctccagct	aa		2322

(SEQ ID NO:75)

Signal sequence is residue 1 to 60

5 Mature protein sequence of Anti-CD37 X TSC453:

	EVQLVQSGAE VKKPGESLKI SCKGSGYSFT GYNMNVWRQM PGKGLEWMGN IDPYYGGTTY	60
	NRKFKGQVTI SADKSISTAY LQWSSLKASD TAMYYCARSV GPFDSWGQGT LVTVSSGGGG	120
10	SGGGGSGGGG SGGGSGGGG SEIVLTQSPA TLSLSPGERA TLSCRAENV YSYLAWYQQK	180
	PGQAPRLLIY FAKTLAEGIP ARFSGSGSGT DFTLTISSE PEDFAVYQC HHSDNPWTFG	240
	QGTKVEIKSS SEPKSSDKTH TCFPCPAPEA AGAPSVFLFP PKPKDTLMIS RTPEVTCVVV	300
	DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKAYACAVS	360
15	NKALPAPIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN	420
	GQFENNYKTT PPVLDSGGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL	480
	FGQRHNSSL NTGTQAGHS PNSQVQLVQS GPEVKKPGSS VKVCKASGY TFSRSTMHWV	540
	RQAPGGGLEW IGYNPSSAY TYNQKFKDR VTITADKSTS TAYMELSSLR SEDTAVYYCA	600
	RPQVHYDNG FPYWGQGLV TVSSGGGGSG GGGSGGGSG GGGSDIQMTQ SPSSLSASVG	660
20	DRVMTCSAS SSVSYMNWYQ QKPGKAPKRW IYDSSKLASG VPARFSGSGS GTDYTLTIS	720
	LQPEDFATYY CQQWSRNPPT FGGGTLKQIT SSS	753

(SEQ ID NO:76)**25 DNA sequence of Anti-CD37 X TSC454:**

	atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt	60
	gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt	120
	tcctgttaagg gctccgggta ctcatctact ggctacaata tgaactgggt gcgccagatg	180
30	cccggaagag gctcggagtg gatgggcaat attgatcctt attatgggtg tactacctac	240
	aaccgggaagt tcaaggggcca ggtcactatc tccgcgcaca agtccatcag caccgcctac	300
	ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc accctcagtc	360
	ggcccttttcg actcctgggg ccaggggcacc ctgggtcactg tctcctcttg gggtggaggc	420
	tctgttgggc gtggctcttg cggaggtgga tccgttgccg gcggatctgg cgggggtggc	480
	tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc	540
35	accctctctt gccaggaag tgaaaatggt tacagctact tagcctggta ccaacagaaa	600
	cctggccagg ctcttaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca	660
	gccaggttca gtggcagtg ctccgggaca gacttcactc tcaccatcag cagcctagag	720
	cctgaagatt ttgcagttta ttactgtcaa catcattccg ataactccgtg gacattcggc	780
40	caagggaaca aggtggaaa caaatcctcg agtgagccca aatcttctga caaaactcac	840
	acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagttt cctcttcccc	900
	ccaaaaccca aggacaccct catgatctcc cggaccctcg aggtcacatg cgtgggtggtg	960
	gacgtgagcc acgaagaccc tgaggtcaag ttcaactggg acgtggacgg cgtggaggtg	1020
	cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
45	gtcctcaccc tcttcgacca ggactggctg aatggcaagg catacgcgtg cgcgggtctc	1140
	aacaaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1200
	gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
	ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
	gggcagccgg agaacaacta caagaccacg cctcccggtg tggactccga cggctccttc	1380
50	ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca	1440
	tgctccgtga tgcagtggc tctgcacaac cactacacgg agaagagcct ctccctgtct	1500
	ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct	1560
	ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg	1620
	gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg	1680
55	cgacagggcc ctggacaagg gcttgagtg ataggatata ttaactctag cagtgcctat	1740
	actaattaca atcagaaatt caaggacaga gtcacgatta ccgaggacaa atccacgagc	1800
	acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg	1860
	agaccccaag tccactatga ttacaacggg ttctcttact ggggccaagg aacctgtgtc	1920
	accgtctctt caggtggagg cgggttcaggc ggaggtggat ccggcggtgg cggatcgggt	1980
	ggcgggcgat ctgacatcca gatgaccag tctccttcca ccctgtctgc atctgtagga	2040
60	gacagagtca ccatgacttg cagtgcacgc tcaagtgtaa gttacatgaa ctgggtatcag	2100
	cagaaaccag ggaagacccc taagagatgg atttatgact catccaaact ggcttctggg	2160
	gtcccaccaa ggttcagcgg cagtggatct gggacagatt tcaactctac catcagcagc	2220
	ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccaccact	2280
	ttcggcggag ggaccaaggt ggagatcaaa cggctctcca gctaa	2325

(SEQ ID NO:77)

Signal sequence is residue 1 to 60

5 Mature protein sequence of Anti-CD37 X TSC454:

	EVQLVQSGAE	VKKPGESLKI	SCKSGSGYSFT	GYNMNVWRQM	PGKGLEWMGN	IDPYYGGTTY	60
	NRKFKGQVTI	SADKSISTAY	LQWSSLKASD	TAMYYCARSV	GPFDSWGQGT	LVTVSSGGGG	120
10	SGGGGSGGGG	SGGGGSGGGG	SEIVLTQSPA	TLSLSPGERA	TLSCRAENV	YSLAWYQQK	180
	PGQAPRLLIY	FAKTLAEGIP	ARFSGSGSGT	DFTLTITSSLE	PEDEAVYYCQ	HHSDNPWTFG	240
	QGTKVEIKSS	SEPKSSDKTH	TCPPCPAPEA	AGAPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	300
	DVSHEDPEVK	FNWYVDGVEV	HNAKTKPREE	QYNSTYRVVS	VLTVLHQDWL	NGKAYACAVS	360
	NKALPAPIEK	TISKAKGQPR	EPQVYTLPPS	RDELTKNQVS	LTCLVKGFYP	SDIAVEWESN	420
15	GQFENNYKTT	PPVLDSGGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTQKSLSL	480
	FGQRHNNSSL	NTGTQMAGHS	PNSQVQLVQS	GPEVKKPGSS	VKVSCKASGY	TFSRSTMHWV	540
	RQAPGGGLEW	IGYINPSSAY	TNYNQKFKDR	VTITADKSTS	TAYMELSSLR	SEDTAVYYCA	600
	RPQVHYDYNG	FPYWGQGTILV	TVSSGGGGSG	GGGSGGGGSG	GGGSDIQMTQ	SPSTLSASVG	660
	DRVMTTCSAS	SSVSVMWYQ	QKPGKAPKRW	IYDSSKLASG	VPSRFSGSGS	GTDFTLTIS	720
20	LQPDDEFATYY	CQQWSRNPPT	FGGGTKVEIK	RSSS			754

(SEQ ID NO:78)**25 DNA sequence of Anti-CD37 X TSC455:**

	atggaagcac	cagcgcagct	tctcttcctc	ctgctactct	ggctcccaga	taccaccggg	60
	gaggtgcagc	tgggtgcagtc	tggagcagag	gtgaaaaagc	ccggagagtc	tctgaagatt	120
	tcctgttaagg	gtcccggtta	ctcattcact	ggctacaata	tgaactgggt	gcgccagatg	180
	cccggaagag	gcctggagtg	gatgggcaat	attgatcctt	attatgggtg	tactacctac	240
30	aaccggaagt	tcaagggcca	ggtcactatc	tcggccgaca	agtccatcag	caccgcctac	300
	ctgcaatgga	gcagccctgaa	ggcctcggac	accgccatgt	attactgtgc	acgctcagtc	360
	ggccctttcg	actcctgggg	ccagggcacc	ctgggtcactg	tctcctcttg	gggtggaggc	420
	tctgttgggg	gtggctcttg	cggaggtgga	tcgggtggcg	gcggatctgg	cgggggtggc	480
	tctgaaattg	tgttgacaca	gtctccagcc	accctgtctt	tgtctccagg	cgaaagagcc	540
35	accctctctt	gccgagcaag	tgaaaatggt	tacagctact	tagcctggta	ccaacagaaa	600
	cctggccagg	ctcctaggtt	cctcatctat	tttgcaaaaa	ccttagcaga	aggtattcca	660
	gccaggttca	gtggcagtg	ctccgggaca	gacttcactc	tcaccatcag	cagcctagag	720
	cctgaagatt	ttgcagttta	ttactgtcaa	catcattccg	ataatccgtg	gacattcggc	780
	caagggaaca	aggtggaaat	caaatcctcg	agtgaagcca	aatcttctga	caaaaactcac	840
40	acatgcccac	ctgtcccagc	acctgaagcc	cggggtgcac	cgtcagttct	cctcttcccc	900
	ccaaaaccca	aggacaccct	catgatctcc	cggaccctcg	aggtcacatg	cgtgggtggtg	960
	gacgtgagcc	acgaagaccc	tgaggtcaag	ttcaactggg	acgtggacgg	cgtggaggtg	1020
	cataatgcca	agacaaagcc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtgggtcagc	1080
	gtcctcaccc	tcttcgacca	ggactggctg	aatggcaagg	catacgcgtg	cgcgggtctcc	1140
45	aacaaaagccc	tcccagcccc	catcgagaaa	accatctcca	aagccaaaagg	gcagcccccga	1200
	gaaccacagg	tgtacaccct	gcccccatcc	cgggatgagc	tgaccaagaa	ccaggtcagc	1260
	ctgacctgcc	tgggtcaaagg	cttctatcca	agcgacatcg	ccgtggagtg	ggagagcaat	1320
	gggcagccgg	agaacaacta	caagaccacg	cctcccgtgc	tggactccga	cggctccttc	1380
	ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcaggggaa	cgtcttctca	1440
50	tgctccgtga	tgcatgagc	tctgcacaac	catacacagg	agaagagcct	ctccctgtct	1500
	ccgggtcaga	ggcacaacaa	ttcttccctg	aatacaggaa	ctcagatggc	aggtcattct	1560
	ccgaattctc	aggtccagct	gggtgcaatct	gggcctgagg	tgaagaagcc	tgggtcctcg	1620
	gtgaaggtct	cctgcaaggc	ttctggatat	accttcagca	gatctacgat	gcactgggtg	1680
	cgacagggcc	ctggacaagg	gcttgagtg	ataggatata	ttaactcctag	cagtgcttat	1740
55	actaattaca	atcagaaaat	caaggacaga	gtcacgatta	ccgcggacaa	atccacgagc	1800
	acagcctaca	tggagctgag	cagcctgaga	tctgaggaca	cggccgtgta	ttactgtgcg	1860
	agaccccaag	ttcactatga	ttacaacggg	tttcttact	ggggccaagg	aaccttggtc	1920
	accgtctcct	caggtggagg	cggttcaggc	ggaggtggat	ccggcggtgg	cggatcgggt	1980
	ggcggcggat	ctgacatcca	gatgaccag	tctccttcca	ccctgtctgc	atctgtagga	2040
	gacagagtca	ccatgacttg	cagtgccagc	tcaagtgtaa	gttcatatga	ctgggtatcag	2100
	cagaaaccag	ggaaaagcccc	taagagatgg	atcttatgact	catccaaact	ggcttctggg	2160
	gtcccaccaa	ggttcagcgg	cagtggtatct	gggacagagt	atactctcac	catcagcagc	2220
	ctgcagcctg	atgatttttg	aaacttattac	tgccaacagt	ggagtcgtaa	cccaccacat	2280
60	ttcggcggag	ggaccaaggt	ggagatcaaa	cggctctcca	gctaa		2325

(SEQ ID NO:79)

Signal sequence is residue 1 to 60

5 Mature protein sequence of Anti-CD37 X TSC455:

	EVQLVQSGAE	VKKPGESLKI	SCKGSGYSFT	GYNMNWRQM	PGKGLEWMGN	IDPYYGGTTY	60
	NRKFKGQVTI	SADKSISTAY	LQWSSLKASD	TAMYYCARSV	GPFDSWGQGT	LVTVSSGGGG	120
	SGGGGSGGGG	SGGGGSGGGG	SEIVLTQSPA	TLSLSPGERA	TLSCRASENV	YSLAWYQQK	180
10	PGQAPRLLIY	FAKTLAEGIP	ARFSGSGSGT	DFTLTISSE	PEDFAVYYCQ	HHSDNPWTFG	240
	QGTKVEIKSS	SEPKSSDKTH	TCPPCPAPEA	AGAPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	300
	DVSHEDPEVK	FNWYVDGVEV	HNAKTKPREE	QYNSTYRVVS	VLTVLHQDWL	NGKAYACAVS	360
	NKALPAPIEK	TISKAKGQPR	EPQVYTLPPS	RDELTKNQVS	LTCLVKGFYP	SDIAVEWESN	420
	GQFENNYKTT	PPVLDSDGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	HYTQKSLSLS	480
15	PGQRHNSSL	NTGTQMAGHS	PNSQVQLVQS	GPEVKKPGSS	VKVCKASGY	TFSRSTMHWV	540
	RQAPGGGLEW	IGYINPSSAY	TNYNQKFKDR	VTITADKSTS	TAYMELSSLR	SEDTAVYYCA	600
	RPQVHYDYNG	FPYWGQGTIV	TVSSGGGGSG	GGGSGGGSGG	GGGSDIQMTQ	SPSTLSASVG	660
	DRVMTMCSAS	SSVSVMWYQ	QKPGKAPKRW	IYDSSKLASG	VPSRFGSGGS	GTEYTLTIS	720
	LQPDDEFATYY	CQQWSRNPP	FGGGTKVEIK	RSSS			754

20 (SEQ ID NO:80)**DNA sequence of Anti-CD37 X TSC456:**

	atggaagcac	cagcgagcgt	tctcttcctc	ctgctactct	ggctcccaga	taccacccgt	60
25	gagggtgcagc	tgggtgcagtc	tggagcagag	gtgaaaaagc	ccggagagtc	tctgaagatt	120
	tctgtgaagg	gctccggtta	ctcattcact	ggctacaata	tgaactgggt	gcgccagatg	180
	cccgggaaag	gcttggagtg	gatgggcaat	attgatcctt	attatgggtg	tactacctac	240
	aaccgggaagt	tcaagggcca	ggtcactatc	tccgcgcaga	agtcctatcag	caccgcctac	300
	ctgcaatgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	acgctcagtc	360
30	ggccctttcg	actcctgggg	ccagggcacc	ctggtcactg	tctcctctgg	gggtggaggc	420
	tctggtggcg	gtggctcttg	cggaggtgga	tccggtggcg	gcggatctgg	cgggggtggc	480
	tctgaaattg	tgttgacaca	gtctccagcc	accctgtctt	tgtctccagg	cgaaagagcc	540
	accctctect	gccgagcaag	tgaaaatggt	tacagctact	tagcctggta	ccaacagaaa	600
	cctggccagg	ctcctaggct	cctcatctat	tttgcaaaaa	ccttagcaga	aggtattcca	660
35	gccaggttca	gtggcagtg	ctccgggaca	gacttcactc	tcaccatcag	cagcctagag	720
	cctgaagatt	ttcgagttaa	ttactgtcaa	catcattcog	ataatccgtg	gacattcggc	780
	caagggaacca	aggtggaaat	caaatcctcg	agttagccca	aatcttctga	caaaaactcac	840
	acatgcccac	cgtgcccagc	acctgaagcc	gcgggtgcac	cgtcagttct	cctcttcccc	900
	ccaaaaccca	aggacaccct	catgatctcc	cggaccctcg	aggtcacatg	cgtgggtggtg	960
40	gacgtgagcc	acgaagaccc	tgaggtcaag	ttcaactggg	acgtggacgg	cgtggagggtg	1020
	cataatgcca	agacaaaagc	gcgggaggag	cagtaacaac	gcacgtaccg	tgtggtcagc	1080
	gtcctacccg	tctgcacca	ggactggctg	aatggcaagg	catacgcgtg	cgcggtctcc	1140
	aacaaaagccc	tcccagcccc	catcgagaaa	accatctcca	aagccaaaagg	gcagccccga	1200
	gaaccacagg	tgtacaccct	gcccccatcc	cgggatgagc	tgaccaagaa	ccagggtcagc	1260
45	ctgacctgcc	tgggtcaaagg	cttctatcca	agcgacatcg	ccgtggagtg	ggagagcaat	1320
	gggcagccgg	agaacaacta	caagaccacg	cctcccgtgc	tggactccga	cggtctcttc	1380
	ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcaggggaa	cgtcttctca	1440
	tgctccgtga	tgcagtaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1500
	ccgggtcaga	ggcacaacaa	ttcttccctg	aatacaggaa	ctcagatggc	aggtcattct	1560
50	ccgaattctc	agggtccagct	gggtgcaatct	gggcctgagg	tgaagaagcc	tgggtcctcg	1620
	gtgaaggctc	cctgcaaggc	ttctggatat	accttcagca	gatctacgat	gcactgggtg	1680
	cgacaggccc	ctggacaagg	gcttgagtgg	ataggatata	ttaatcctag	cagtgcttat	1740
	actaattaca	atcagaaatt	caaggacaga	gtcacgatta	ccgcggacaa	atccacgagc	1800
	acagcctaca	tggagctgag	cagcctgaga	tctgaggaca	cggccgtgta	ttactgtgcg	1860
55	agaccccaag	tccactatga	ttacaacggg	tttccttact	ggggccaagg	aacctctgtc	1920
	accgtctcct	cagggtggagg	cgggttcaggc	ggaggtggat	ccggcggtgg	cggatcgggt	1980
	ggcggcggat	ctgacatcca	gatgacccag	tctccttcca	ccctgtctgc	atctgttagga	2040
	gacagagtca	ccatgacttg	cagtgccagc	tcaagtgtaa	gttacatgaa	ctggatcag	2100
	cagaaaaccag	ggaaaagccc	taagagatgg	atttttgact	catccaaaact	ggcttctggg	2160
60	gtcccatcaa	ggttcagcgg	cagtggtatct	gggacagatt	atactctcac	catcagcagc	2220
	ctgcagcctg	atgatttttg	aacttattac	tgccaacagt	ggagtctgta	cccacccact	2280
	ttcggcggag	ggaccaaggt	ggagatcaaa	cggctctcca	gctaa		2325

(SEQ ID NO:81)

Signal sequence is residue 1 to 60

Mature protein sequence of Anti-CD37 X TSC456:

5 EVQLVQSGAE VKKPGESLKI SCKGSGYSFT GYNMNWVRQM PGKGLEWMGN IDPHYGGTTY 60
 NRKFKGQVTI SADKSISTAY LQWSSLKASD TAMYYCARSV GPFDSWGQGT LVTVSSGGGG 120
 SGGGGSGGGG SGGGGSGGGG SEIVLTQSPA TSLSPGERA TLSCRASENV YSYLAWYQQK 180
 10 PGQAPRLLIY FAKTLAEGIP ARFSGSGSGT DFTLTISSE PEDFAVYYCQ HHSDNPWTFG 240
 QGTVKVEIKSS SEPKSSDKTH TCPPCPAPEA AGAPSVFLFP PKPKDTLMIS RTPEVTCVVV 300
 DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKAYACAVS 360
 NKALPAPIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS LTCLVKGEYF SDIAVEWESN 420
 GQPENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSL 480
 15 PGQRHNSSL NTGTQAGHS PNSQVQLVQS GPEVKKPGSS VKVSKASGY TFSRSTMHWV 540
 RQAPGQGLEW IGYINPSSAY TNYNQKFKDR VTITADKSTS TAYMELSSLR SEDTAVYYCA 600
 RPQVHYDNG FPYWGQGTTLV TVSSGGGGSG GGGSGGGSG GGGSDIQMTQ SPSTLSASVG 660
 DRVTMTCSAS SSVSYMNWYQ QKPGKAPKRW IYDSSKLASG VPSRFGSGSGS GTDYTLTIS 720
 LQPDDEATYY CQQWSRNPT FGGGTVKVEIK RSSS 754

(SEQ ID NO:82)

Protein sequence of TSC455 anti-CD3 scFv

25 QVQLVQSGPEVKKPGSSVKVSKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVTITADK
 STSTAYMELSSLRSED TAVYYCARPQVHYDNGFPYWGQGTTLVTVSSGGGGSGGGSGGGSGGGSDIQMTQS
 PSTLSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKLASGVPSRFGSGSGSGTEYTLTISLQPD
 FATYYCQQWSRNPTFFGGGTVKVEIKRSSS

(SEQ ID NO:83)

Protein sequence of TSC456 anti-CD3 scFv

35 QVQLVQSGPEVKKPGSSVKVSKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVTITADK
 STSTAYMELSSLRSED TAVYYCARPQVHYDNGFPYWGQGTTLVTVSSGGGGSGGGSGGGSGGGSDIQMTQS
 PSTLSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKLASGVPSRFGSGSGSGTDYTLTISLQPD
 FATYYCQQWSRNPTFFGGGTVKVEIKRSSS

(SEQ ID NO:84)

Protein sequence of DRA222 anti-CD3 scFv

45 QVQLVESGGGVVQPGSRSLRLSCKASGYTFTRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRFTISADK
 SKSTAFQMDSLRPEDTG VYFCARPQVHYDNGFPYWGQGTPTVTVSSGGGGSGGGSGGGGSAQDIQMTQSPSS
 LSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKLASGVPARFSGSGSGTDYTLTISLQPEDFAT
 YYCQQWSRNPTFFGGGTVKVEIKRSSS

(SEQ ID NO:85)

Protein sequence of TSC455 and TSC456 variable heavy domain

50 QVQLVQSGPEVKKPGSSVKVSKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVTITADK
 STSTAYMELSSLRSED TAVYYCARPQVHYDNGFPYWGQGTTLVTVSS

(SEQ ID NO:86)

Protein sequence of DRA222 variable heavy domain

55 QVQLVESGGGVVQPGSRSLRLSCKASGYTFTRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRFTISADK
 SKSTAFQMDSLRPEDTG VYFCARPQVHYDNGFPYWGQGTPTVTVSS

(SEQ ID NO:87)

Protein sequence of TSC455 variable light domain

DIQMTQSPSTLSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKSLASGVPSRFSGSG
SGTEYTLTISSLQPDFATYYCQQWSRNPPTFGGGTKVEIKRS

5 (SEQ ID NO:88)

Protein sequence of TSC456 variable light domain

DIQMTQSPSTLSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKSLASGVPSRFSGSG
SGTDYTLTISSLQPDFATYYCQQWSRNPPTFGGGTKVEIKRS

10 (SEQ ID NO:89)

Protein sequence of DRA222 variable light domain

DIQMTQSPSSLSASVGDRVTMTCSASSSVSYMNWYQQKPGKAPKRWIYDSSKSLASGVPARFSGSG
SGTDYTLTISSLQPEDFATYYCQQWSRNPPTFGGGTKLQITS

15 (SEQ ID NO:90)

Cris7 and DRA222 VH CDR1 (Kabat)

RSTMH (SEQ ID NO:91)

20 Cris7 and DRA222 VH CDR2 (Kabat)

YINPSSAYTNYNQKFK (SEQ ID

NO:92)

Cris7 and DRA222 VH CDR3 (Kabat)

QVHYDYNNGFPY (SEQ ID NO:93)

Cris7 and DRA222 VL CDR1 (Kabat)

SASSSVSYMN (SEQ ID NO:94)

Cris7 and DRA222 VL CDR2 (Kabat)

DSSKSLAS (SEQ ID NO:95)

25 Cris7 and DRA222 VL CDR3 (Kabat)

QQWSRNPPT (SEQ ID NO:96)

Cris7 and DRA222 VH CDR1 (IMGT)

GYTFTRST (SEQ ID NO:199)

Cris7 and DRA222 VH CDR2 (IMGT)

INPSSAYT (SEQ ID NO:200)

Cris7 and DRA222 VH CDR3 (IMGT)

ARPQVHYDYNNGFPY (SEQ ID

30 NO:201)

Cris7 and DRA222 VL CDR1 (IMGT)

ASSSVSY (SEQ ID NO:202)

Cris7 and DRA222 VL CDR2 (IMGT)

DSS (SEQ ID NO:203)

Cris7 and DRA222 VL CDR3 (IMGT)

QQWSRNPPT (SEQ ID NO:204)

35

DNA sequence of ROR133:

atggaagcaccagcgcagcttctctctctgctactctggctcccagataccaccggtgacatccagatgaccagtgccc
cctcctcctgtccgcctcgtggcgaccgggtgacctcaactgccaggcctcccagtgccatgactccaacctggcct
gggtccagcagaagcccggaagcccccaagctgctgatctaccgggctccaacctggcctccggcggtgccctccc
40 gttctccggctccggctccggcaccgacttcacctgacctctcctcctgcagcccaggagctggccacctactactg
cctggcgcggtggcgccgtgtcctaccggacctctcctggcgggcgccaccaaggtggagatcaagggtggaggcg
gttcaggcggaggtggatccggcggtggcggtccgggtggcgggcgatctgaggtgcagctggtggagtccggcggc
ggcctggtgcagcccggcggtccctgctgctgcaccgcctccggctccgacatcaacgactacccatctcctg
ggtgcggcaggccccggcaaggcgctggagtggatcggttcacatccggcggtccacctggtacgcctcctgg
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 (SEQ ID NO:97)

Mature protein sequence of ROR133:

diqmtqspsslsasvgrvtineqasqidsnlawfqkpgkppklliyasnlsgvpsrfsfsgsgtdftltisslqpedvatyyclggv
 gavsyrtsfgggtkveikggggsgggsgggsgggsgggsgggsevlvesggglvqpgrslrlsctasgsdindypiswvrqapgkglewigf
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 20 agapsvflfppkpkdltlmisrtpetvrvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvsvltvlhqdwlngkeyk
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 ssgggsgggsgggsgggsgaqqdiqmtqspsslsasvgrvtmtcsasssvsynmwyqqkpgkapkrwiydssklasgvparfsgsgs
 25 gtdytlitisslqpedfatyyccqwsrnpptfgggtklqitss
 (SEQ ID NO:98)

DNA sequence of ROR193:

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 10 aaccacccacttctggcgagggaccaaggtggagatcaaacggtcctccagctaa
 (SEQ ID NO:99)

Mature protein sequence of ROR193:

Diqmtqspsslsasvdrvtnincqasqsidsnlawfqqkpgkppklliyrasnlsgvpsrfsrgsgsgtdftlisslqpedvatyyclgg
 15 vgavsyrtsfgggtkveikggggsgggsgggsgggsgggseqlvsgggglvqpgsrslrscstasgsdindypiswvrqapgkglewi
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 rfsgsgsgteytlisslqpdffatyycqqrwnpftfgggtkveikrsss
 (SEQ ID NO:100)

DNA sequence of ROR134:

atggaagcaccagcgcagcttctcttctcctgctactctggctcccagataccaccgggtgacatccagatgacccagtcctccctcctcctg
 tccgctcctcgtggcgaccgggtgacatcaactgccaggcctccagtcctcgaactcgaactcgaactcgaactcgaactcgaactcga
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 5 caccacgttcggagggggaccaagctacaaattacatctccagctaa
 (SEQ ID NO:101)

Mature protein sequence of ROR134:

Diqmtqspsslsasvgrvtincqasqsidsnlawfqkpgkppklliyrasnlasgvpsrfsrgsgsgtdftltisslqpedvatyyclgg
 vgavsyrtsfgggtkveikggggsgggsgggsgggsevgqlvesggglvqpgslrlscasgsdindypiswvrqapgkglewi
 gfinssgstwyadsvkgrftisrhsskntlylqmnsdraedtavyfcargystyygdfniwgqgtlvtvssepksdkthtccppc
 15 aagapsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvsvltvlhqdwlngkey
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 (SEQ ID NO:102)

DNA sequence of ROR189:

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 35 aaaccaaggacacctcatgatctcccgacccctgaggtcatatcggtggtggtgacgtgagccacgaagacctgaggtcaagttc
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5 (SEQ ID NO:103)

10 diqmtqspsslsasvgrvtincasqsidsnlawfqkpgkppklliyrasnlasgvpsrfssgsgsgtdftltisslqpedvatyyclggv
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20 DNA sequence of ROR154:

20 **DNA sequence of ROR154:**
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(SEQ ID NO:105)

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15

20

40

45

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5 ssgtdytltisslqpedfatyycqqwsrnpptfgggtklqitss
(SEQ ID NO:110)

DNA sequence of ROR186:

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 (SEQ ID NO:111)

Mature protein sequence of ROR186:

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 aagapsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvsvltvlhqdwlngkey
 35 kcavsnkalpapiektiskakgqprepvytlppsrdeltknqvsllclvkgfypsdiavewesngqpennyktpvldsdgsfflys
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 40 (SEQ ID NO:112)

DNA sequence of ROR181:

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 (SEQ ID NO:113)

30

Mature protein sequence of ROR181:

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 finsggstwyadsvkgrftisrhsskntlylqmnslraedtavvfargystyrdfniwgqgtlvtssepkssdkthtppcpapeaa
 35 gapsvflfpkpkdltlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvsvltvlhqdwlngkeykc
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 40 gtdytlitisslqpedfatyyccqqwsrnpptfgggtklqitsss
 (SEQ ID NO:114)

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Mature protein sequence of ROR191:

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127

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[illegible]

128

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Chimeric bispecific anti-CD123 (VHVL) x anti-CD3 (TSC456) scFv-Fc-scFv

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DNA sequence of TSC471:

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Diqmtqspsslsasvgdrvtincqasqsidsnlawfqkpgqppklliyrasnlasgvpdrfsgsgsgtdftltissleaedvatyyclgg
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5 **DNA sequence of TSC266:**

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10 gaaatcaaacgaggtggcgagggtgtctgggggtggcggtatccggaggtggtgggtctctcaggtccagctggtacagtctggggctgaggt
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25 ttaaggacaggttcacaatcagcgcagacaaatccaagagcacagccttctgcagatggacagcctgaggcccaggacacgggct
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30 ctgcagcccgaagatttgcacatttactgcccagcagtggaagtctgaaccacccacgttcggaggggggaccaagctacaaattacat
cctccagctaa (SEQ ID NO:209)

Proten sequence of TSC266:

35 Diqmtqspamsasvgrvttitcrasksiskeylawfqkpgkvpklrihsgstlqsgvpsrfsfgsgsgteftltisslqpedfatyycqqh
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DNA sequence of ROR206:

45 atggaagcaccagcgcagcttctctcctctgctactctggctcccagataccaccgggtgacatccagatgaccagtgccccctcctcctg
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Protein sequence of ROR206:

MEAPAQLLFLLLLWLPDITGDIQMTQSPSSLSASVGDRTVINCQASQSIDSNLAWFQQKP
 GKPPKLLIYRASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLGGVGAVSYRTSF
 GGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSLRLSCTASGSDI
 30 NDYPITWVRQAPGKGLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
 DTAVYYCARGYSTYYRDFNIWGQGLTVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL
 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
 35 QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVESGGGV
 VQPGRSLRLSCKASGYTFTRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRFTI
 SADKSKSTAFLQMDSLRLPEDTGVYFCARPQVHYDYNFGPYWGQGTPTVTVSSGGGGSG
 GGGSGGGGSAQDIQMTQSPSSLSASVGDRTVMTCSASSSVSYMNWYQQKPGKAPKRWI
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 40 SS (SEQ ID NO:212)

DNA sequence of ROR207:

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 45 aagcccccaagctgctgatctaccgggctccaacctggcctcggcgtgcccctccgggttctcggctcgggtcctccggcaccgacttca
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 acattaatcttagcagtgcttatactaattacaatcagaatcaaggacagagtcacgattaccgcggaacaaatccacgagcacagcctaca
 tggagctgagcagcctgagatctgaggacacggcggtgtattactgtgcgagacccccaaagtcactatgattacaacgggttcttactgg
 ggccaaggaaacctggtacccgtctcctcaggtggagggcggttcaggcgagggtggatccggcggtggcggtatcggtggcgcggtat
 ctgacatccagatgaccagctctctccacccctgctgcatctgtaggagacagagtcaccatgactgtagtccagctcaagtgtaa
 20 acatgaactggtatcagcagaaaccagggaagccctaaagagatggatttatgactcatcaaaactgcttctgggtgctccatcaaggttc
 agcggcagtggtatctgggacagattatactctcaccatcagcagcctgcagcctgatgatttgaacttattactgccaacagtggagtcgt
 aaccacccacttccggcgaggggaccaagggtggagatcaaacggtcctccagc (SEQ ID NO:213)

Protein sequence of ROR207:

25 MEAPAQLLLFLLLWLPDITGDIQMTQSPSSLSASVGDRVITNCQASQSIDSNLAWFQQKP
 GKPPKLLIYRASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLGGVGAVSYRTSF
 GGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSLRLSCTASGSDI
 NDYPITWVRQAPGKGLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
 DTAVYYCARGYSTYYRDFNIWGQGLTVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
 30 FPPKPKDITLMISRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL
 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVQSGPEV
 KKPSSSVKVSCKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRV
 35 ITADKSTSTAYMELSSLRSEDTAVYYCARPQVHYDYNFPYWGQGLTVTVSSGGGGSG
 GGGSGGGGSGGGGSDIQTQSPSTLSASVGDRVITMTCASSSSVSYMNWYQQKPKGAP
 KRWIYDSSKLASGVPSRFSGSGSGTDYTLTISSLQPDFAFYQCQWSRNPPTFGGGTKV
 EIKRSSS (SEQ ID NO:214)

DNA sequence of ROR208:

40 atggaagcaccagcgcagcttctctctctctgctactctggtccagataccaccggtgacatccagatgacccagtcctccctcctcctg
 tccgctcccggtggcgacccgggtgacatcaactgccaggcctccagtcctcagactccaacctggcctggttccagcagaagcccggc
 cagcccccaagctgctgatctaccgggctccaacctggcctccggcggtgcccagccggttctccggtcctgggtcctggcaccgacttc
 accctgacatctctcctggaggcgaggacgtggccacctactactgctggggcggtggtggcgccgtgtctaccggacctccttc
 45 ggcggcgccaccaaggtggagatcaagggtggaggcggttcaggcgagggtggatccggcggtggtgggtcctgggtggcgcggtatc
 tgagggtcagctggtggagtccggcgggcggtggtgagcccggtcctgctgctgacccgctccgggtcctgacatca

acgactaccccatcaactgggtgcggcaggccccggccagggcctggagtggatcggcttcatcaactccggcggtccacctggtac
 gctcctcgggtgaaggccgggttcacatctccgggacgactccaagtcacatgcctacctgcagatgaactccctgaagaccgaggac
 accgcctgtactattgcgccccgggctactccacctactaccgggacttcaacatctggggccagggcaccctggtagcctgtctcga
 gtgagcccaatcttctgacaaaactcacatgcccaccgtgcccagcacctgaagccgcgggtgcacccgtcagttctcttccccca
 5 aaaccaaggacaccctcatgatctcccgaccctgaggtcacatgcgtgggtggagcgtgagccacgaagaccctgaggtcaagttc
 aactggtagcgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcg
 tectaccgtcctgcaccaggactggctgaatggcaaggatacaagtgccggtctccaacaaagccctccagcccccatcgagaaaa
 ccatctccaaagccaaaggcagccccgagaaccacaggtgtacaccctgcccccatcccggtgatgagctgaccaagaaccaggtcag
 cctgacctgcctggtaaaaggcttctatccaagcgacatgcctgggagtgaggagcaatgggcagccggagaacaactacaagacca
 10 cgcctccgtgctggactccgacggctccttctctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgttctc
 atgctccgtgatgcatgaggtctctgcacaaccactacacgcagaagagcctctccctgtctcgggttctgggtggaggcgggttcaggcgga
 ggtggctccggcggtgctggatgcgggctctcaggtccagctgggtggagtctggggcgaggagtggtgagcctggcggtcactga
 ggctgtcctgcaaggcttctggctacaccttactagatctacgatgcactgggtgaaggcaggccccctggacaaggcttggaatggattgga
 tacattaatcctagcagtgcttatactaattacaatcagaattcaaggacaggttcacaatcagcgcagacaaatccaagagcacagccttc
 15 ctgcagatggacagcctgaggccccgaggacaccggcgtctatttctgtgcacggcccccaagtccactatgattacaacgggttctctactg
 gggccaagggaactccgtcactgtctctagcgggtggcgagggtctgggggtggcggtatccggagggtggtgctctgcacaagacatcc
 agatgaccagcttccaagcagcctgtctgcaagcgtgggggacaggggtaccatgacctgcagtgccagctcaagtgttaagtacatga
 actggtaccagcagaagccgggcaaggcccccaaaagatggattatgactcatccaaactggcttctggagtccctgtctcgttcagtgg
 cagtgggtctgggaccgactataccctcacaatcagcagcctgcagccgaagatttcgccacttattactgcagcagtggtgagtcgtaacc
 20 caccacgttcggaggggggaccaagctacaaattacatctccagc (SEQ ID NO:215)

Protein sequence of ROR208:

MEAPAQLFLLLLWLPDTTGDIMQTSPLSLASVGDRTINCQASQSIDSNLAWFQQKP
 GQPPKLLIYRASNLASGVDRFSGSGSGTDFTLTISSLEAEDVATYYCLGGVGAVSRTS
 25 FGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSLRLSCTASGSDI
 NDYPITWVRQAPGQGLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
 DTAIVYYCARGYSTYYRDFNIWGQGLTVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
 FPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL
 30 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVESGGGV
 VQGRSLRLSCKASGYTFTRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRFTI
 SADKSKSTAFLQMDSLRPEDTGVYFCARPQVHYDNGFPYWGQGTPTVTVSSGGGGSG
 GGGSGGGGSAQDIQMTQSPSSLSASVGDRTMTCSASSSVSYMNWYQQKPGKAPKRWI
 35 YDSSKLASGVPARFSGSGSGTDYTLTISSLQPEDFATYYCQQWSRNPPTFGGGTKLQITS
 SS (SEQ ID NO:216)

DNA sequence of ROR209:

atggaagcaccagcgcagcttcttctcctcgtctactctggctccagataaccaccgtgacatccagatgacccagtcctccctcctcctg
 40 tccgcctcctggtggcgaccgggtgaccatcaactgccaggcctccagtcacatgcactccaactggcctggttcagcagaagcccggc
 cagcccccaagctgctgactaccgggctcccaactggcctccggcgtgcccagccggtctcggctccggctccggcaccgacttc
 accctgaccatctcctccctggaggccgaggacgtggccacctactactgctggcgccgctggggcgccgtgtctaccggacctccttc
 ggcggcgccaccaaggtggagatcaagggtggaggcgggttcaggcggaggtggatccggcggtggcggtcctgggtggcgcggtatc
 tgagggtcagctggtggagtcggcgggcgtggtgcagcccggcgggtcctcggtgctgtctgcaccgctccggctccgacatca
 45 acgactaccccatcaactgggtgcggcaggccccggccagggcctggagtggatcggcttcatcaactccggcggtccacctggtac
 gcctcctgggtgaaggccgggttcacatctccgggacgactccaagtcacatgcctacctgcagatgaactccctgaagaccgaggac

accgcegtgtactattgcgcccggggctactccactactaccgggacttcaacatctggggccagggcacccctggtgaccgtgtcctcga
gtgagcccaaatcttctgacaaaactcacacatgccaccgtgccagcacctgaagccggggtgcaccgtcagttcttcttccccca
aaacccaaggacacccctcatgatctcccgaccctgagggtcacatgcgtgggtgggacgtgagccacgaagacccctgagggtcaagttc
aactggtagcgtggacggcggtggagggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtgtcagcg
5 tectaccgtcctgcaccaggactggctgaatggcaaggatacaagtgcgcggtctccaacaaagccctccagcccccatcgagaaaa
ccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccccatccgggatgagctgaccaagaaccagggtcag
cctgacctgectgggtcaaaaggcttctatccaagcgacatgcggtggagtgaggagagcaatgggcagccgggagaacaactacaagacca
cgctcccggtgctggactccgaaggctccttctcctctacagcaagctaccgtggacaagagcaggtggcagcaggggaacgttctc
atgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtctggtggagcggttcaggcgga
10 ggtggctccggcggtggcggtatgcggggctctcaggtccagctggtgcaatctggcctgaggtgaagaagcctgggtcctcggtgaa
ggtctcctgcaaggcttctgcatataccttcagcagatctacgatgcactgggtgcagcagccctggacaagggtgagtgataggat
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tgagctgagcagcctgagatctgaggacacggcggtgtattactgtgcgagaccccaagtcactatgattacaacgggttcttactgg
ggcgaaggaaacctgggtaccgtctcctcaggtggagggcggttcaggcgaggtggatccggcggtggcggtatgggtggcgcggt
15 ctgacatccagatgaccagctctcctccacccctgtctgcactctgtaggagacagagtcaccatgactgagtgccagctcaagtgaagt
acatgaactggatcagcagaaaccagggaaggccccctaaagatggattatgactcatccaaactggcttctgggggtcccatcaagggtc
agcggcagtggtgctgggacagattatactctaccatcagcagcctgcagcctgatgatttgcacttattactgccaacagtggagtcgt
aaccacccacttctggcgaggaggaccaagggtggagatcaaacggctcctccagc (SEQ ID NO:217)

Protein sequence of ROR209:

MEAPAQLLFLLLLWLPDITGDIQMTQSPSSLSASVGDRTVINCQASQSIDSNLAWFQQKP
GQPPKLLIYRASNLASGVPDRFSGSGSGTDFTLTISLSLEAEDVATYYCLGGVGAVSYRTS
FGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSRLSCTASGSDI
NDYPITWVRQAPGQGLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
25 DTAVYYCARGYSTYYRDFNIWGQGLVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
FPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVQSGPEV
30 KKPSSSVKVSCKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVT
ITADKSTSTAYMELSSLRSEDTAVYYCARPQVHYDYNQFPYWGQGLVTVSSGGGGSG
GGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRTVMTCSASSSVSYMNWYQQKPGKAP
KRWIYDSSKLASGVPSRFSGSGSGTDYTLTISLQPDDEATYYCQQWSRNPPTFGGGTKV
EIKRSSS (SEQ ID NO:218)

DNA sequence of ROR231:

atggaggcaccgcgccagctgctgttctgtgtgctgtgtggctccctgataccaccggagacatccagatgacccaatccccctctagtctct
ccgctagcgtcgagaccgcgtgaccatcaattgtcaagcatctcagagtattgacagcaatctcgctgtttcagcagaagccaggaaa
gccaccaagctcctgattatagggttagcaacctggcttctgtgtccctagtaggttcagcggctctgggagtggtgcacagacttcacct
40 gaccattagtagtctgcagcccgaagatgtcgtacctaactgctcggaggagtggtgcccgttctatcgacctaattggagtggtgc
accaaagtggagatcaaaagggtgtggcggtccgggggtggcggtcagggggggagggtctggaggcggtggtatcagaagtca
gctgtgtggaatctggaggaggtctgtgtgcagccaggcaggtccctccggctgagctgcaactgcatccggtctgacattaatgactacct
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aaggacgcttcacaattagtagagcagactctaagtctatcgcatatctgcagatgaatagcttgaagacagaggacaccccggtgtactatt
45 gtgcaagaggatactccacttactacgcgatttcaatatctggggccagggaacctggtgacagtgtctcagagtggcccaaatcttctg
acaaaactcacacatgccaccgtgccagcacctgaagccgcggtgacccgtcagttcttcttcccccaaaacccaaggacacc

5 tcattgatctcccgaccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttaactggtacgtggacg
 gctgtgaggtgcataatgccaagacaaagccgaggaggagcagtaacagcacgtaccgtgtggtcagcgtctcaccgtctgcac
 caggactggctgaatggcaaggaaatacaagtgcgcggtctccaacaaagccctccagccccatcgagaaaacctctccaaagccaa
 agggcagocccgagaaccaaggtgtacacctgccccatcccggtatgagctgaccaagaaccaggtcagcctgacctgctgtggtc
 10 aaaggcttctatccaagcgacatgcctgtgagtgaggagagcaatgggcagccggagaaactacaagaccagcctcccggtgctgg
 actccgacggctccttctctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgtccgtgatgcat
 gaggtctctgcacaaccactacacgcagaagagcctctcctgtctccgggttccggaggcgggcggtccggcgggcgggcagcggc
 ggcgggcggcagcccggtatcccggtgagctggtgagctgtggtcctgaggtgaaaaagcctggctccagcgtgaagggtgctctgcaa
 ggccagcgggatacacttttagccgggtccaccatgcattgggtgagcagcgtcctggacagggcctggagtgatcggtcatcaaccc
 15 cagcagcgttataccaactacaatcagaagttaaggaccgggtgaccatcaccggcgaataagtcaccagcaccgctcatgagct
 gtccagcctgaggagcagagatacccggtgtactattgcgccccggccccagggtccattacgactacaacggcttccctattggggcca
 gggaaccctggtgacctgttccagcgggagggcgggcagcggcgggcgggcggcagcggcgggaggagcagcggcgggaggaggctc
 cgacattcagatgaccagtcacctccacctgtccgctagcgtggcgatcggtgacctgacctgacgcgcagcagctccgtgtc
 ctacatgaactggtaccagcagaagcccggaaggctcccaagagtggtattacgactccagcaagctggcctgtggtgtcccgagcag
 20 gttctctggtagcggcagcggcacagactacacctgacctctcctccctgagcccgacgatttcgccactactattgccagcagtggt
 cccggaatccccctaccttggcgggcggcaccaaggtggagatcaagaggagctccagc (SEQ ID NO:219)

Protein sequence of ROR231:

20 MEAPAQLLFLLLLWLPDITGDIQMTQSPSSLSASVGDRTVINCQASQSIDSNLAWFQQKP
 GKPPKLLIYRASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLGGVGAVSYRTSF
 GGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSLRLSCTASGSDI
 NDYPITWVRQAPGKLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
 DTA VYYCARGYSTYYRDFNIWQGGLTVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
 25 FPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL T
 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVQSGPEV
 KKP GSSVKVSKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVT
 ITADKSTSTAYMELSSLRSEDTA VYYCARPQVHYDYNQFPYWGQGLTVTVSSGGGGSG
 30 GGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRTVMTCSASSSVSYMNWYQQKPKGAP
 KRWIYDSSKLASGVPSRFSGSGSGTDYTLTISSLQPDDFATYYCQQWSRNPPTFGGGTKV
 EIKRSSS (SEQ ID NO:220)

DNA sequence of ROR233:

35 atggaggctcccgtcagctgctgttctcctgctgctctggtgctcccgacaccacaggcgacatccagatgaccagtcctcctcct
 gtccgctagcgtggcgatagggtgacctcaactgccaggcctccagtcattgactccaatctggcctggttccagcagaagccggg
 acagcccccaagctgctgatttacagggectccaacctggtctccggcgtgctgacaggttctccggatccggcagcggcaccgacttc
 accctgacctatctcctcctggaggcggaggtgtcgccacctactactgtctggcgggcgtggcgctgtgagctatcggaacctcttcg
 gcgggcgccaccaaggtggagatcaaggcgggcgggcagcggcgggcgggcagcggcgggcgggaggtcctggcgggcgggcgggc
 40 agcgaggtgcaagctggtgaaagcgaggaggcctggtgagcctggaaggtccctgaggtgtctgtcacagccagcggctccgac
 atcaacgactacccatcacctgggtgaggcaggctcctggccaggcctggaatggatcggtttatcaacagcggcgggcagcacctg
 gtatgcttctgggtgaaggggccggttaccattagcagggacgactccaagtccattgacctgagatgaacctccctgaagaccgag
 gacaccgcccgttactactgcgccaggggctacagcacctattaccgggactttaacctgtggggcaggggcacactgtgacacctgtcct
 cgagtgtgacccaaatcttctgacaaaactcacatgcccaccgtgcccagacactgaagccgcggtgacacgtcagcttcttctccc
 45 cccaaaacccaaggacacctcatgatctcccgacccctgaggtcacatgcgtggtggtggacgtgagccacgaagacctgaggtca
 agttcaactggtacgtggacggcggtggaggtgcataatgccaagacaaagccgaggaggagcagtaacagcacgtaccgtgtggtc

agcgtcctcaccgtcctgcaccaggactggctgaatggcaaggaatacaagtgcgcggtctccaacaaagccctcccagccccatcga
 gaaaaccatctccaaagccaaaggcagccccgagaaccacaggtgtacacctgccccatccccgggatgagctgaccaagaaccag
 gtcagcctgacctgcctggctcaaggcttctatccaagcgacatcgccgtggagtgaggagagcaatgggcagccggagaaactataa
 gaccaagcctcccgctgctggactccgacggctccttctctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgt
 5 cttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtccggaggcggcgctcc
 ggcgggcggcagcgccggcgggcagccccggatcccaggtgcagctggtgcagctggtcctgaggtgaaaaagcctggctcc
 agcgtgaagggtgctctgcaaggccagcgggatacacctttagccgggtccacatgcattgggtgaggcaggtcctggacagggcctgga
 gtggatcggctacatcaaccccagcagcgttataccaactacaatcagaaggttaaggaccgggtgaccatcacgcggataagtccacc
 agcaccgcctacatggagctgtccagcctgaggagcgaggataccgcctgtactattgcgccggccccaggtccattacgactacaac
 10 ggcttccctattggggccagggaacctgtgtaccgtgtccagcggaggcgggcggcagcgggcgggcggcagcgggcgaggagg
 cagcgggcgaggaggctccgacattcagatgaccagtcctccctccacctgtccgtagcgtggcgatcggggtgacctgacctgca
 gcgcagcagctccgtgtcctacatgaactggtagcagcagaagcccggaaggctccaagaggtgattacgactccagcaagctg
 gcctctggtgtccccagcaggttctctggtagcggcagcggcacagactacacctgacctctctccctgcagcccgacgatttcgcca
 cctactattgccagcagtggtgccgggaatccccctacctttggcgggcgccaccaagggtggagatcaagaggagctccagc (SEQ ID
 15 NO:221)

Protein sequence of ROR233:

MEAPAQLLFLLLLWLPDITGDIQMTQSPSSLSASVGDRVITNCQASQSIDSNLAWFQQKP
 GQPPKLLIYRASNLASGVPDRFSGSGSGTDFTLTISLEAEDVATYYCLGGVGAVSYRTS
 20 FGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGRSLRLSCTASGSDI
 NDYPITWVRQAPGQGLEWIGFINSGGSTWYASWVKGRFTISRDDSKSIAYLQMNSLKTE
 DTAIVYYCARGYSTYYRDFNIWGQGTLVTVSSSEPKSSDKTHTCPPCPAPEAAGAPSVFL
 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
 25 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSGGGGSPGSQVQLVQSGPEV
 KKPSSSVKVSCKASGYTFSRSTMHWVRQAPGQGLEWIGYINPSSAYTNYNQKFKDRVIT
 ITADKSTSTAYMELSSLRSEDTAIVYYCARPQVHYDYNQFPYWGQGLVTVSSGGGGSG
 GGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVITMTCASSSVSVMNWFYQQKPKGAP
 30 KRWIYDSSKLASGVPSRFSGSGSGTDYTLTISSLQPDDEATYYCQQWSRNPPTFGGGTKV
 EIKRSSS (SEQ ID NO:222)

Table 15. Summary of SEQ ID NOs

Designation	Description	DNA SEQ ID NO	Protein SEQ ID NO
TSC311 or TSC312	Fc DRA222	1	2
TSC313	Fc H7L1	3	4
TSC314	Fc H7L4	5	6
TSC315	Fc H7L5	7	8
TSC316	Fc H8L1	9	10
TSC317	Fc H8L4	11	12
TSC318	Fc H8L5	13	14
TSC319	Fc H9L1	15	16
TSC320	Fc H9L4	17	18
TSC321	Fc H9L5	19	20
TSC322	Fc H10L1	21	22
TSC323	Fc H10L4	23	24
TSC324	Fc H10L5	25	26
TSC334	Fc H7L6	27	28
TSC335	Fc H7L7	29	30
TSC336	Fc H7L8	31	32
TSC337	Fc H8L6	33	34
TSC338	Fc H8L7	35	36
TSC339	Fc H8L8	37	38
TSC340	Fc H10L6	39	40
TSC341	Fc H10L7	41	42
TSC342	Fc H10L8	43	44
TSC370	TSC342 G27Y	45	46
TSC371	TSC342 M53I	47	48
TSC372	TSC342 I21M	49	50
TSC390	TSC370 A9P	51	52
TSC391	TSC370 A9P M53I	53	54
TSC392	TSC370 A9P I21M	55	56
TSC393	TSC370 M53I I21M	57	58
TSC394	TSC370 A9P M53I I21M	59	60
TSC408	Anti-PSMA X TSC391	61	62
TSC409	Anti-PSMA X TSC392	63	64
TSC410	Anti-PSMA X TSC393	65	66
TSC411	Anti-PSMA X TSC394	67	68
TSC471	Anti-PSMA X TSC456	205	206
TSC266	Anti-PSMA X DRA222 (huVL-VH 107-1A4 scFv-Fc-DRA222 scFv)	209	210
CAS105	Anti-CD37 X DRA222	69	70
Anti-CD37 X TSC445	Anti-CD37 X TSC394	71	72
Anti-CD37 X TSC452	Anti-CD37 X (TSC394 VL + DRA222 VH)	73	74
Anti-CD37 X	Anti-CD37 X (TSC394 VH + DRA222 VL)	75	76

TSC453			
Anti-CD37 X TSC454	Anti-CD37 X TSC394 E86D	77	78
Anti-CD37 X TSC455	Anti-CD37 X TSC394 F87Y	79	80
Anti-CD37 X TSC456	Anti-CD37 X TSC394 E86D F87Y	81	82
TSC455	TSC394 F87Y scFv (anti-CD3 scFv)		83
TSC456	TSC394 E86D F87Y scFv (anti-CD3 scFv)		84
DRA222	Anti-CD3 scFv		85
TSC455 and TSC456 VH	TSC455 and TSC456 variable heavy domain		86
DRA222 VH	DRA222 variable heavy domain		87
TSC455 VL	TSC455 variable light domain		88
TSC456 VL	TSC456 variable light domain		89
DRA222 VL	DRA222 variable light domain		90
Cris7 and DRA222 VH CDR1 (Kabat)	Anti-CD3 VH CDR1		91
Cris7 and DRA222 VH CDR2 (Kabat)	Anti-CD3 VH CDR2		92
Cris7 and DRA222 VH CDR3 (Kabat)	Anti-CD3 VH CDR3		93
Cris7 and DRA222 VL CDR1 (Kabat)	Anti-CD3 VL CDR1		94
Cris7 and DRA222 VL CDR2 (Kabat)	Anti-CD3 VL CDR2		95
Cris7 and DRA222 VL CDR3 (Kabat)	Anti-CD3 VL CDR3		96
Cris7 and DRA222 VH CDR1 (IMGT)	Anti-CD3 VH CDR1		199
Cris7 and DRA222 VH CDR2 (IMGT)	Anti-CD3 VH CDR2		200
Cris7 and DRA222 VH CDR3 (IMGT)	Anti-CD3 VH CDR3		201
Cris7 and DRA222 VL CDR1 (IMGT)	Anti-CD3 VL CDR1		202
Cris7 and DRA222 VL CDR2 (IMGT)	Anti-CD3 VL CDR2		203
Cris7 and DRA222 VL CDR3 (IMGT)	Anti-CD3 VL CDR3		204
ROR133	Anti-ROR1 (R11 L7H15) X DRA222	97	98
ROR193	Anti-ROR1 (R11 L7H15) X TSC394 F87Y	99	100
ROR134	Anti-ROR1 (R11 L7H10) X DRA222	101	102
ROR189	Anti-ROR1 (R11 L7H10) X TSC394 E86D F87Y	103	104
ROR154	Anti-ROR1 (R11 L7H16) X DRA222	105	106
ROR185	Anti-ROR1 (R11 L7H15) X TSC394 E86D	107	108

	F87Y		
ROR179	Anti-ROR1 (R11 L8H16) X DRA222	109	110
ROR186	Anti-ROR1 (R11 L8H16) X TSC394 E86D F87Y	111	112
ROR181	Anti-ROR1 (R11 L7H17) X DRA222	113	114
ROR191	Anti-ROR1 (R11 L7H17) X TSC394 E86D F87Y	115	116
ROR182	Anti-ROR1 (R11 L9H18) X DRA222	117	118
ROR192	Anti-ROR1 (R11 L9H18) X TSC394 E86D F87Y	119	120
ROR243	Humanized, codon optimized anti- ROR1 X anti-CD3 (parent anti-ROR1 molecule is ROR192) scFv-Fc-scFv	207	208
ROR206	ROR133 S40T G113R x DRA222 Fc ADCC- K322A-H111 in pEE12.4	211	212
ROR207	ROR133 S40T G113R x TSC456 Fc ADCC- K322A-H111 in pEE12.4	213	214
ROR208	ROR174 S40T G113R x DRA222 Fc ADCC- K322A-H111 in pEE12.4	215	216
ROR209	ROR174 S40T G113R x TSC456 Fc ADCC- K322A-H111 in pEE12.4	217	218
ROR231	Anti-ROR1 X anti-CD3	219	220
ROR233	Anti-ROR1 X anti-CD3	221	222
	Chimeric bispecific anti-CD123 (VLVH) x anti-CD3 (TSC456) scFv-Fc- scFv		197
	Chimeric bispecific anti-CD123 (VHVL) x anti-CD3 (TSC456) scFv-Fc- scFv		198

- Throughout the specification and claims, unless the context requires otherwise, 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.

CLAIMS:

1. A CD3-binding polypeptide comprising a CD3-binding domain that binds specifically to human CD3 and that comprises a humanized immunoglobulin light chain region and a humanized immunoglobulin heavy chain region,
5 wherein the immunoglobulin light chain variable region comprises an LCDR1 amino acid sequence of SEQ ID NO:94, an LCDR2 amino acid sequence of SEQ ID NO:95, and an LCDR3 amino acid sequence of SEQ ID NO:96 and wherein the immunoglobulin heavy chain variable region comprises an HCDR1 amino acid
10 sequence of SEQ ID NO:91, an HCDR2 amino acid sequence of SEQ ID NO:92, and an HCDR3 amino acid sequence of SEQ ID NO:93;

wherein the amino acid at position 9 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is proline; and

wherein the amino acid at position 21 according to the IMGT numbering system of the immunoglobulin light chain variable region is methionine; and

wherein the amino acid at position 87 according to the IMGT numbering system of the immunoglobulin light chain variable region is tyrosine, and

wherein

(a) the immunoglobulin light chain variable region comprises an amino
20 acid sequence that is at least 95% identical to SEQ ID NO:88 and the immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least 95% identical to SEQ ID NO:86 ; or

(b) the immunoglobulin light chain variable region comprises an amino
acid sequence that is at least 95% identical to SEQ ID NO:89 and the
25 immunoglobulin heavy chain variable region comprises an amino acid sequence that is at least 95% identical to SEQ ID NO:86.

2. The CD3-binding polypeptide of claim 1, wherein

(a) the immunoglobulin light chain variable region comprises SEQ ID NO:88
30 and the immunological heavy chain variable region comprises SEQ ID NO: 86; or

(b) the immunological light chain variable region comprises SEQ ID NO:89
and the immunoglobulin heavy chain variable region comprises SEQ ID NO:86.

3. The CD3-binding polypeptide of claim 1, wherein the amino acid
35 residue at position 52 according to the IMGT numbering system of the immunoglobulin light chain variable region is arginine and/or the amino acid residue

at position 53 according to the IMGT numbering system of the immunoglobulin light chain variable region is tryptophan.

4. The CD3-binding polypeptide of claim 1, wherein the amino acid
5 residue at position 27 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is tyrosine.

5. The CD3-binding polypeptide of claim 1, wherein the amino acid
10 residue at position 53 according to the IMGT numbering system of the immunoglobulin heavy chain variable region is isoleucine.

6. The CD3-binding polypeptide of claim 1, wherein the amino acid
15 residue at position 86 according to the IMGT numbering system of the immunoglobulin light chain variable region is aspartic acid.

7. The CD3-binding polypeptide of any one of claims 1-6, wherein the CD3-binding domain comprises SEQ ID NO:83 or SEQ ID NO:84.

8. The CD3-binding polypeptide of any one of claims 1-7, wherein the
20 CD3-binding domain is a single chain variable fragment (scFv).

9. The CD3-binding polypeptide of claim 8, wherein said scFv comprises a linker between the heavy chain variable region and the light chain variable region of said scFv and wherein said linker comprises the amino acid sequence
25 QRHNSSSLNTGTQMAGHSPNS (SEQ ID NO:148).

10. The CD3-binding polypeptide of claim 8, wherein the heavy chain variable region of said scFv is amino-terminal to the light chain variable region of said scFv.
30

11. The CD3-binding polypeptide of any one of claims 1-10, further comprising a second binding domain.

12. The CD3-binding polypeptide of claim 11, wherein said CD3-binding
35 polypeptide comprises, in order from amino-terminus to carboxyl-terminus, (i) the second-binding domain, (ii) a hinge region, (iii) an immunoglobulin constant region, (iv) a carboxyl-terminus linker, and (v) the CD3-binding domain.

13. The CD3-binding polypeptide of claim 12, wherein said immunoglobulin constant region comprises a human IgG1 CH2 domain containing the substitutions L234A, L235A, G237A, and K322A, according to the EU numbering system.

14. The CD3-binding polypeptide of claim 11 or 13, wherein the second binding domain comprises (a) an immunoglobulin light chain variable region comprising LCDR1, LCDR2, and LCDR3, and (b) an immunoglobulin heavy chain variable region comprising HCDR1, HCDR2, and HCDR3.

15. The CD3-binding polypeptide of any one of claims 12-14, wherein the hinge region is derived from an immunoglobulin hinge region.

16. The CD3-binding polypeptide of any one of claims 12-15, wherein the carboxyl-terminus linker comprises or consists of SEQ ID NO:196.

17. The CD3-binding polypeptide of any one of claims 12-16, wherein the immunoglobulin constant region comprises immunoglobulin CH2 and CH3 domains of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2 or IgD.

18. The CD3-binding polypeptide of claim 12, wherein the immunoglobulin constant region comprises a human IgG1 CH2 domain comprising the substitutions L234A, L235A, G237A, and K322A, according to the EU numbering system.

19. The CD3-binding polypeptide of any one of claims 11-18, wherein the CD3-binding polypeptide induces redirected T-cell cytotoxicity (RTCC).

20. The CD3-binding polypeptide of claim 19, wherein the CD3-binding polypeptide induces RTCC with an EC50 of about 30 pM or lower.

21. The CD3-binding polypeptide of any one of claims 11-20, wherein the second binding domain is a single chain variable fragment (scFv).

22. The CD3-binding polypeptide of any one of claims 11-21, wherein the second binding domain binds or interacts with a tumor associated antigen.

23. The CD3-binding polypeptide of claim 22, wherein said CD3-binding polypeptide induces T-cell-dependent lysis of cells expressing the tumor associated antigen.

5 24. The CD3-binding polypeptide of claim 22, wherein the tumor associated antigen is selected from the group consisting of PSMA, CD19, CD20, CD37, CD38, CD123, Her2, ROR1, RON, glycoprotein A33 antigen (gpA33), and CEA.

10 25. An isolated nucleic acid molecule encoding the CD3-binding polypeptide of any one of claims 1-24 or a portion of said CD3-binding polypeptide, wherein the portion comprises the humanized immunoglobulin light chain variable region and the humanized immunoglobulin heavy chain variable region.

15 26. An expression vector comprising a nucleic acid segment encoding the CD3-binding polypeptide of any one of claims 1-24, wherein the nucleic acid segment is operatively linked to regulatory sequences suitable for expression of the nucleic acid segment in a host cell.

20 27. A recombinant host cell comprising the expression vector of claim 26.

28. A method for producing a CD3-binding polypeptide, the method comprising
culturing a recombinant host cell comprising the expression vector of claim 26
25 under conditions whereby the nucleic acid segment is expressed, thereby producing the CD3-binding polypeptide; and
recovering the CD3-binding polypeptide.

30 29. A pharmaceutical composition comprising the CD3-binding polypeptide of any one of claims 1-24, and a pharmaceutically acceptable carrier, diluent, or excipient.

35 30. A method when used to induce redirected T-cell cytotoxicity (RTCC) against a cell expressing the tumor associated antigen, the method comprising:
contacting said tumor associated antigen-expressing cell with the CD3-binding polypeptide of any one of claims 22-24, wherein said contacting is under conditions whereby RTCC against the tumor associated antigen-expressing cell is induced.

5 31. A method when used to inhibit tumor growth in a subject in need thereof, comprising administering a therapeutically effective amount of the CD3-binding polypeptide of any one of claims 1-24, or the composition of claim 29 to the subject.

10 32. A method when used in treating cancer or a T-cell-mediated autoimmune disorder in a subject in need thereof, comprising administering a therapeutically effective amount of the CD3-binding polypeptide of any one of claims 1-24, or the composition of claim 29 to the subject.

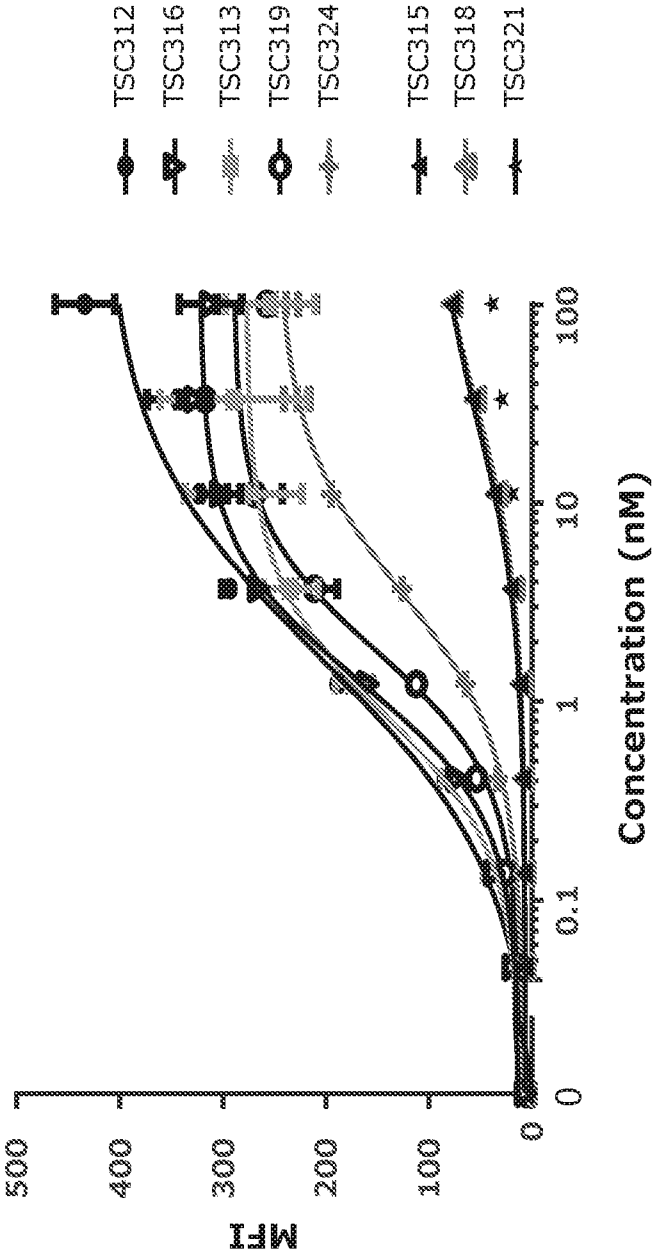
15 33. The method of claim 32, wherein the cancer is prostate cancer, colorectal cancer, renal cell carcinoma, bladder cancer, salivary gland cancer, pancreatic cancer, ovarian cancer, non-small cell lung cancer, breast cancer (e.g., triple negative breast cancer), melanoma, adrenal cancer, mantle cell lymphoma, acute lymphoblastic leukemia, chronic lymphocytic leukemia, Non-Hodgkin's lymphoma, acute myeloid leukemia (AML), B-lymphoid leukemia, blastic plasmacytoid dendritic neoplasm (BPDCN), or hairy cell leukemia.

20 34. A CD3-binding protein that is a dimer of two identical polypeptides, wherein each polypeptide is the CD3-binding polypeptide of any one of claims 1-24.

25 35. The CD3-binding polypeptide of any one of claims 1-24, wherein the CD3-binding polypeptide does not exhibit or exhibits minimal antibody-dependent cell-mediated cytotoxicity (ADCC) activity and/or complement-dependent cytotoxicity (CDC) activity.

Figure 1

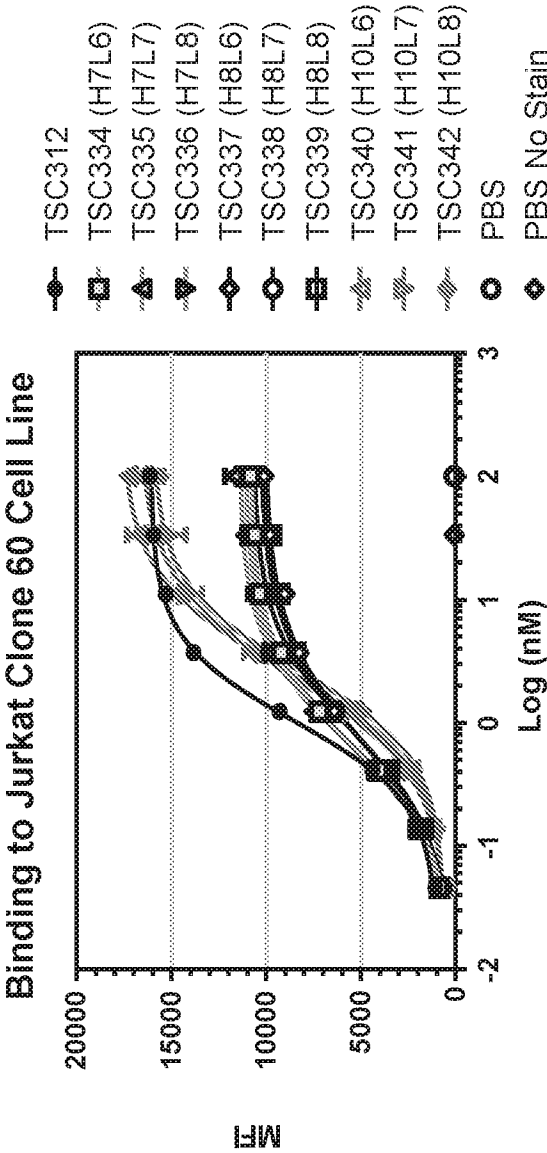
Binding to CD3 on Jurkat T cells



EC₅₀ for CD3 binding

TSC312	1.7 +/- 0.4 nM
TSC313	0.87 +/- 0.3 nM
TSC315	na
TSC316	1.3 +/- 0.2 nM
TSC318	na
TSC319	1.8 +/- 0.4 nM
TSC321	na
TSC324	3.6 +/- 0.3 nM

Figure 2



	Top		EC50	
	Mean	SEM	Mean	SEM
TSC312	16106	86	1.04	0.03
TSC334 (H7L6)	10839	95	0.70	0.04
TSC335 (H7L7)	11431	168	0.74	0.07
TSC336 (H7L8)	11133	151	0.67	0.06
TSC337 (H8L6)	10073	143	0.73	0.07
TSC338 (H8L7)	10702	142	0.86	0.07
TSC339 (H8L8)	10334	206	0.78	0.10
TSC340 (H10L6)	17626	80	2.76	0.05
TSC341 (H10L7)	15963	229	2.67	0.15
TSC342 (H10L8)	16702	461	2.32	0.25

Figure 3

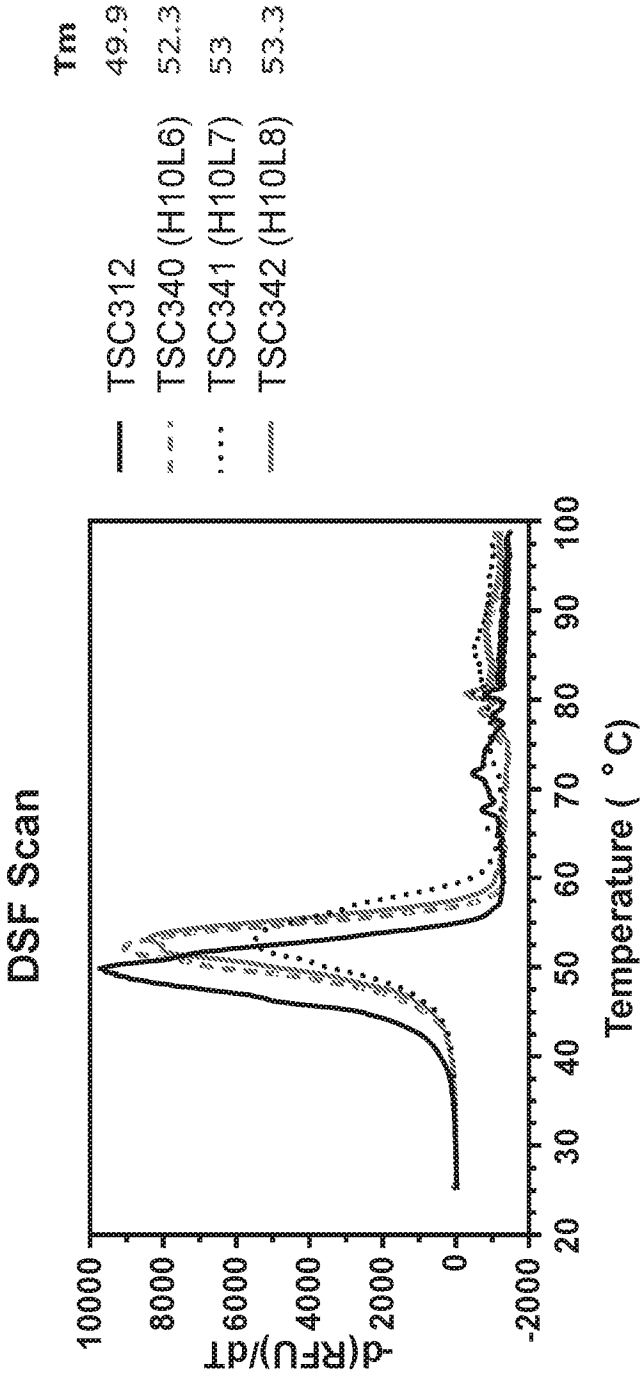
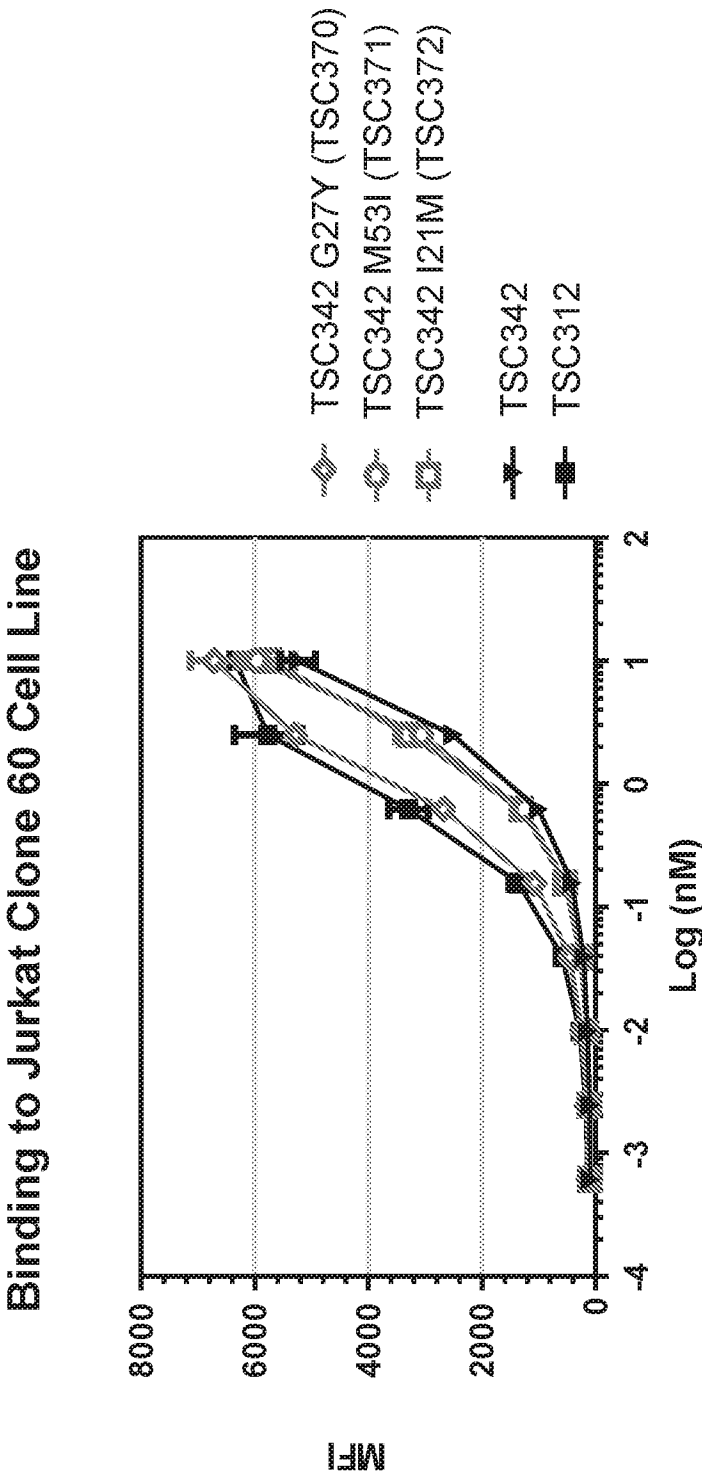


Figure 4



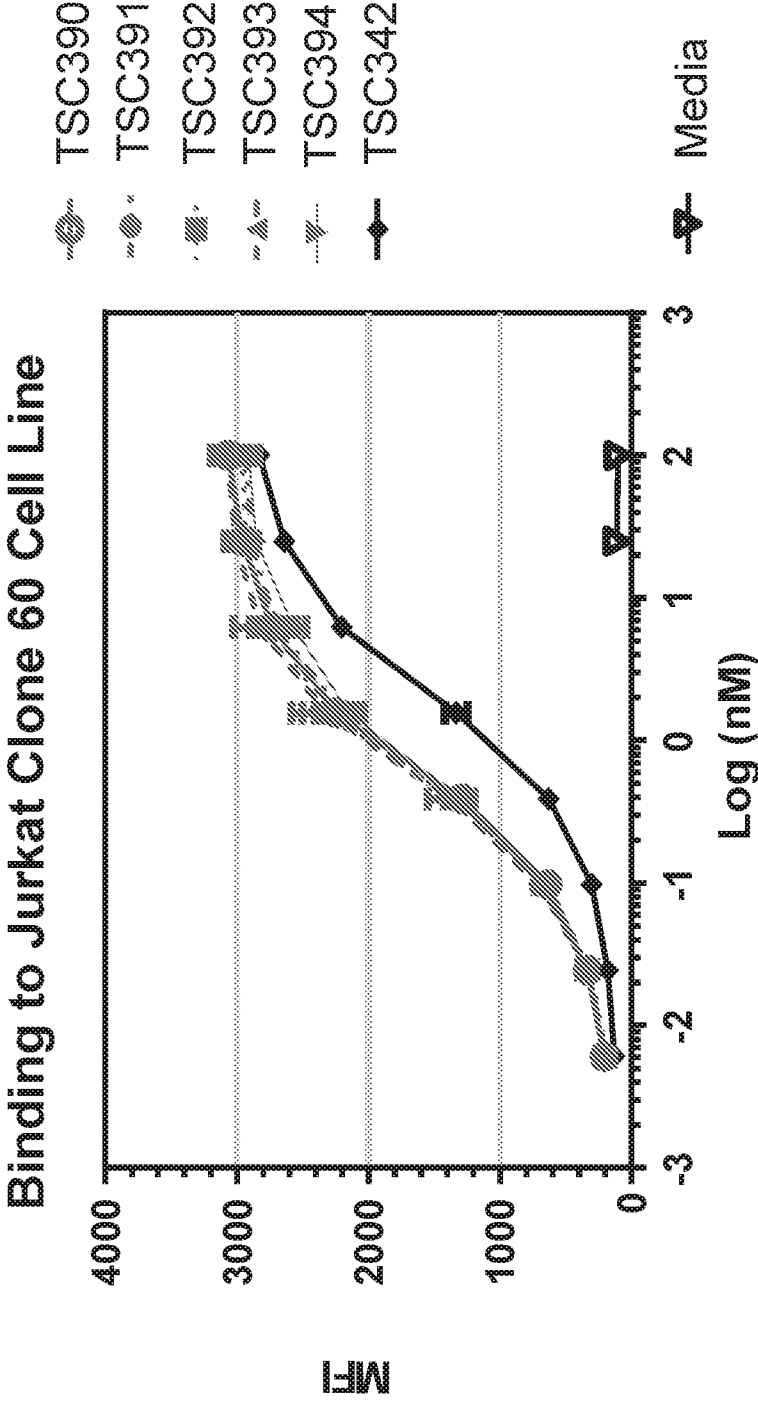
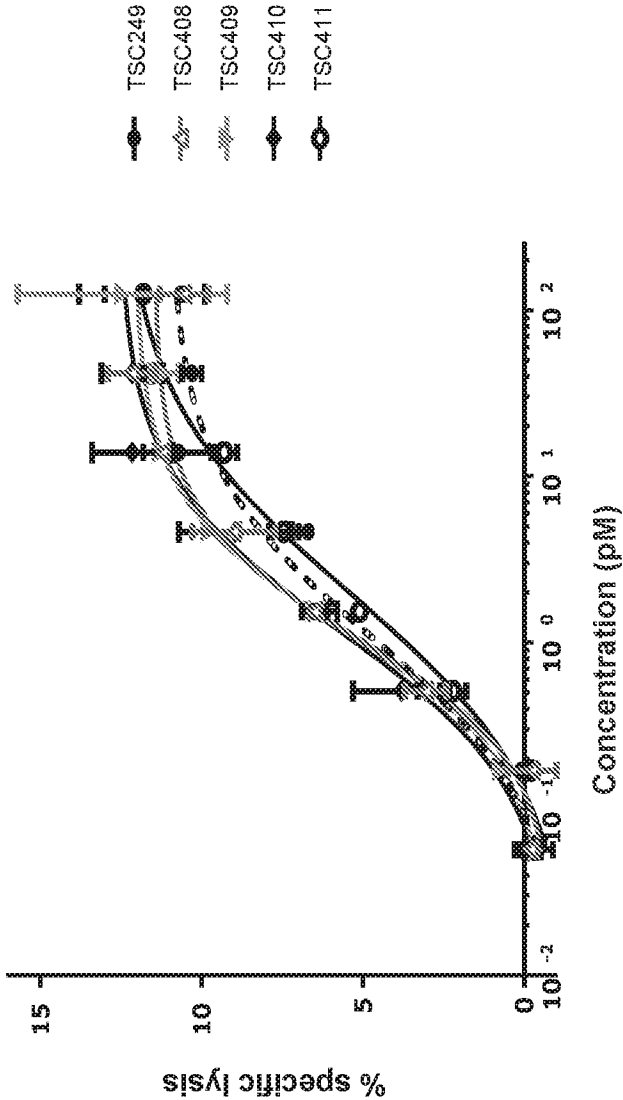


Figure 5

Figure 6

RTCC activity of PSMAxCD3 bispecifics
with alternate CD3 domains

⁵¹Cr release assay, 4 hr, C4-2B target cells



	EC ₅₀ for RTCC
TSC249	1.12 +/- 0.42 pM
TSC408	1.10 +/- 0.26 pM
TSC409	1.20 +/- 0.39 pM
TSC410	1.18 +/- 0.52 pM
TSC411	2.03 +/- 0.53 pM

Figure 7A

Binding to Cynomolgus T cells
Chinese-Cyno #141325

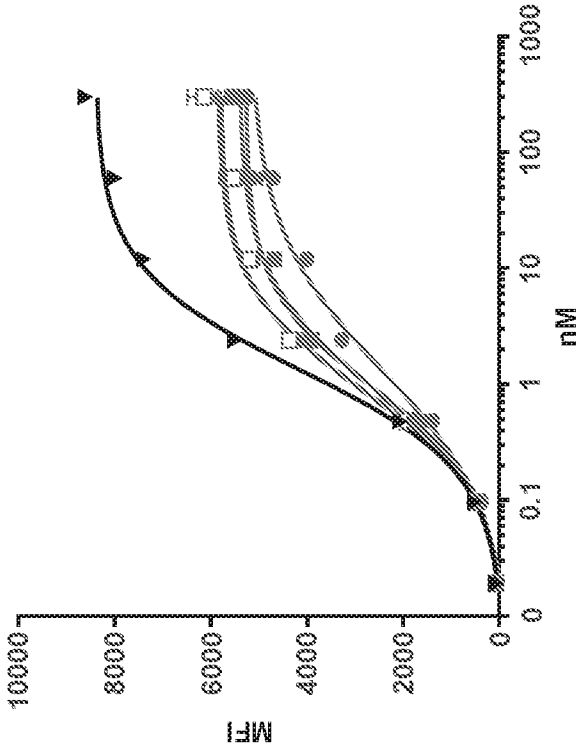


Figure 7B

Binding to Cynomolgus T cells
Chinese-Cyno #141334

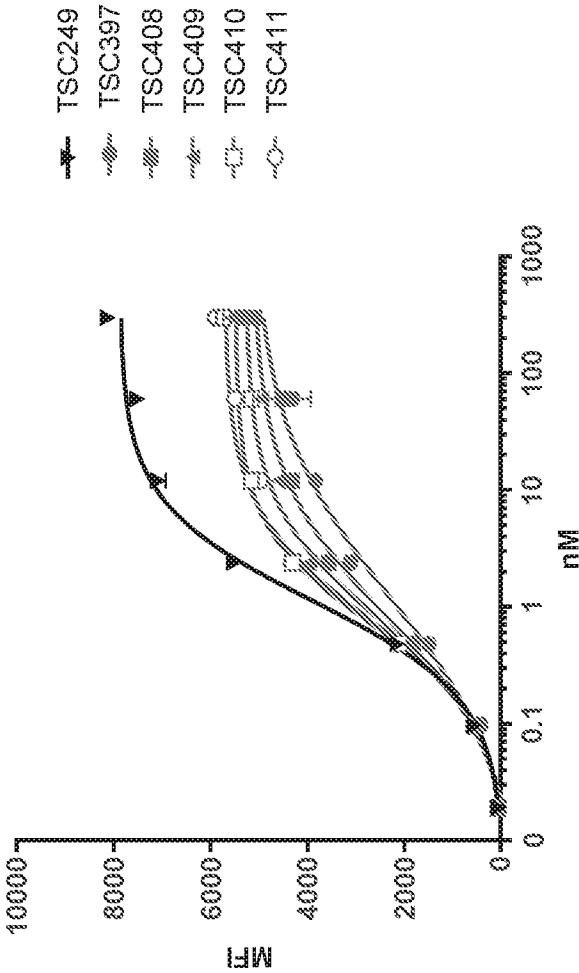


Figure 8A

RTCC of C4-2B cells with Cynomolgus PBMC
4 hr ⁵¹Cr release assay
Cyno # 141325

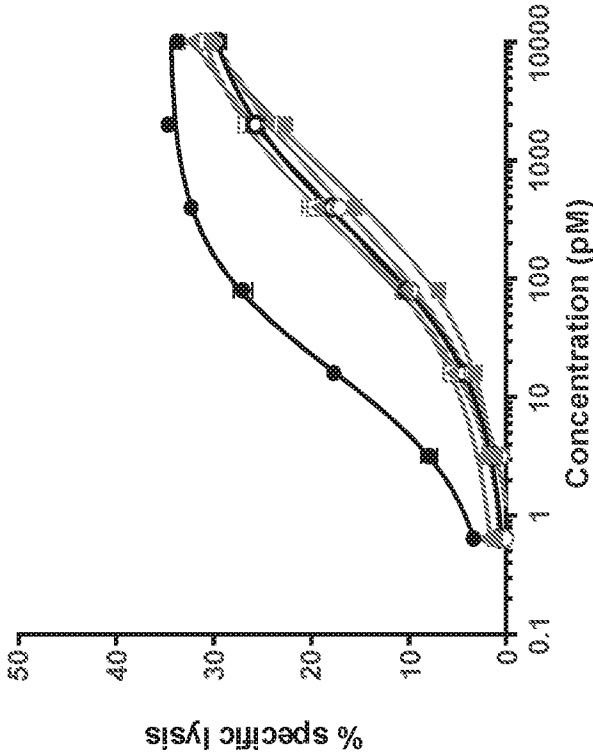


Figure 8B

RTCC of C4-2B cells with Cynomolgus PBMC
4 hr ⁵¹Cr release assay
Cyno #141334

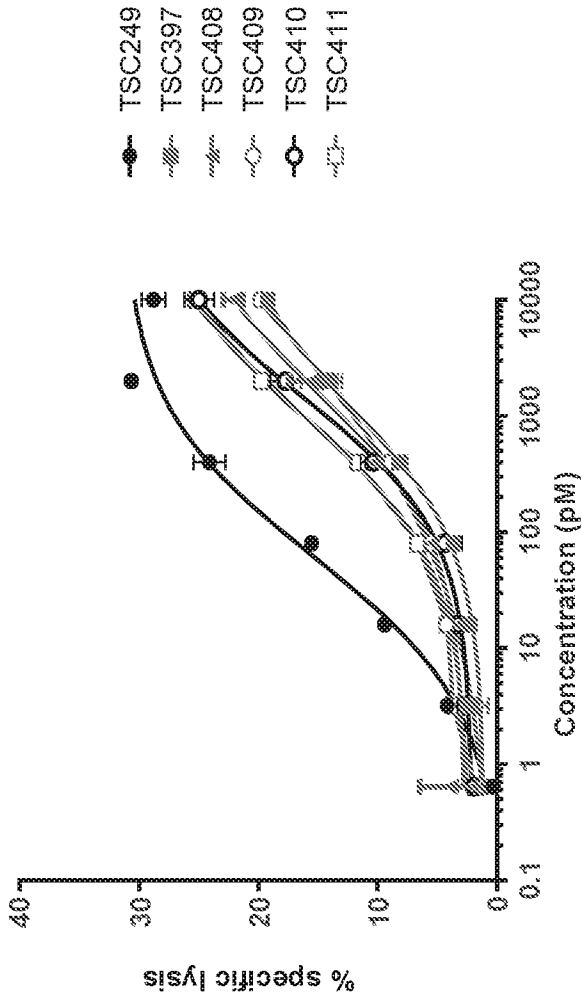


Figure 9

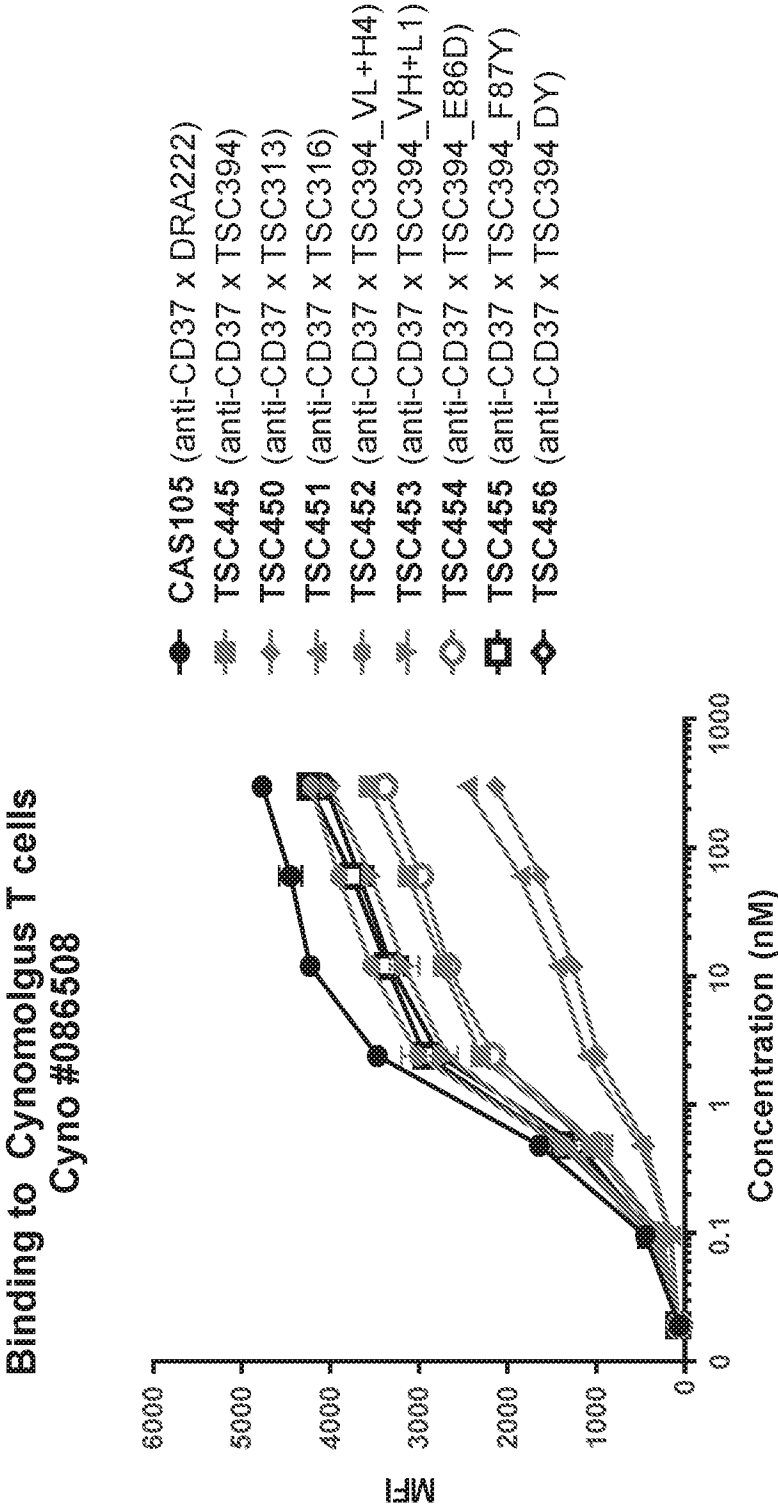
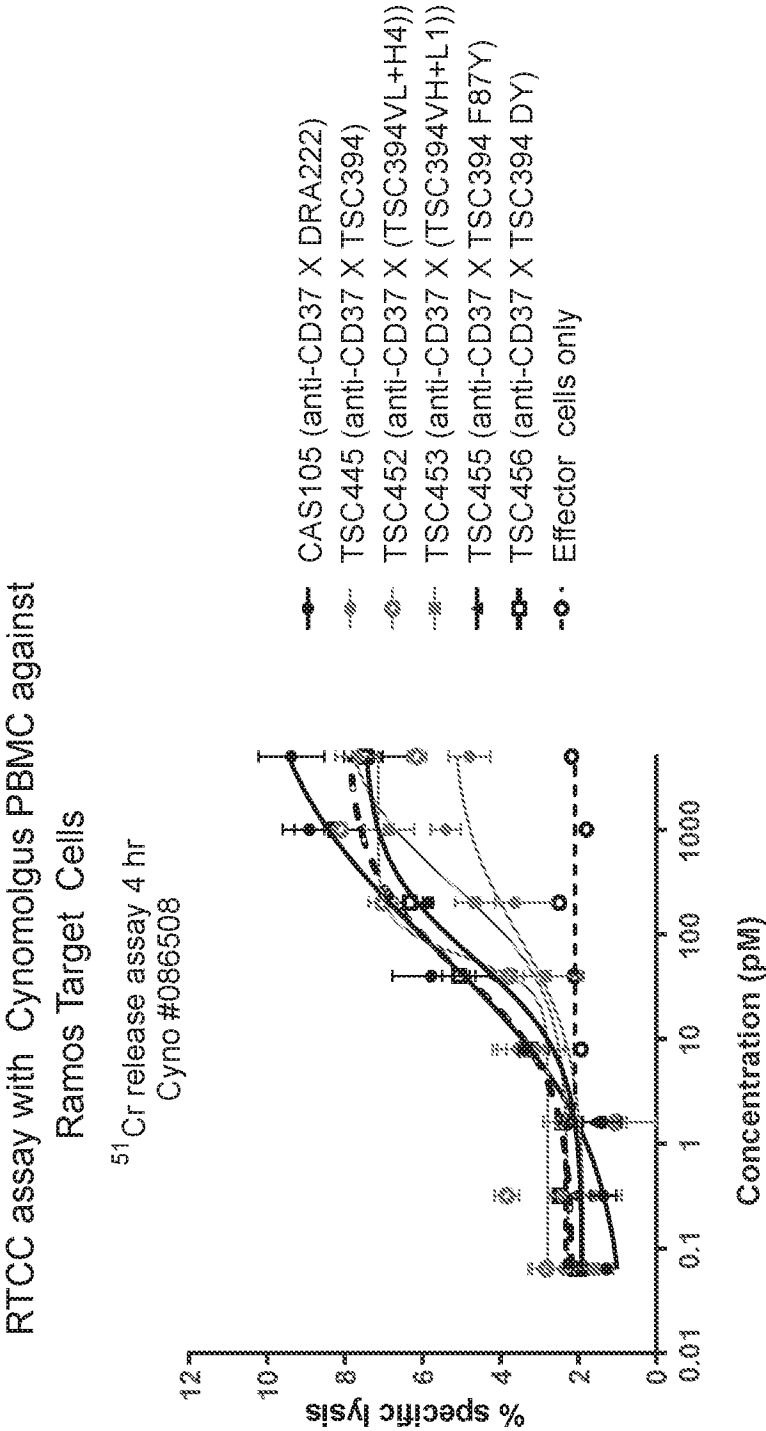
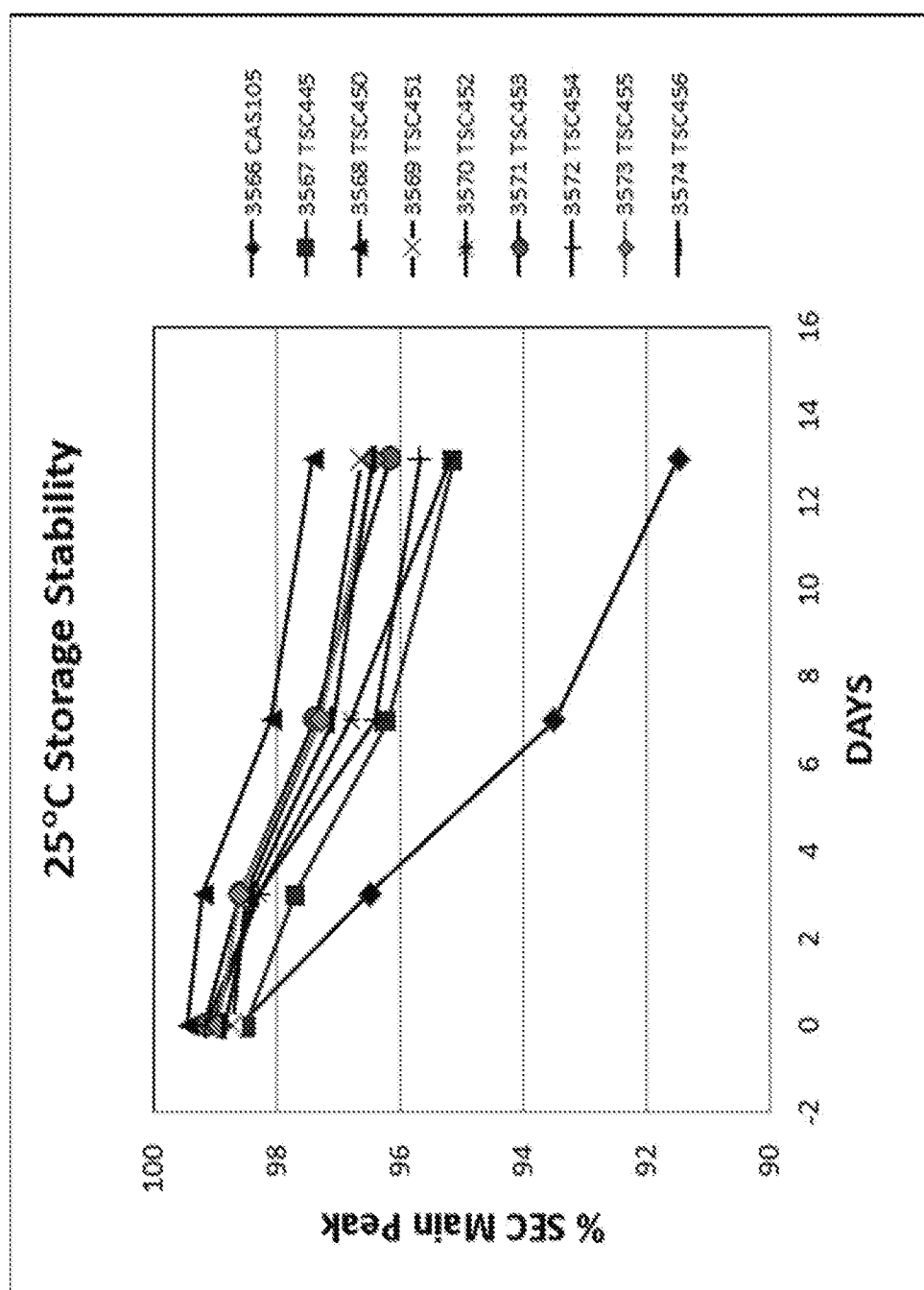


Figure 10

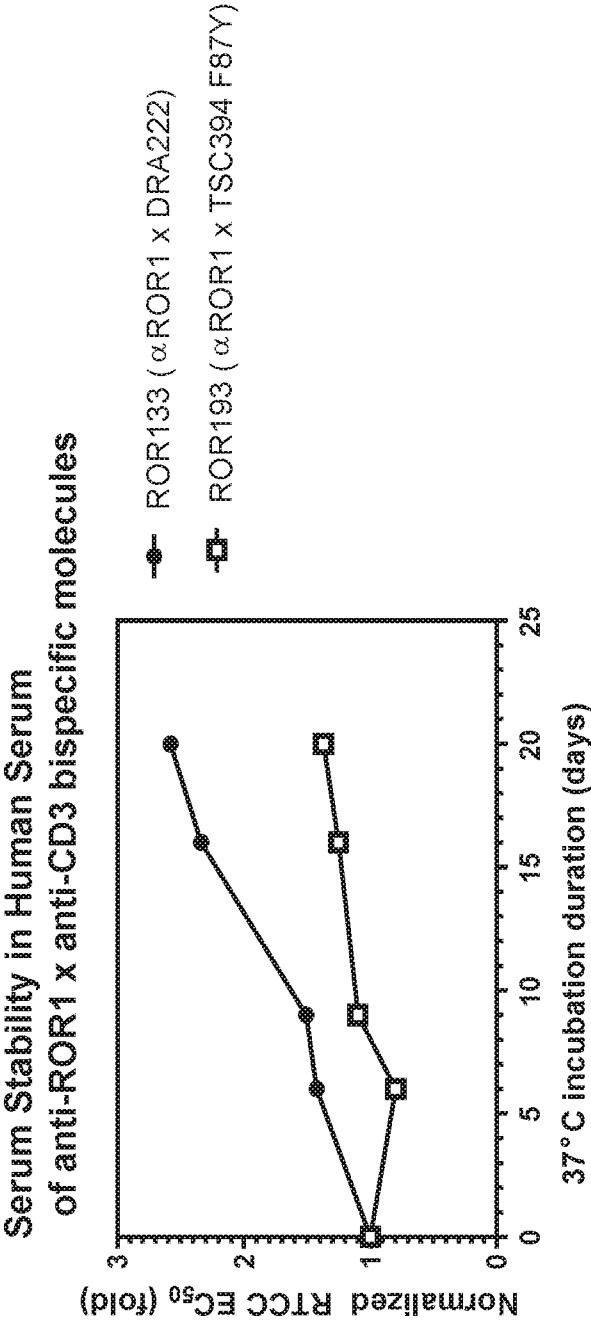


10:1 E:T		EC50 for RTCC
Ramos	CAS105	69.47 +/- 57.6 pM
Cyno #086508	TSC445	101.3 +/- 142.1 pM
	TSC452	61.65 +/- 45.57 pM
	TSC453	298.6 +/- 218.9 pM
	TSC455	60.18 +/- 21.51 pM
	TSC456	44.78 +/- 19.9 pM



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Figure 12



		(1)	1	10	20	30	40	50	60	70	82
DRA222	scFv	(1)	QVQLVSSGGGVVQPGKSLRLSCKASGYYTFASTHFWVQAPQGGLWIGYINPSSAYTHYNQKPFDEPTISADZSKSTAFLEQ								
TSC455	scFv	(1)	QVQLVQSGGPEVKEPGSSVYVSCKASGYYTFSRSTHFWVQAPQGGLWIGYINPSSAYTHYNQKPFDEVTITADZSTSTAYME								
TSC456	scFv	(1)	QVQLVQSGGPEVKEPGSSVYVSCKASGYYTFSKSTHFWVQAPQGGLWIGYINPSSAYTHYNQKPFDRVTITADKSTSTAYME								
----- Section 2 -----											
		(83)	83	90	100	110	120	130	140	150	164
DRA222	scFv	(83)	MESLPEDTGVYFCARPQVHYIDYNGFFPYWQGTPTVTVSSGGGGSGGGSGGGGGG---								
TSC455	scFv	(83)	LSSLRSKDTAVYYCARPQVHYIDYNGFFPYWQGTPTVTVSSGGGGSGGGSGGGSGGGGGSDIQTQSPSSLASVGDRTVMT								
TSC456	scFv	(83)	LSSLRSKDTAVYYCARPQVHYIDYNGFFPYWQGTPTVTVSSGGGGSGGGSGGGSGGGGGSDIQTQSPSSLASVGDRTVMT								
----- Section 3 -----											
		(165)	165	170	180	190	200	210	220	230	246
DRA222	scFv	(162)	SASSSVSYMNWYQKPKQZAPKRWIYDSSEKLASGVPARFSGSGSGTDYTLTISSLQPEDFATYYCQQWGRNPPTFGGGTLEI								
TSC455	scFv	(165)	SASSSVSYMNWYQKPKQZAPKRWIYDSSEKLASGVPARFSGSGSGTDYTLTISSLQPEDFATYYCQQWGRNPPTFGGGTLEI								
TSC456	scFv	(165)	SASSSVSYMNWYQKPKQZAPKRWIYDSSEKLASGVPARFSGSGSGTDYTLTISSLQPEDFATYYCQQWGRNPPTFGGGTLEI								
----- Section 4 -----											
		(247)	247	251							
DRA222	scFv	(244)	TSSS-								
TSC455	scFv	(247)	KRSSS								
TSC456	scFv	(247)	KRSSS								

SUBSTITUTE SHEET (RULE 26)

Figure 14

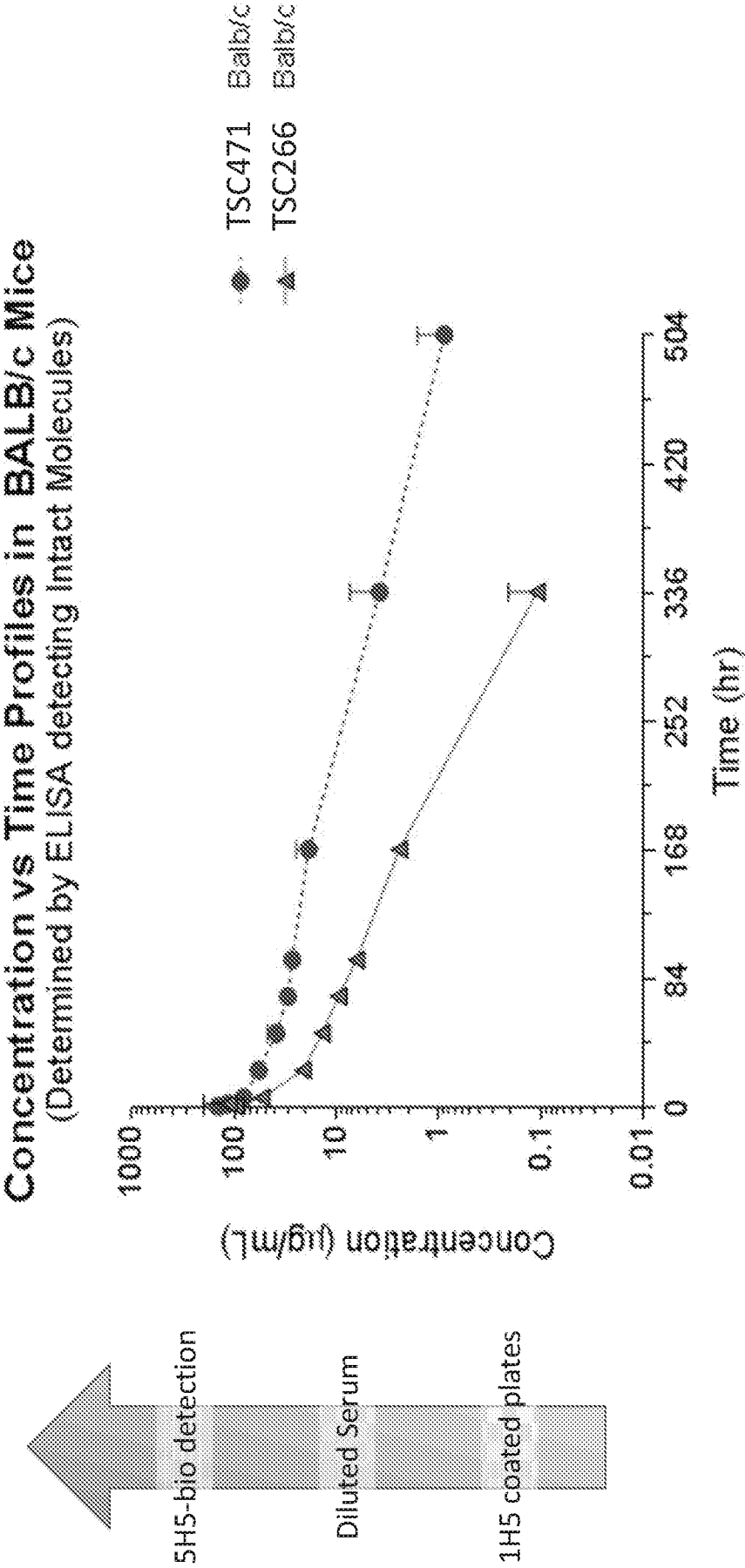


Figure 15

NCA Parameter	Units	TSC471	TSC266
HL_Lambda_z	hr	83.631	41.5
Cmax (Tmax)	ug/mL	144.0 (at 0.25 hr)	114.33 (at 2 hrs)
AUCall	hr*ug/mL	8561	2673.7
AUCINF_obs	hr*ug/mL	8668	2671
Vz_obs	mL/kg	150.5	238.7
Cl_obs	mL/hr/kg	1.247	3.9872
Vss_obs	mL/kg	137.70	197.8

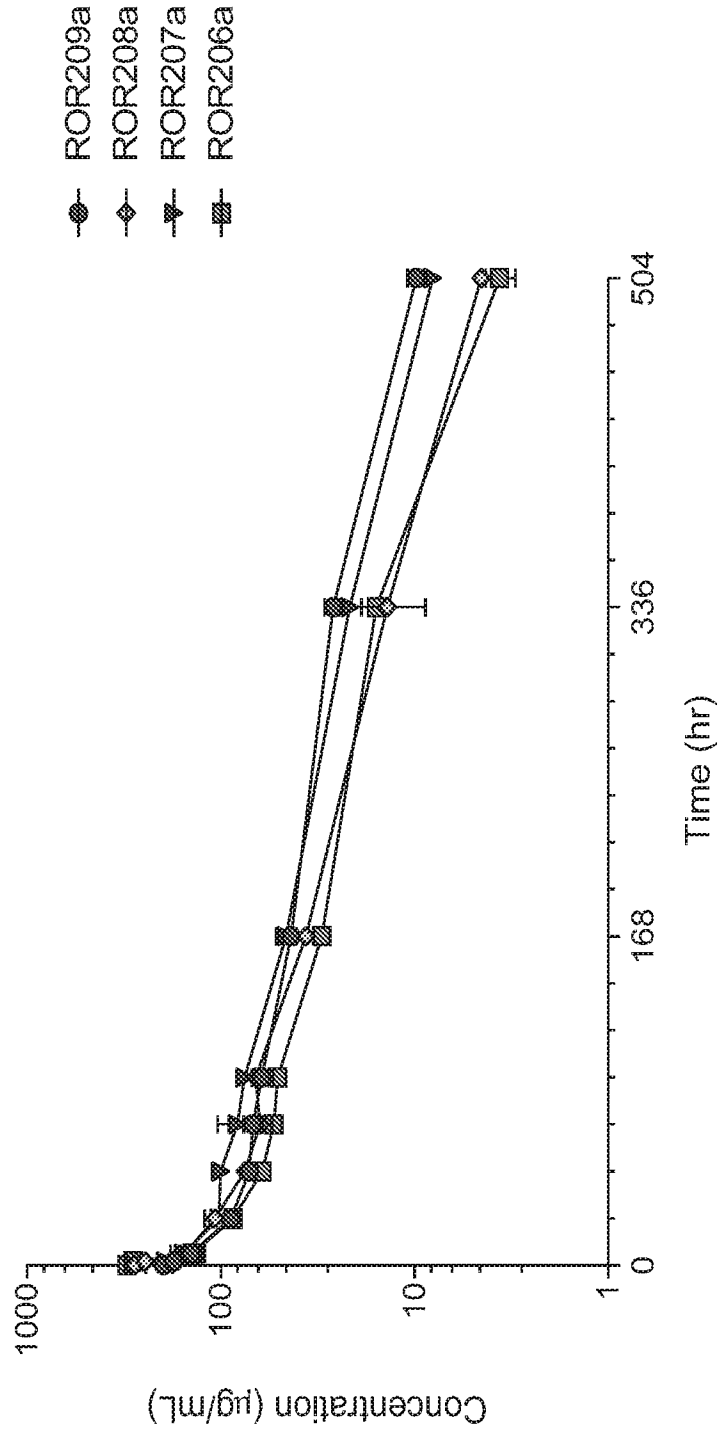


Figure 16

Figure 17A

Parameter Estimate	HL	Cmax	AUC all	AUC inf	Volume	Clearance
Units	hr	ug/mL	hr*ug/mL	hr*ug/mL	mL/kg	mL/hr/kg
ROR206a	116.8	306.3	16306	16920	100.1	0.594
ROR207a	128.5	280.6	22617	24113	78.1	0.421
ROR208a	112.1	278.7	18545	19279	87.4	0.540
ROR209a	163.3	198.2	20941	23252	107.8	0.458

Figure 17B

Parameter Estimate	CL	CLD2	V1	V2	Alpha HL	Beta HL	AUC
Units	mL/hr/kg	mL/hr/kg	mL/kg	mL/kg	hr	hr	hr*ug/mL
ROR206a	0.635	4.197	29.9	70.3	3.22	117.8	15818
ROR207a	0.440	6.165	35.6	44.6	2.18	129.2	23042
ROR208a	0.581	3.940	35.6	49.9	3.48	107.3	17926
ROR209a	0.469	3.069	53.5	56.0	5.93	168.3	22666

Figure 18

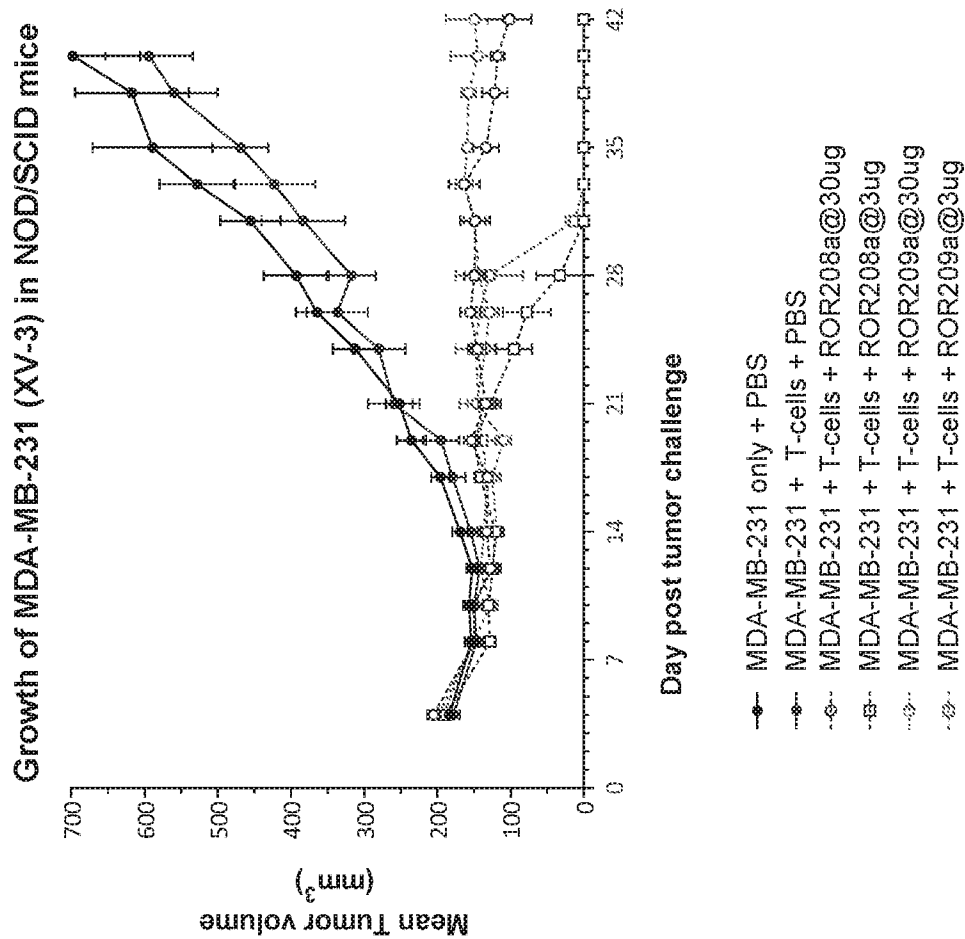
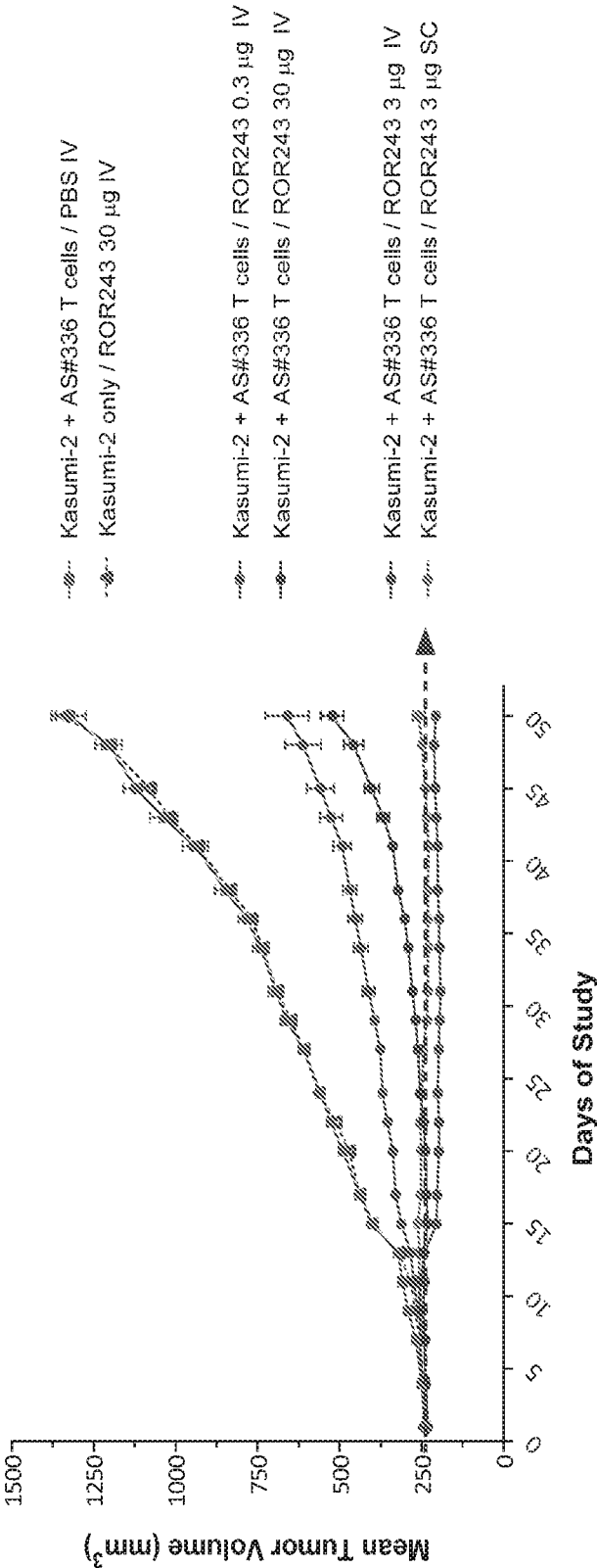


Figure 19

Growth of Kasumi-2 Tumor



*Tumor volumes are plotted as the mean + SEM of tumor volume measurement

*Tumor volumes are plotted until first mouse in study reached the endpoint

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<110>  APTEVO RESEARCH AND DEVELOPMENT LLC
        Tan, Philip
        Blankenship, John W.

<120>  CD3 BINDING POLYPEPTIDES

<130>  APVO-052/01W0

<150>  US 62/221,190
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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
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Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
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 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
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 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900
 ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacaggggtc 1020
 accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080
 gacgacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcgatctg acatccagat gaccagctct 1260
 ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgacg tgccagctca 1320
 agtgtaagtt acatgaactg gtatcagcag aaaccagga aagcccctaa gtcctgatc 1380
 tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440
 acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

SeqList.txt

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

<210> 8
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L5 (TSC315) CD3-binding domain

<400> 8

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

SeqList.txt
220

210

215

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

Glu Ile Lys Arg Ser Ser Ser
500

<210> 9
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L1 (TSC316) CD3-binding domain

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<400> 9
atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctctcttctc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg      840
gctgaggtga agaagcctgg ggcctcagtg aaggtttctt gcaaggcatc tggatacacc      900
ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
accatgacca gggacacgtc cagagcaca gtctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct     1260
ccaagcagcc tgtctgcaag cgtggggggac agggtcacca tgacctgcag tgccagctca     1320
agtgtaaagt acatgaactg gtaccagcag aagccgggca agggcccca aagatggatt     1380
tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg     1440
accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc     1500
cagcagtgga gtcgtaacct acccagttc ggagggggga ccaagctaca aattacatcc     1560

```

tccagctaa

<210> 10
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H8L1 (TSC316) CD3-binding domain

<400> 10

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

SeqList.txt

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 405 410 415
 Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430
 Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 450 455 460
 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480
 Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

SeqList.txt

Gln Ile Thr Ser Ser Ser
500

<210> 11
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L4 (TSC317) CD3-binding domain

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<400> 11
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg      840
gctgaggatga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc      900
ttcaccagat ctacgatgca ctgggtgcca caggccccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
accatgacca gggacacgtc cagcagcaca gtctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct     1260
ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca     1320
agtgtaaagt acatgaactg gtaccaacag aaacctggcc aggctcccag gtcctcatc     1380
tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg     1440
acagacttca ctctcacat cagcagccta gagcctgaag attttgagcgt ttattactgt     1500
cagcagtgga gtcgtaaccc acccactttc ggcgagggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

SeqList.txt

<210> 12
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H8L4 (TSC317) CD3-binding domain

<400> 12

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 Page 17

SeqList.txt

225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
 385 390 395 400
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415
 Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460
 Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 465 470 475 480
 Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495
 Glu Ile Lys Arg Ser Ser Ser

500

<210> 13
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H8L5 (TSC318) CD3-binding domain

<400> 13
 atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aaggtttctt gcaaggcatc tggatacacc 900
 ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
 accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacggggtt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct 1260
 ccctcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgacg tgccagctca 1320
 agtgaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gtcctgatc 1380
 tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440
 acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500
 caacagtgga gtcgtaacct acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
 tcctccagct aa 1572

<210> 14

SeqList.txt

<211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H8L5 (TSC318) CD3-binding domain

<400> 14

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

SeqList.txt

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415
 Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445
 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460
 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480
 Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495
 Glu Ile Lys Arg Ser Ser Ser
 500

SeqList.txt

<210> 15
 <211> 1569
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H9L1 (TSC319) CD3-binding domain

<400> 15
 atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180
 accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaaggga gccccgagaa ccacaggtgt acaccctgcc cccatcccg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactaaa gaccacgcct 600
 cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840
 gctgaggtga agaagcctgg ggcctcagtg aaggtttctt gcaaggcttc tggctacacc 900
 tttagtagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020
 accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct 1080
 gaagacacgg ctgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct 1260
 ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 1320
 agtgtaagtt acatgaactg gtaccagcag aagccgggca agggcccaa aagatggatt 1380
 tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1440
 accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 1500
 cagcagtgga gtcgtaacc acccacgttc ggagggggga ccaagctaca aattacatcc 1560
 tccagctaa 1569

<210> 16
 <211> 502
 <212> PRT

<213> Artificial Sequence

<220>

<223> Fc H9L1 (TSC319) CD3-binding domain

<400> 16

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu

SeqList.txt

245

250

255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 405 410 415
 Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430
 Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 450 455 460
 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480
 Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495
 Gln Ile Thr Ser Ser Ser
 500

<210> 17

SeqList.txt

<211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H9L4 (TSC320) CD3-binding domain

<400> 17
 atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctgggtgaat 360
 ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctccttcctc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840
 gctgaggatga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc 900
 ttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020
 accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct 1080
 gaagacacgg ctgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcgatctg aaattgtgtt gacacagtct 1260
 ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320
 agtghtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gtcctcatc 1380
 tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg 1440
 acagacttca ctctcacat cagcagccta gagcctgaag attttgagcgt ttattactgt 1500
 cagcagtgga gtcgtaaccc acccactttc ggcgagggga ccaaggtgga gatcaaacgg 1560
 tcctccagct aa 1572

<210> 18
 <211> 503
 <212> PRT
 <213> Artificial Sequence

SeqList.txt

<220>

<223> Fc H9L4 (TSC320) CD3-binding domain

<400> 18

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

SeqList.txt

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
 385 390 395 400
 Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415
 Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460
 Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 465 470 475 480
 Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495
 Glu Ile Lys Arg Ser Ser Ser
 500

<210> 19
 <211> 1572
 <212> DNA

<213> Artificial Sequence

<220>

<223> Fc H9L5 (TSC321) CD3-binding domain

<400> 19

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaa at cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      180
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc      660
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tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg      840
gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc      900
tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacaggggtc     1020
accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaagacacgg ctgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaaggaa cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct     1260
ccatcctccc tgtctgcatc ttaggagac agagtcacca tcaattgcag tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gtcctgatc     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg     1440
acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt     1500
caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                           1572

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<210> 20

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc H9L5 (TSC321) CD3-binding domain

SeqList.txt

<400> 20

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val

SeqList.txt

260

265

270

Ser Cys Lys₂₇₅ Ala Ser Gly Tyr Thr₂₈₀ Phe Thr Arg Ser Thr₂₈₅ Met His Trp

Val Arg₂₉₀ Gln Ala Pro Gly₂₉₅ Gln Arg Leu Glu Trp Met₃₀₀ Gly Tyr Ile Asn

Pro₃₀₅ Ser Ser Ala Tyr Thr₃₁₀ Asn Tyr Asn Gln Lys₃₁₅ Phe Lys Asp Arg Val₃₂₀

Thr Ile Thr Arg₃₂₅ Asp Thr Ser Ala Ser Thr₃₃₀ Ala Tyr Met Glu Leu₃₃₅ Ser

Ser Leu Arg Ser₃₄₀ Glu Asp Thr Ala Val₃₄₅ Tyr Tyr Cys Ala Arg₃₅₀ Pro Gln

Val His Tyr₃₅₅ Asp Tyr Asn Gly₃₆₀ Phe Pro Tyr Trp Gly₃₆₅ Gln Gly Thr Leu

Val Thr₃₇₀ Val Ser Ser Gly₃₇₅ Gly Gly Gly Ser Gly₃₈₀ Gly Gly Ser Gly

Gly₃₈₅ Gly Gly Ser Gly₃₉₀ Gly Gly Gly Ser Asp Ile₃₉₅ Gln Met Thr Gln Ser₄₀₀

Pro Ser Ser Leu₄₀₅ Ser Ala Ser Val Gly₄₁₀ Asp Arg Val Thr Ile₄₁₅ Thr Cys

Ser Ala Ser₄₂₀ Ser Val Ser Tyr Met₄₂₅ Asn Trp Tyr Gln Gln₄₃₀ Lys Pro

Gly Lys Ala₄₃₅ Pro Lys Leu Leu Ile₄₄₀ Tyr Asp Ser Ser Lys₄₄₅ Leu Ala Ser

Gly Val₄₅₀ Pro Ser Arg Phe₄₅₅ Ser Gly Ser Gly Ser₄₆₀ Thr Asp Phe Thr

Leu Thr Ile Ser Ser Leu₄₇₀ Gln Pro Glu Asp Phe₄₇₅ Ala Thr Tyr Tyr Cys₄₈₀

Gln Gln Trp Ser Arg₄₈₅ Asn Pro Pro Thr Phe₄₉₀ Gly Gly Gly Thr Lys₄₉₅ Val

Glu Ile Lys Arg₅₀₀ Ser Ser Ser

<210> 21

<211> 1569

<212> DNA

<213> Artificial Sequence

SeqList.txt

<220>

<223> Fc H10L1 (TSC322) CD3-binding domain

<400> 21

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      180
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctgggtgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactaaa gaccacgcct      600
cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggtatctg acatccagat gaccagctct     1260
ccaagcagcc tgtctgcaag cgtggggggac agggtcacca tgacctgcag tgccagctca     1320
agtgtaaagt acatgaactg gtaccagcag aagccgggca agggcccaa aagatggatt     1380
tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg     1440
accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc     1500
cagcagtgga gtcgtaacc acccacgttc ggagggggga ccaagctaca aattacatcc     1560
tccagctaa                                     1569

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<210> 22

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc H10L1 (TSC322) CD3-binding domain

<400> 22

SeqList.txt

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15
 Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270

SeqList.txt

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Gln Ile Thr Ser Ser Ser
 500

<210> 23
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H10L4 (TSC323) CD3-binding domain
 Page 33

SeqList.txt

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<400> 23
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ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtgc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgctgctg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
gctgaggatga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggccccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cagcagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcggtggc ggcgatctg aaattgtgtt gacacagtct     1260
ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca     1320
agtgtaaagt acatgaactg gtaccaacag aaacctggcc aggtcccag gtcctcatc     1380
tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg     1440
acagacttca ctctcaccat cagcagccta gagcctgaag attttgagcgt ttattactgt     1500
cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

```

<210> 24
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H10L4 (TSC323) CD3-binding domain

```

```

<400> 24
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

```

SeqList.txt

1		5						10					15				
Pro	Glu	Ala	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
			20					25					30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
		35					40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
	50					55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
				85					90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Ala	Tyr	Ala	Cys	Ala	Val	Ser	Asn	Lys	Ala		
			100					105					110				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
		115					120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
	130					135					140						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
145					150					155					160		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
				165					170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr		
			180					185					190				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
		195					200					205					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
	210					215					220						
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Gln	Arg	His	Asn	Asn	Ser	Ser	Leu	Asn		
225					230					235					240		
Thr	Gly	Thr	Gln	Met	Ala	Gly	His	Ser	Pro	Asn	Ser	Gln	Val	Gln	Leu		
				245					250					255			
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser	Val	Lys	Val		
			260					265					270				
Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Arg	Ser	Thr	Met	His	Trp		

SeqList.txt

275

280

285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
 385 390 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 25

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc H10L5 (TSC324) CD3-binding domain

<400> 25

SeqList.txt

```

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      180
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggga gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660
agggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggg gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtt tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaagAAC cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcgatctg acatccagat gaccagctct     1260
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcaattgcag tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gctcctgac     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg     1440
acagatttca ctctaccat cagcagtctg caacctgaag attttgcaac ttactactgt     1500
caacagtgga gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                           1572

```

<210> 26
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H10L5 (TSC324) CD3-binding domain
 <400> 26

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

SeqList.txt

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285

SeqList.txt

```

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290          295          300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305          310          315          320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
          325          330          335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
          340          345          350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355          360          365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370          375          380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385          390          395          400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
          405          410          415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
          420          425          430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435          440          445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450          455          460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465          470          475          480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
          485          490          495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 27
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L6 (TSC334) CD3-binding domain

<400> 27
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt

```

60

SeqList.txt

```

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      180
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg      840
gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc      900
ttcaccagat ctacgatgca ctgggtgcca caggcccctg gacaagggtt tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc     1020
accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct     1080
gacgacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcgatctg acatccagat gaccagctct     1260
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgagc tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg     1440
acagatttca ctctcacat cagcagtctg caacctgaag attttgcaac ttactactgt     1500
caacagtgga gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

```

<210> 28
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H7L6 (TSC334) CD3-binding domain
<400> 28

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

```

SeqList.txt

20

25

30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn

SeqList.txt
300

290

295

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 29
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L7 (TSC335) CD3-binding domain

<400> 29
atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt 60
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120

SeqList.txt

```

ggtgcaccgt cagtcttctt cttcccccca aaacccaagg acaccctcat gatctcccgg 180
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccatt cgagaaaacc 420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900
ttcaccagat ctacgatgca ctgggtgcca caggcccctg gacaagggct tgagtggatg 960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020
accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080
gacgacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt 1140
ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct 1260
ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320
agtgtaaagt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380
tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg 1440
acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt 1500
cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

```

```

<210> 30
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H7L7 (TSC335) CD3-binding domain

```

```
<400> 30
```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1           5           10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```


SeqList.txt

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

SeqList.txt

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 31

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc H7L8 (TSC336) CD3-binding domain

<400> 31

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180

SeqList.txt

```

accctgagg tcacatgCGT ggtggtggac gtgagccacg aagaccctga ggtcaagtTC 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgCGc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctcccttcttc ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900
ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg 960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacaggggtc 1020
accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080
gacgacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt 1140
ccttactggg gccaaagAAC cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct 1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgCag tgccagctca 1320
agtgtAagtt acatgaactg gtatcagcag aaaccagggA aagcccctaa gagatggatt 1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
caacagtggA gtcgtaaccC acccactttc ggcgagggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

```

```

<210> 32
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H7L8 (TSC336) CD3-binding domain

```

```
<400> 32
```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1           5           10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

```

SeqList.txt

35

40

45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val

SeqList.txt

```

305                310                315                320
Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                330                335
Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
                340                345                350
Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
                355                360                365
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                370                375                380
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                390                395                400
Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                410                415
Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
                420                425                430
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
                435                440                445
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
                450                455                460
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                470                475                480
Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                490                495
Glu Ile Lys Arg Ser Ser Ser
                500

```

```

<210> 33
<211> 1572
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Fc H8L6 (TSC337) CD3-binding domain

```

```

<400> 33
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaaggg acaccctcat gatctcccg      180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

```

SeqList.txt

```

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcccttctc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg      840
gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc      900
ttcaccagat ctacgatgca ctgggtgcca caggcccctg gacaagggtc tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct     1260
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgagc tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg     1440
acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt     1500
caacagtgga gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

<210> 34
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H8L6 (TSC337) CD3-binding domain
 <400> 34

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

SeqList.txt

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

SeqList.txt

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 35

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc H8L7 (TSC338) CD3-binding domain

<400> 35

atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccg 180

acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

SeqList.txt

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg 840
gctgaggtga agaagcctgg ggcctcagtg aaggtttctt gcaaggcatc tggatacacc 900
ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
accatgacca gggacacgtc cagcagcaca gtctacatgg agctgagcag cctgagatct 1080
gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacggggtt 1140
ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggatggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct 1260
ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320
agtgttaagt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380
tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg 1440
acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt 1500
cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

<210> 36
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L7 (TSC338) CD3-binding domain
<400> 36

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

SeqList.txt

50

55

60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
Page 53

SeqList.txt

325

330

335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
 385 390 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 37

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc H8L8 (TSC339) CD3-binding domain

<400> 37

atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg 180

accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

SeqList.txt

```

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcccttctt ctctacagca agctcaccgt ggacaagagc      660
agggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggg gcagtctggg      840
gctgaggtga agaagcctgg ggcctcagtg aaggtttctt gcaaggcatc tggatacacc      900
ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgctaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggtatccg gcgggtggcg atcgggtggc ggcggatctg acatccagat gaccagctct     1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgagc tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg     1440
acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc     1500
caacagtgga gtcgtaacct acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

```

<210> 38
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H8L8 (TSC339) CD3-binding domain

```

```

<400> 38

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50          55          60

```

SeqList.txt

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
 325 330 335

SeqList.txt

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 39
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H10L6 (TSC340) CD3-binding domain

<400> 39
 atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420

SeqList.txt

```

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccggtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaagAAC cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
gggtggatccg gcggtggcgg atcgggtggc ggcggtatctg acatccagat gaccagctct     1260
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcaG tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagggA aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg     1440
acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt     1500
caacagtgga gtcgtaacc acccactttc ggcgagggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

```

<210> 40
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H10L6 (TSC340) CD3-binding domain

```

```

<400> 40

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

```

SeqList.txt

65					70					75					80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	
Asp	Trp	Leu	Asn	Gly	Lys	Ala	Tyr	Ala	Cys	Ala	Val	Ser	Asn	Lys	Ala
			100					105					110		
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145					150					155					160
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Gln	Arg	His	Asn	Asn	Ser	Ser	Leu	Asn
225					230					235					240
Thr	Gly	Thr	Gln	Met	Ala	Gly	His	Ser	Pro	Asn	Ser	Gln	Val	Gln	Leu
				245					250					255	
Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser	Val	Lys	Val
			260					265					270		
Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Arg	Ser	Thr	Met	His	Trp
		275					280					285			
Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Tyr	Ile	Asn
	290					295					300				
Pro	Ser	Ser	Ala	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Arg	Val
305					310					315					320
Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser
				325					330					335	
Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Pro	Gln

SeqList.txt

340

345

350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 41
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H10L7 (TSC341) CD3-binding domain

<400> 41
 atggaagcac cagcgagct tctcttctc ctgctactct ggctcccaga taccaccggt 60
 gagccaaat cttctgaaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttct cttccccca aaaccaagg acaccctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaaggga gccccgagaa ccacaggtgt acaccctgcc cccatcccg 480

SeqList.txt

```

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggctctct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcca caggcccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cagagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggatggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct     1260
ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca     1320
agtgtaaagt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt     1380
tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg     1440
acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt     1500
cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                                1572

```

```

<210> 42
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fc H10L7 (TSC341) CD3-binding domain
<400> 42

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
          65          70          75          80

```

SeqList.txt

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

SeqList.txt

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
 385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 43
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fc H10L8 (TSC342) CD3-binding domain

<400> 43
 atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

SeqList.txt

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctcccttctt ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagctggg gcaatctggg 840
 gctgaggtga agaagcctgg gtcctcgggtg aaggtctcct gcaaggcttc tggaggcacc 900
 ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
 acgattaccg cggacaaatc cagagcaca gcctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260
 ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgca gtcagctca 1320
 agtghtaagtt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt 1380
 tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
 acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
 caacagtggg gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
 tcctccagct aa 1572

<210> 44
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fc H10L8 (TSC342) CD3-binding domain
 <400> 44

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 Page 64

SeqList.txt

85

90

95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 Page 65

SeqList.txt

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 45
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TSC370 CD3-binding domain

<400> 45
 atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

SeqList.txt

```

cccggtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
tacacgcaga agagcctctc cctgtctccg ggctcagaggc acaacaattc ttccctgaat 780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840
gctgaggtga agaagcctgg gtcctcgggtg aaggctctct gcaaggcttc tggatatacc 900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggatg 960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
ccttactggg gccaaagAAC cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggatggatccg gcggtggcgg atcgggtggc ggcggtatctg acatccagat gaccagctct 1260
ccttccacc tgctctgcat ttaggagac agagtcacca tcacttgcag tgccagctca 1320
agtgaagtt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt 1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
caacagtgga gtcgtaacc acccactttc ggcgaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

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<210> 46

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> TSC370 CD3-binding domain

<400> 46

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

SeqList.txt

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

SeqList.txt

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 47
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC371 CD3-binding domain

<400> 47
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccg 180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
atctccaaag ccaaaggga gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

SeqList.txt

```

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtt tgagtggata      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cagcagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct     1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgca tgcagctca      1320
agtgtaaagt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg     1440
acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc     1500
caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                              1572

```

<210> 48
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TSC371 CD3-binding domain

<400> 48

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala

SeqList.txt

100

105

110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

SeqList.txt
380

370

375

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 49
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC372 CD3-binding domain

<400> 49
atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt 60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
gggtgcaccgt cagtcttctt cttccccca aaaccaagg acaccctcat gatctcccgg 180
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

SeqList.txt

```

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggg gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtt tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt     1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggtatcc gcggtggcgg atcggtggc ggcgatctg acatccagat gacccagtct     1260
ccttccaccc tgtctgcatc ttaggagac agagtcacca tgacttgagc tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg     1440
acagaattca ctctcacat cagcagcctg cagcctgatg attttgcaac ttattactgc     1500
caacagtgga gtcgtaacc acccactttc ggcgaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                           1572

```

```

<210> 50
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TSC372 CD3-binding domain

```

```

<400> 50

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1           5           10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65          70          75          80

```

```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
          85          90          95

```

```

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
          100          105          110

```

SeqList.txt

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

SeqList.txt

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 51
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC390 CD3-binding domain

<400> 51
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
atctccaaag ccaaaggga gcccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc 660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

SeqList.txt

```

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840
cctgaggtga agaagcctgg gtcctcggtg aaggctctct gcaaggcttc tggatatacc      900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtt tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct     1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt     1140
ccttactggg gccaaagAAC cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga     1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagctct     1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca     1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt     1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg     1440
acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc     1500
caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg     1560
tcctccagct aa                                                              1572

```

```

<210> 52
<211> 503
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> TSC390 CD3-binding domain

```

```

<400> 52

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65          70          75          80

```

```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
          85          90          95

```

```

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
          100          105          110

```

```

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

```

SeqList.txt

115

120

125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
 290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 Page 77

SeqList.txt

385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 53
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TSC391 CD3-binding domain

<400> 53
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 gagcccaa at cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

SeqList.txt

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatataacc 900
 ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggtc tgagtggata 960
 ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020
 acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080
 gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt 1140
 ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
 ggtggatccg gcggtggcgg atcgggtggc ggcgatctg acatccagat gacccagtct 1260
 ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320
 agtgaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt 1380
 tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
 acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
 caacagtgga gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
 tcctccagct aa 1572

<210> 54

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> TSC391 CD3-binding domain

<400> 54

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

SeqList.txt

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400

SeqList.txt

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 55
 <211> 1572
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TSC392 CD3-binding domain

<400> 55
 atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt 60
 gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120
 ggtgcaccgt cagtcttctt cttccccca aaaccaagg acaccctcat gatctcccgg 180
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtcc 240
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360
 ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc 420
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600
 cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 660
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720
 tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780
 acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840
 cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

SeqList.txt

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ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg      960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc      1020
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct      1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt      1140
ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga      1200
ggatggatccg gcgggtggcg atcgggtggc ggcggatctg acatccagat gacccagtct      1260
ccttccaccc tgtctgcatc ttaggagac agagtcacca tgacttgca tgccagctca      1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt      1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg      1440
acagagttca ctctacccat cagcagcctg cagcctgatg attttgcaac ttattactgc      1500
caacagtgga gtcgtaacc acccactttc ggcggaggga ccaaggtgga gatcaaacgg      1560
tcctccagct aa                                                              1572

```

```

<210> 56
<211> 503
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TSC392 CD3-binding domain

```

```

<400> 56

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65          70          75          80

```

```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
          85          90          95

```

```

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
          100          105          110

```

```

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
          115          120          125

```

```

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

```

SeqList.txt
140

130

135

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
Page 83

405

410

415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 57

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> TSC393 CD3-binding domain

<400> 57

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gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120
ggtgcaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      180
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      420
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg      480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc      660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggg gcaatctggg      840
gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc      900
ttcagcagat ctacgatgca ctgggtgcca caggcccctg gacaagggct tgagtggata      960

```

SeqList.txt

```

ggatacatta atcctagcag tgcttataact aattacaatc agaaattcaa ggacagagtc 1020
acgattaccg cggacaaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacggggtt 1140
ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gaccagtcct 1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgacag tgccagctca 1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt 1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

```

```

<210> 58
<211> 503
<212> PRT
<213> Artificial Sequence

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<220>
<223> TSC393 CD3-binding domain

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```

<400> 58

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```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1          5          10          15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          20          25          30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          35          40          45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          50          55          60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65          70          75          80

```

```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
          85          90          95

```

```

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
          100          105          110

```

```

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
          115          120          125

```

```

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
          130          135          140

```

SeqList.txt

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
 225 230 235 240
 Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
 245 250 255
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 260 265 270
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
 275 280 285
 Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 290 295 300
 Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 305 310 315 320
 Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 325 330 335
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 340 345 350
 Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 355 360 365
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 385 390 395 400
 Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 405 410 415

SeqList.txt

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 59

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> TSC394 CD3-binding domain

<400> 59

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt	60
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg	120
ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg	180
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	240
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	300
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	360
ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc	420
atctccaaag ccaaaggga gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	480
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc	540
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	600
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	660
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	720
tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat	780
acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg	840
cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc	900
ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata	960
ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc	1020

SeqList.txt

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080
gaggacacgg ccgtgtatta ctgtgcgaga cccaagtcc actatgatta caacgggttt 1140
ccttactggg gccaaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200
ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260
ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca 1320
agtgtaaagt acatgaactg gtatcagcag aaaccagga aagcccctaa gagatggatt 1380
tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440
acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500
caacagtgga gtcgtaacct acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560
tcctccagct aa 1572

<210> 60
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC394 CD3-binding domain

<400> 60

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

SeqList.txt

145		150		155		160									
Asp	Ile	Ala	Val	Glu 165	Trp	Glu	Ser	Asn	Gly 170	Gln	Pro	Glu	Asn	Asn	Tyr
Lys	Thr	Thr	Pro 180	Pro	Val	Leu	Asp	Ser 185	Asp	Gly	Ser	Phe	Phe 190	Leu	Tyr
Ser	Lys	Leu 195	Thr	Val	Asp	Lys	Ser 200	Arg	Trp	Gln	Gln	Gly 205	Asn	Val	Phe
Ser	Cys 210	Ser	Val	Met	His	Glu 215	Ala	Leu	His	Asn	His 220	Tyr	Thr	Gln	Lys
Ser 225	Leu	Ser	Leu	Ser	Pro 230	Gly	Gln	Arg	His	Asn 235	Asn	Ser	Ser	Leu	Asn 240
Thr	Gly	Thr	Gln	Met 245	Ala	Gly	His	Ser	Pro 250	Asn	Ser	Gln	Val	Gln 255	Leu
Val	Gln	Ser	Gly 260	Pro	Glu	Val	Lys	Lys 265	Pro	Gly	Ser	Ser	Val	Lys	Val
Ser	Cys	Lys 275	Ala	Ser	Gly	Tyr	Thr 280	Phe	Ser	Arg	Ser	Thr 285	Met	His	Trp
Val	Arg 290	Gln	Ala	Pro	Gly	Gln 295	Gly	Leu	Glu	Trp	Ile 300	Gly	Tyr	Ile	Asn
Pro 305	Ser	Ser	Ala	Tyr	Thr 310	Asn	Tyr	Asn	Gln	Lys 315	Phe	Lys	Asp	Arg	Val 320
Thr	Ile	Thr	Ala	Asp 325	Lys	Ser	Thr	Ser	Thr 330	Ala	Tyr	Met	Glu	Leu	Ser 335
Ser	Leu	Arg	Ser 340	Glu	Asp	Thr	Ala	Val 345	Tyr	Tyr	Cys	Ala	Arg 350	Pro	Gln
Val	His	Tyr 355	Asp	Tyr	Asn	Gly	Phe 360	Pro	Tyr	Trp	Gly	Gln 365	Gly	Thr	Leu
Val	Thr 370	Val	Ser	Ser	Gly	Gly 375	Gly	Gly	Ser	Gly	Gly 380	Gly	Gly	Ser	Gly
Gly 385	Gly	Gly	Ser	Gly	Gly 390	Gly	Gly	Ser	Asp	Ile 395	Gln	Met	Thr	Gln	Ser 400
Pro	Ser	Thr	Leu	Ser 405	Ala	Ser	Val	Gly	Asp 410	Arg	Val	Thr	Met	Thr 415	Cys
Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro

420

425

430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 485 490 495

Glu Ile Lys Arg Ser Ser Ser
 500

<210> 61
 <211> 2301
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TSC408 Anti-PSMA X anti-CD3 bispecific molecule

<400> 61
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 gatatccaga tgaccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120
 atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180
 gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240
 cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300
 gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360
 gggaccaagg tggaaatcaa acgaggtggc ggaggggtctg ggggtggcgg atccggaggt 420
 ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480
 gtgaaggctc cctgcaaggc ttctggatac acattcactg actactacat gactgggtg 540
 cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600
 actagatacg cacagaagtt ccagggcaga gtcacatga ccagggacac gtctatcagc 660
 acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720
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 tcctcgagtg agcccaaadc ttctgacaaa actcacacat gccaccgtg cccagcacct 840
 gaagccgcgg gtgcaccgtc agtcttctc ttcccccaa aaccaagga caccctcatg 900
 atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

SeqList.txt

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gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
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tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500
tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctgggtg 1560
caatctgggc ctgaggtgaa gaagcctggg tcctcgggtga aggtctcctg caaggcttct 1620
ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccttg acaagggtt 1680
gagtggatag gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag 1740
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ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac 1860
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accagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat cacttgcagt 2040
gccagtcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100
agatggattt atgactcatc caaactggct tctgggggtcc catcaagggt cagcggcagt 2160
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tattactgcc aacagtggag tcgtaacca cccactttcg gcggaggggac caaggtggag 2280
atcaaacggt cctccagcta a 2301

```

<210> 62

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<223> TSC408 Anti-PSMA X anti-CD3 bispecific molecule

<400> 62

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
1           5           10          15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20          25          30

```

```

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Arg Ile
35          40          45

```

```

His Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60

```


SeqList.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
 100 105 110
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val
 115 120 125
 Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 130 135 140
 Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
 145 150 155 160
 Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
 165 170 175
 Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
 180 185 190
 Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
 195 200 205
 Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
 210 215 220
 Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 225 230 235 240
 Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335

SeqList.txt

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
 340 345 350
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
 465 470 475 480
 Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
 485 490 495
 Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
 500 505 510
 Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
 515 520 525
 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 530 535 540
 Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 545 550 555 560
 Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
 565 570 575
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 580 585 590
 Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
 595 600 605

SeqList.txt

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
625 630 635 640

Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr
645 650 655

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
660 665 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
675 680 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
690 695 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
705 710 715 720

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
725 730 735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745

<210> 63
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC409 Anti-PSMA X anti-CD3 bispecific molecule

<400> 63
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SeqList.txt

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<210> 64
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TSC409 Anti-PSMA X anti-CD3 bispecific molecule

<400> 64

Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly

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His Ser Gly Ser 50	Thr Leu Gln Ser	Gly Val Pro Ser 55	Arg Phe Ser Gly 60
Ser Gly Ser Gly 65	Thr Glu Phe Thr	Leu Thr Ile Ser 70	Ser Ser Leu Gln Pro 75
Glu Asp Phe Ala 85	Thr Tyr Tyr Cys	Gln Gln His Ile 90	Glu Tyr Pro Trp 95
Thr Phe Gly Gln 100	Gly Thr Lys Val	Glu Ile Lys Arg 105	Gly Gly Gly Gly 110
Ser Gly Gly Gly 115	Gly Gly Ser Gly	Gly Gly Gly Ser 120	Gln Val Gln Leu Val 125
Gln Ser Gly Ala 130	Glu Val Lys Lys	Pro Gly Ala Ser 135	Val Lys Val Ser 140
Cys Lys Ala Ser 145	Gly Tyr Thr Phe	Thr Asp Tyr Tyr 150	Met His Trp Val 155
Arg Gln Ala Pro 165	Gly Gln Gly Leu	Glu Trp Met Gly 170	Tyr Phe Asn Pro 175
Tyr Asn Asp Tyr 180	Thr Arg Tyr Ala	Gln Lys Phe Gln 185	Gly Arg Val Thr 190
Met Thr Arg Asp 195	Thr Ser Ile Ser	Thr Ala Tyr Met 200	Glu Leu Ser Ser 205
Leu Arg Ser Asp 210	Asp Thr Ala Val	Tyr Tyr Cys Ala 215	Arg Ser Asp Gly 220
Tyr Tyr Asp Ala 225	Met Asp Tyr Trp	Gly Gln Gly Thr 230	Thr Thr Val Thr 235
Ser Ser Ser Glu 245	Pro Lys Ser Ser	Asp Lys Thr His 250	Thr Cys Pro Pro 255
Cys Pro Ala Pro 260	Glu Ala Ala Gly	Ala Pro Ser Val 265	Phe Leu Phe Pro 270
Pro Lys Pro Lys 280	Asp Thr Leu Met	Ile Ser Arg Thr 285	Pro Glu Val Thr 290

SeqList.txt

275

280

285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
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Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
 340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
 465 470 475 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
 485 490 495

Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
 500 505 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
 515 520 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 530 535 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys

SeqList.txt

SeqList.txt

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<210> 66
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TSC410 Anti-PSMA X anti-CD3 bispecific molecule

<400> 66

Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
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Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Arg Ile
 35 40 45

His Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val
 115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
 145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
 165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
 180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
 195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
 210 215 220

SeqList.txt

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
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 Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335
 Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
 340 345 350
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
 465 470 475 480
 Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
 485 490 495

SeqList.txt

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser
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 Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
 515 520 525
 Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 530 535 540
 Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 545 550 555 560
 Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
 565 570 575
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 580 585 590
 Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
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 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
 625 630 635 640
 Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 645 650 655
 Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
 660 665 670
 Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
 675 680 685
 Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 690 695 700
 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
 705 710 715 720
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 Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
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<210> 67
 <211> 2301
 <212> DNA

<213> Artificial Sequence

<220>

<223> TSC411 Anti-PSMA X anti-CD3 bispecific molecule

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 gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100
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<210> 68

<211> 746

<212> PRT

<213> Artificial Sequence

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<223> TSC411 Anti-PSMA X anti-CD3 bispecific molecule

<400> 68

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Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Arg Ile
 35 40 45

His Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
 115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
 130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
 145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
 Page 104

SeqList.txt

165

170

175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
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 Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
 195 200 205
 Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
 210 215 220
 Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
 225 230 235 240
 Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
 245 250 255
 Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
 260 265 270
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 275 280 285
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 290 295 300
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 305 310 315 320
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 325 330 335
 Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
 340 345 350
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 355 360 365
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 370 375 380
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 385 390 395 400
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 405 410 415
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

SeqList.txt

435

440

445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
 465 470 475 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
 485 490 495

Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
 500 505 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
 515 520 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 530 535 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
 545 550 555 560

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
 565 570 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 580 585 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
 595 600 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
 625 630 635 640

Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 645 650 655

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
 660 665 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
 675 680 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 690 695 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
 Page 106

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
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725

730

735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745

740

745

<210>	69
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<212>	DNA
<213>	Artificial Sequence

$\langle 211 \rangle$ 2313

<212> DNA

<213> Artificial Sequence

<220>
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<223> CAS105 Anti-CD37 X anti-CD3 bispecific molecule

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 <211> 750
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAS105 Anti-CD37 X anti-CD3 bispecific molecule

<400> 70

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 20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

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Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
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 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
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 145 150 155 160
 Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 180 185 190
 Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220
 Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240
 Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350
 Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380

SeqList.txt

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
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 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 450 455 460
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 465 470 475 480
 Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
 485 490 495
 Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly
 500 505 510
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
 515 520 525
 Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
 530 535 540
 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
 545 550 555 560
 Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp
 565 570 575
 Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 580 585 590
 Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
 595 600 605
 Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 610 615 620
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
 625 630 635 640
 Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 645 650 655

SeqList.txt

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745 750

<210> 71

<211> 2325

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-CD37 X TSC445 anti-CD3 bispecific molecule

<400> 71

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SeqList.txt

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<210> 72

<211> 754

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD37 X TSC445 anti-CD3 bispecific molecule

<400> 72

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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
Page 112

SeqList.txt
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50

55

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
180 185 190

Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
210 215 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
260 265 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
Page 113

SeqList.txt

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330

335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 465 470 475 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
 485 490 495

Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Pro
 500 505 510

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
 515 520 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
 530 535 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
 545 550 555 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
 565 570 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
 580 585 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr

SeqList.txt

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600

605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 610 615 620

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 625 630 635 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 645 650 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
 660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
 690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
 705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
 725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
 740 745 750

Ser Ser

<210> 73

<211> 2325

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-CD37 X TSC452 anti-CD3 bispecific molecule

<400> 73

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gtcccatcaa	ggttcagcgg	cagtggatct	gggacagagt	tcactctcac	catcagcagc	2220
ctgcagcctg	atgattttgc	aacttattac	tgccaacagt	ggagtcgtaa	cccaccact	2280
ttcggcggag	ggaccaaggt	ggagatcaaa	cggtcctcca	gctaa		2325

<210> 74
 <211> 754
 <212> PRT
 <213> Artificial Sequence

SeqList.txt

<220>

<223> Anti-CD37 X TSC452 anti-CD3 bispecific molecule

<400> 74

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
 130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 180 185 190

Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255

SeqList.txt

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350
 Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 385 390 395 400
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 450 455 460
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 465 470 475 480
 Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
 485 490 495
 Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly
 500 505 510
 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
 515 520 525

SeqList.txt

Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
 530 535 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
 545 550 555 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp
 565 570 575

Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
 580 585 590

Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
 595 600 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 610 615 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 625 630 635 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 645 650 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
 660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
 690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
 705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
 725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
 740 745 750

Ser Ser

<210> 75
 <211> 2322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Anti-CD37 X TSC453 anti-CD3 bispecific molecule

SeqList.txt

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<400> 75
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
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tcctgtaagg gctccgggta ctcatctact ggctacaata tgaactgggt gcgccagatg      180
cccgggaaaag gcctggagtg gatgggcaat attgatcctt attatgggtg tactacctac      240
aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac      300
ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc      360
ggcccttttcg actcctgggg ccagggcacc ctgggtcactg tctcctctgg ggggtggaggc      420
tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc      480
tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc      540
accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa      600
cctggccagg ctctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca      660
gccaggttca gtggcagtggt ctccgggaca gacttcactc tcaccatcag cagcctagag      720
cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc      780
caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac      840
acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtcct cctcttcccc      900
ccaaaacca aggacacct catgatctcc cggacccttg aggtcacatg cgtggtgggtg      960
gacgtgagcc acgaagacct tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg     1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc     1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc     1140
aaciaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga     1200
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc     1260
ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat     1320
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc     1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca     1440
tgctccgtga tgcagtaggc tctgcacaac cactacacgc agaagagcct ctccctgtct     1500
ccgggtcaga ggcacaacia ttcttccttg aatacaggaa ctcatatggc aggtcattct     1560
ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg     1620
gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg     1680
cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgttat     1740
actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc     1800
acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg     1860
agacccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc     1920
accgtctcct caggtggagg cggttcaggc ggaggtggat ccggaggtgg tggctctggt     1980

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SeqList.txt

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ggcggcgcat ctgacatcca gatgaccag tctccaagca gcctgtctgc aagcgtgggg 2040
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cagaagccgg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 2160
gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc 2220
ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccaccacg 2280
ttcggagggg ggaccaagct acaaattaca tcctccagct aa 2322

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<210> 76
 <211> 753
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-CD37 X TSC453 anti-CD3 bispecific molecule

<400> 76

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
 130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 Page 121

SeqList.txt

180

185

190

Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 Page 122

SeqList.txt
460

450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
485 490 495

Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Pro
500 505 510

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
515 520 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
530 535 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545 550 555 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
565 570 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
580 585 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
595 600 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
610 615 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
645 650 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
705 710 715 720

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser
 740 745 750

Ser

<210> 77
 <211> 2325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Anti-CD37 X TSC454 anti-CD3 bispecific molecule

<400> 77
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 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cgggagagtc tctgaagatt 120
 tcctgtaagg gctccggtta ctcatcact ggctacaata tgaactgggt gcgccagatg 180
 cccgggaaaag gcctggagtg gatgggcaat attgatcctt attatgggtg tactacctac 240
 aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300
 ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360
 ggccctttcg actcctgggg ccagggcacc ctgggtcactg tctcctctgg ggggtggaggc 420
 tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480
 tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540
 accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600
 cctggccagg ctcttaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660
 gccaggttca gtggcagtggt ctccgggaca gacttcactc tcaccatcag cagcctagag 720
 cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780
 caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840
 acatgcccac cgtgccagc acctgaagcc gcgggtgcac cgtcagtcct cctcttcccc 900
 ccaaaacca aggacacct catgatctcc cggaccctg aggtcacatg cgtggtggtg 960
 gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 1020
 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200
 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
 ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320
 gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1380
 ttctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

SeqList.txt

tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct	1500
ccgggtcaga ggcacaacaa ttcttccttg aatacaggaa ctcatatggc aggtcattct	1560
ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg	1620
gtgaaggctc cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg	1680
cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcattat	1740
actaattaca atcagaaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc	1800
acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg	1860
agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc	1920
accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt	1980
ggcggcggat ctgacatcca gatgaccag tctccttcca ccctgtctgc atctgtagga	2040
gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag	2100
cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg	2160
gtcccatcaa gggtcagcgg cagtggatct gggacagatt tcactctcac catcagcagc	2220
ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccaccact	2280
ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa	2325

<210> 78

<211> 754

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD37 X TSC454 anti-CD3 bispecific molecule

<400> 78

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
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Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr
			20					25					30		

Asn	Met	Asn	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly	Asn	Ile	Asp	Pro	Tyr	Tyr	Gly	Gly	Thr	Thr	Tyr	Asn	Arg	Lys	Phe
	50					55					60				

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

Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Ser	Val	Gly	Pro	Phe	Asp	Ser	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		

SeqList.txt

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
 130 135 140
 Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160
 Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 180 185 190
 Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220
 Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240
 Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350
 Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380

SeqList.txt

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 385 390 395 400
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 450 455 460
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 465 470 475 480
 Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
 485 490 495
 Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Pro
 500 505 510
 Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
 515 520 525
 Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
 530 535 540
 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
 545 550 555 560
 Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
 565 570 575
 Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
 580 585 590
 Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
 595 600 605
 Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 610 615 620
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 625 630 635 640
 Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 645 650 655

SeqList.txt

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 79
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC455 anti-CD3 bispecific molecule

<400> 79
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gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt 120
tcctgtaagg gctccggtta ctcatctact ggctacaata tgaactgggt gcgccagatg 180
cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac 240
aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300
ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360
ggccctttcg actcctgggg ccagggcacc ctgggtcactg tctcctctgg ggggtggaggc 420
tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480
tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540
accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600
cctggccagg ctctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660
gccaggttca gtggcagtggt ctccgggaca gacttcactc tcaccatcag cagcctagag 720
cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780
caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840
acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

SeqList.txt

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ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg      960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg      1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc      1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcggtg cgcggtctcc      1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga      1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc      1260
ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat      1320
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc      1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca      1440
tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct      1500
ccgggtcaga ggcacaacaa ttcttccttg aatacaggaa ctcatatggc aggtcattct      1560
ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg      1620
gtgaaggctc cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg      1680
cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgccttat      1740
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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg      1860
agacccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctgggtc      1920
accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt      1980
ggcggcggtg ctgacatcca gatgaccag tctccttcca ccctgtctgc atctgtagga      2040
gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag      2100
cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg      2160
gtcccatcaa gggtcagcgg cagtggatct gggacagagt atactctcac catcagcagc      2220
ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccaccact      2280
ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa      2325

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<210> 80

<211> 754

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD37 X TSC455 anti-CD3 bispecific molecule

<400> 80

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met

SeqList.txt

35

40

45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
 130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 180 185 190

Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 Page 130

SeqList.txt

305					310					315					320
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
				325					330					335	
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
			340					345					350		
Lys	Ala	Tyr	Ala	Cys	Ala	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
		355					360					365			
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
	370					375					380				
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
385					390					395					400
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
				405					410					415	
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
			420					425					430		
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
		435					440					445			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
	450					455					460				
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
465					470					475					480
Pro	Gly	Gln	Arg	His	Asn	Asn	Ser	Ser	Leu	Asn	Thr	Gly	Thr	Gln	Met
				485					490					495	
Ala	Gly	His	Ser	Pro	Asn	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro
			500					505					510		
Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser
		515					520					525			
Gly	Tyr	Thr	Phe	Ser	Arg	Ser	Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro
	530					535					540				
Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Ser	Ala	Tyr
545					550					555					560
Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Arg	Val	Thr	Ile	Thr	Ala	Asp
				565					570					575	
Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu

580

585

590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
 595 600 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 610 615 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 625 630 635 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 645 650 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
 660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
 690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser
 705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
 725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
 740 745 750

Ser Ser

<210> 81
 <211> 2325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Anti-CD37 X TSC456 anti-CD3 bispecific molecule

<400> 81
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 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt 120
 tcctgtaagg gctccggtta ctcatcact ggctacaata tgaactgggt gcgccagatg 180
 cccgggaaag gcctggagt gatgggcaat attgatcctt attatggtgg tactacctac 240
 aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300
 ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360

SeqList.txt

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tctgggtggcg	gtgggtcttg	cggaggtgga	tccgggtggcg	gcggatctgg	cgggggtggc	480
tctgaaattg	tggtgacaca	gtctccagcc	accctgtctt	tgtctccagg	cgaaagagcc	540
accctctcct	gccgagcaag	tgaaaatgtt	tacagctact	tagcctggta	ccaacagaaa	600
cctggccagg	ctcctaggct	cctcatctat	tttgcaaaaa	ccttagcaga	aggtattcca	660
gccaggttca	gtggcagtgg	ctccgggaca	gacttcactc	tcaccatcag	cagcctagag	720
cctgaagatt	ttgcagttta	ttactgtcaa	catcattccg	ataatccgtg	gacattcggc	780
caagggacca	aggtggaaat	caaatcctcg	agttagccca	aatcttctga	caaaactcac	840
acatgcccac	cgtgcccagc	acctgaagcc	gcgggtgcac	cgtcagtctt	cctcttcccc	900
ccaaaaccca	aggacaccct	catgatctcc	cggacccttg	aggtcacatg	cgtgggtggg	960
gacgtgagcc	acgaagaccc	tgaggtcaag	ttcaactggg	acgtggacgg	cgtggaggtg	1020
cataatgcca	agacaaagcc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtggtcagc	1080
gtcctcaccg	tcctgcacca	ggactggctg	aatggcaagg	catacgcgtg	cgcggtctcc	1140
aacaaagccc	tcccagcccc	catcgagaaa	accatctcca	aagccaaagg	gcagccccga	1200
gaaccacagg	tgtacaccct	gccccatcc	cgggatgagc	tgaccaagaa	ccaggtcagc	1260
ctgacctgcc	tggtcaaagg	cttctatcca	agcgacatcg	ccgtggagtg	ggagagcaat	1320
gggcagccgg	agaacaacta	caagaccacg	cctcccgtgc	tggactccga	cggctccttc	1380
ttcctctaca	gcaagctcac	cgtggacaag	agcaggtggc	agcaggggaa	cgtcttctca	1440
tgctccgtga	tgcatgaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1500
ccgggtcaga	ggcacaacaa	ttcttccttg	aatacaggaa	ctcagatggc	aggtcattct	1560
ccgaattctc	aggtccagct	ggtgcaatct	gggcctgagg	tgaagaagcc	tgggtcctcg	1620
gtgaaggctc	cctgcaaggc	ttctggatat	accttcagca	gatctacgat	gcactgggtg	1680
cgacaggccc	ctggacaagg	gcttgagtgg	ataggataca	ttaatcctag	cagtgccttat	1740
actaattaca	atcagaaatt	caaggacaga	gtcacgatta	ccgcggacaa	atccacgagc	1800
acagcctaca	tggagctgag	cagcctgaga	tctgaggaca	cggccgtgta	ttactgtgcg	1860
agaccccaag	tccactatga	ttacaacggg	tttccttact	ggggccaagg	aaccctggtc	1920
accgtctcct	caggtggagg	cggttcaggc	ggaggtggat	ccggcggtgg	cggatcgggt	1980
ggcggcggat	ctgacatcca	gatgaccag	tctccttcca	ccctgtctgc	atctgtagga	2040
gacagagtca	ccatgacttg	cagtgccagc	tcaagtgtaa	gttacatgaa	ctggtatcag	2100
cagaaaccag	ggaaagcccc	taagagatgg	atttatgact	catccaaact	ggcttctggg	2160
gtcccatcaa	ggttcagcgg	cagtggatct	gggacagatt	atactctcac	catcagcagc	2220
ctgcagcctg	atgattttgc	aacttattac	tgccaacagt	ggagtcgtaa	cccaccact	2280
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SeqList.txt

<211> 754
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Anti-CD37 X TSC456 anti-CD3 bispecific molecule

<400> 82

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30

Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
 130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
 145 150 155 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
 180 185 190

Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 210 215 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
 225 230 235 240

SeqList.txt

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
 245 250 255
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 260 265 270
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350
 Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 370 375 380
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 385 390 395 400
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 405 410 415
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 420 425 430
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 435 440 445
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 450 455 460
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 465 470 475 480
 Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
 485 490 495
 Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Pro
 500 505 510

SeqList.txt

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
 515 520 525

 Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
 530 535 540

 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
 545 550 555 560

 Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
 565 570 575

 Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
 580 585 590

 Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
 595 600 605

 Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 610 615 620

 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 625 630 635 640

 Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 645 650 655

 Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
 660 665 670

 Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 675 680 685

 Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
 690 695 700

 Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
 705 710 715 720

 Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
 725 730 735

 Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
 740 745 750

 Ser Ser

<210> 83
 <211> 251
 <212> PRT

<213> Artificial Sequence

<220>

<223> TSC455 CD3 scFv CD3-binding domain

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
130 135 140

Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
145 150 155 160

Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser
180 185 190

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser

<210> 84
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TSC456 CD3 scFv CD3-binding domain

<400> 84

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
 130 135 140

Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 145 150 155 160

Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
 165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser
 180 185 190

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
 210 215 220

SeqList.txt

Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
 225 230 235 240

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
 245 250

<210> 85

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> DRA222 CD3 scFv CD3-binding domain

<400> 85

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
 65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95

Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
 100 105 110

Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
 130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
 145 150 155 160

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
 165 170 175

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
 180 185 190

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 Page 139

195

200

205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

Leu Gln Ile Thr Ser Ser Ser
 245

<210> 86

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> TSC455 and TSC456 variable heavy domain CD3-binding domain

<400> 86

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 87

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> DRA222 variable heavy domain CD3-binding domain

<400> 87

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 Page 140

SeqList.txt

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1              5              10              15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
      20      25      30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35      40      45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
      50      55      60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
      65      70      75      80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
      85      90      95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
      100      105      110
Gln Gly Thr Pro Val Thr Val Ser Ser
      115      120

<210> 88
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC455 variable light domain CD3-binding domain

<400> 88
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
      20      25      30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
      35      40      45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
      50      55      60
Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
      65      70      75      80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
      85      90      95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
      100      105

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SeqList.txt

<210> 89
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TSC456 variable light domain CD3-binding domain

<400> 89

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
 100 105

<210> 90
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DRA222 variable light domain CD3-binding domain

<400> 90

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80

SeqList.txt

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser
100 105

<210> 91
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<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR1 (Kabat) CD3-binding domain
<400> 91

Arg Ser Thr Met His
1 5

<210> 92
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR2 (Kabat) CD3-binding domain
<400> 92

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

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<223> Cris7 and DRA222 VH CDR3 (Kabat) CD3-binding domain
<400> 93

Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr
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<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR1 (Kabat) CD3-binding domain
<400> 94

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
1 5 10

<210> 95
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> Cris7 and DRA222 VL CDR2 (Kabat) CD3-binding domain

<400> 95

Asp Ser Ser Lys Leu Ala Ser
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<210> 96

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Cris7 and DRA222 VL CDR3 (Kabat) CD3-binding domain

<400> 96

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1 5

<210> 97

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> ROR133 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 97

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ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc      240
cggttctccg gtcctggctc cggcaccgac ttcacctga ccatctcctc cctgcagccc      300
gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc      360
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ggcgggtggcg gtcctgggtg cggcggatct gaggtgcagc tgggtggagtc cggcggcggc      480
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gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc      600
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aaaccaagg acacctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac      960
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SeqList.txt

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<210> 98
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR133 Anti-ROR1 X anti-CD3 bispecific molecule
 <400> 98

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
          20          25          30

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Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
          35          40          45

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Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

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SeqList.txt
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55

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
195 200 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
210 215 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

SeqList.txt

325

330

335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
 500 505 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
 565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
 580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe

SeqList.txt

595

600

605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
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 625 630 635 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 645 650 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
 675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
 725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
 740 745

<210> 99
 <211> 2316
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR193 Anti-ROR1 X anti-CD3 bispecific molecule

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 atcaactgcc aggctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180
 ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240
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SeqList.txt

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<210> 100

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR193 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 100

SeqList.txt

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 Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45
 Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95
 Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160
 Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270

SeqList.txt

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
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 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540

SeqList.txt

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
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Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
565 570 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
580 585 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625 630 635 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 101
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR134 Anti-ROR1 X anti-CD3 bispecific molecule

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atcaactgcc aggctccca gtccatcgac tccaacctgg cctgggtcca gcagaagccc 180

SeqList.txt

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 ctacaaatta catcctccag ctaa 2304

<210> 102
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR134 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 102

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
 195 200 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
 Page 154

SeqList.txt
220

210

215

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
340 345 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
370 375 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
Page 155

SeqList.txt

485

490

495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
 500 505 510
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540
 Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560
 Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
 565 570 575
 Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
 580 585 590
 Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605
 Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
 625 630 635 640
 Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 645 650 655
 Val Thr Met Thr Cys Ser Ala Ser Ser Val Ser Tyr Met Asn Trp
 660 665 670
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
 675 680 685
 Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 690 695 700
 Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 705 710 715 720
 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
 725 730 735
 Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
 740 745

<210> 103

SeqList.txt

<211> 2316
 <212> DNA
 <213> Artificial Sequence

<220>

<223> ROR189 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 103

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gaggacgtgg ccacctacta ctgcctgggc ggcggtggcg ccgtgtccta ccggacctcc	360
ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc	420
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SeqList.txt

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<210> 104

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR189 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 104

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

SeqList.txt

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
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 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430

SeqList.txt

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
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 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540
 Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560
 Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 565 570 575
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 580 585 590
 Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605
 Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 625 630 635 640
 Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 645 650 655
 Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
 660 665 670
 Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 675 680 685
 Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 690 695 700

SeqList.txt

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
 725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
 740 745 750

<210> 105
 <211> 2304
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR154 Anti-ROR1 X anti-CD3 bispecific molecule

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 ggcggtggcg gtcgggtgg cggcggatct gaggtgcagc tgggtggagtc cggcggcggc 480
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 aatgccaa caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080
 ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140
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SeqList.txt

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 ctacaaatta catcctccag ctaa 2304

<210> 106
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR154 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 106

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 Page 162

SeqList.txt

100

105

110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 Page 163

SeqList.txt
380

370

375

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385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
500 505 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
515 520 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625 630 635 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
 675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
 725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
 740 745

<210> 107
 <211> 2316
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR185 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 107
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SeqList.txt

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<210> 108
 <211> 751
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR185 Anti-ROR1 X anti-CD3 bispecific molecule
 <400> 108

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

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

SeqList.txt

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95
 Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160
 Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320

SeqList.txt

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540
 Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560
 Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 565 570 575
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 580 585 590

SeqList.txt

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625 630 635 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 109
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR179 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 109
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gacatccaga tgaccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120
atcaactgcc aggctccca gtccatcgac tccaacctgg cctgggtcca gcagaagccc 180
ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240
cggttctccg gtcctggctc cggcaccgac ttcacctga ccatctctc cctgcagccc 300
gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ctggacctcc 360
ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcg aggtggatcc 420
ggcgggtggc gtcctgggtg cggcggatct gaggtgcagc tgggtggagtc cggcggcggc 480
ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

SeqList.txt

gactaccca	tcacctgggt	gcggcaggcc	cccggcaagg	gcctggagt	gatcggcttc	600
atcaactccg	gcggctccac	ctggtacgcc	tcctgggtga	agggccggtt	caccatctcc	660
cgggacgact	ccaagtccat	cgcctacctg	cagatgaact	ccctgaagac	cgaggacacc	720
gccgtgtact	attgcgcccc	gggctactcc	acctactacc	gggacttcaa	catctggggc	780
cagggcaccc	tggtgaccgt	gtcctcgagt	gagcccaa	attctgacaa	aactcacaca	840
tgcccaccgt	gccagcacc	tgaagccg	ggtgcaccgt	cagtcttcct	cttcccccca	900
aaaccaagg	acaccctcat	gatctccc	acccctgagg	tcacatgcgt	ggtggtggac	960
gtgagccacg	aagaccctga	ggtcaagttc	aactggtacg	tggacggcgt	ggaggtgcat	1020
aatgccaaga	caaagccg	ggaggagcag	tacaacagca	cgtaccgtgt	ggtcagcgtc	1080
ctcaccgtcc	tgcaccagga	ctggctgaat	ggcaaggaat	acaagtgcgc	ggtctccaac	1140
aaagccctcc	cagcccccat	cgagaaaacc	atctccaaag	ccaaagggca	gccccgagaa	1200
ccacaggtgt	acaccctgcc	cccatccc	gatgagctga	ccaagaacca	ggtcagcctg	1260
acctgcctgg	tcaaaggctt	ctatccaagc	gacatcgccg	tggagtggga	gagcaatggg	1320
cagccggaga	acaactacaa	gaccacgcct	cccgtgctgg	actccgacgg	ctccttcttc	1380
ctctacagca	agctcacctg	ggacaagagc	aggtggcagc	aggggaacgt	cttctcatgc	1440
tccgtgatgc	atgaggctct	gcacaaccac	tacacgcaga	agagcctctc	cctgtctccg	1500
ggttctggtg	gaggcggttc	aggcggaggt	ggctccggcg	gtggcggatc	gccgggctct	1560
caggtccagc	tggtggagtc	tgggggcgga	gtggtgcagc	ctgggcggtc	actgaggctg	1620
tcctgcaagg	cttctggcta	cacctttact	agatctacga	tgcactgggt	aaggcaggcc	1680
cctggacaag	gtctggaatg	gattggatac	attaatccta	gcagtgttta	tactaattac	1740
aatcagaaat	tcaaggacag	gttcacaatc	agcgcagaca	aatccaagag	cacagccttc	1800
ctgcagatgg	acagcctgag	gcccaggagc	accggcgtct	atttctgtgc	acggccccaa	1860
gtccactatg	attacaacgg	gtttccttac	tggggccaag	ggactcccgt	cactgtctct	1920
agcggtggtg	gagggctctg	gggtggcgga	tccggaggtg	gtggctctgc	acaagacatc	1980
cagatgacc	agtctccaag	cagcctgtct	gcaagcgtgg	gggacagggt	caccatgacc	2040
tgcagtgcc	gctcaagtgt	aagttacatg	aactggtacc	agcagaagcc	gggcaaggcc	2100
cccaaaagat	ggatttatga	ctcatccaaa	ctggcttctg	gagtcctctg	tcgcttcagt	2160
ggcagtgggt	ctgggaccga	ctataccctc	acaatcagca	gcctgcagcc	cgaagatttc	2220
gccacttatt	actgccagca	gtggagtcgt	aaccaccca	cgttcggagg	ggggaccaag	2280
ctacaaatta	catcctccag	ctaa				2304

<210> 110

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR179 Anti-ROR1 X anti-CD3 bispecific molecule

SeqList.txt

<400> 110

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

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

Tyr Trp Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 Page 171

SeqList.txt

260

265

270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
 500 505 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly

SeqList.txt
540

530

535

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625 630 635 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
645 650 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 111
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR186 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 111
atggaagcac cagcgcagct tctcttctc ctgtactct ggctcccaga taccaccggt 60
gacatccaga tgaccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

SeqList.txt

atcaactgcc	aggcctccca	gtccatcgac	tccaacctgg	cctggttcca	gcagaagccc	180
ggcaagcccc	ccaagctgct	gatctaccgg	gcctccaacc	tggcctccgg	cgtgcctcc	240
cggttctccg	gctccggctc	cggcaccgac	ttcacctga	ccatctcctc	cctgcagccc	300
gaggacgtgg	ccacctacta	ctgcctgggc	ggcgtgggcg	ccgtgtccta	ctggacctcc	360
ttcggcggcg	gcaccaaggt	ggagatcaag	ggtggaggcg	gttcaggcg	aggtggatcc	420
ggcgggtggcg	gctccgggtg	cggcggatct	gaggtgcagc	tgggtggagtc	cggcggcggc	480
ctggtgcagc	ccggccggtc	cctgcggctg	tcctgcaccg	cctccggctc	cgacatcaac	540
gactacccca	tcacctgggt	gcggcaggcc	cccggcaagg	gcctggagtg	gatcggcttc	600
atcaactccg	gcggctccac	ctggtacgcc	tcctgggtga	agggccgggt	caccatctcc	660
cgggacgact	ccaagtccat	cgcctacctg	cagatgaact	ccctgaagac	cgaggacacc	720
gccgtgtact	attgcgcccc	gggctactcc	acctactacc	gggacttcaa	catctggggc	780
cagggcaccc	tggtgaccgt	gtcctcgagt	gagcccaaat	cttctgacaa	aactcacaca	840
tgccaccgt	gccagcacc	tgaagccgcg	ggtgcaccgt	cagtcttcct	cttcccccca	900
aaacccaagg	acacctcat	gatctcccg	accctgagg	tcacatgct	ggtggtggac	960
gtgagccacg	aagacctga	ggtcaagttc	aactggtacg	tggacggcgt	ggaggtgcat	1020
aatgccaaga	caaagccgcg	ggaggagcag	tacaacagca	cgtaccgtgt	ggtcagcgtc	1080
ctcaccgtcc	tgcaccagga	ctggctgaat	ggcaaggaat	acaagtgcgc	ggtctccaac	1140
aaagccctcc	cagcccccat	cgagaaaacc	atctccaaag	ccaaagggca	gccccgagaa	1200
ccacaggtgt	acacctgcc	cccatcccgg	gatgagctga	ccaagaacca	ggtcagcctg	1260
acctgcctgg	tcaaaggctt	ctatccaagc	gacatcgccg	tggagtggga	gagcaatggg	1320
cagccggaga	acaactacaa	gaccacgcct	cccgtgctgg	actccgacgg	ctccttcttc	1380
ctctacagca	agctcaccgt	ggacaagagc	aggtggcagc	aggggaacgt	cttctcatgc	1440
tccgtgatgc	atgaggctct	gcacaaccac	tacacgcaga	agagcctctc	cctgtctccg	1500
ggttctggtg	gaggcggttc	aggcggaggt	ggctccggcg	gtggcggatc	gccgggctct	1560
caggtccagc	tggtgcaatc	tgggcctgag	gtgaagaagc	ctgggtcctc	ggtgaaggtc	1620
tcctgcaagg	cttctggata	taccttcagc	agatctacga	tgcactgggt	gcgacaggcc	1680
cctggacaag	ggcttgagtg	gataggatac	attaatccta	gcagtgttta	tactaattac	1740
aatcagaaat	tcaaggacag	agtcacgatt	accgcggaca	aatccacgag	cacagcctac	1800
atggagctga	gcagcctgag	atctgaggac	acggccgtgt	attactgtgc	gagaccccaa	1860
gtccactatg	attacaacgg	gtttccttac	tggggccaag	gaaccctgg	caccgtctcc	1920
tcaggtggag	gcggttcagg	cggaggtgga	tccggcgggtg	gcggatcggg	tggcggcgga	1980
tctgacatcc	agatgacca	gtctccttcc	accctgtctg	catctgtagg	agacagagtc	2040
accatgactt	gcagtgccag	ctcaagtgtg	agttacatga	actggtatca	gcagaaacca	2100
gggaaagccc	ctaagagatg	gatttatgac	tcattccaaac	tggcttctgg	ggtcccatca	2160

SeqList.txt

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220
 gatgattttg caacttatta ctgccaacag tggagtcgta acccaccac tttcggcgga 2280
 gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 112
 <211> 751
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR186 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 112

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

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

Tyr Trp Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205

SeqList.txt

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

SeqList.txt

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540
 Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560
 Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 565 570 575
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 580 585 590
 Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605
 Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 625 630 635 640
 Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 645 650 655
 Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
 660 665 670
 Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 675 680 685
 Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 690 695 700
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 705 710 715 720
 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
 725 730 735
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
 740 745 750

SeqList.txt

<210> 113
 <211> 2304
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR181 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 113
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 atcaactgcc aggcctccca gtccatcgac tccaacctgg cctgggtcca gcagaagccc 180
 ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240
 cggttctccg gctccggctc cggcaccgac ttcacctga ccatctcctc cctgcagccc 300
 gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360
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 ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg tgtccggcac cgacatcaac 540
 gactaccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600
 atcaactccg gcggtccac ctggtacgcc gactcggatga agggccggtt caccatctcc 660
 cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc 720
 gccgtgtact tctgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780
 cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840
 tgcccaccgt gccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca 900
 aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960
 gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020
 aatgccaaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080
 ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140
 aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200
 ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260
 acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320
 cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc 1380
 ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
 tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500
 ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560
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SeqList.txt

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cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040
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cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220
gccacttatt actgccagca gtggagtcgt aaccaccca cgttcggagg ggggaccaag 2280
ctacaaatta catcctccag ctaa 2304

<210> 114
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR181 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 114

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
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Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Thr Asp Ile Asn

SeqList.txt

145		150		155		160									
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Trp	Ile	Gly	Phe 180	Ile	Asn	Ser	Gly	Gly 185	Ser	Thr	Trp	Tyr	Ala 190	Asp	Ser
Val	Lys	Gly 195	Arg	Phe	Thr	Ile	Ser 200	Arg	His	Ser	Ser	Lys 205	Asn	Thr	Leu
Tyr	Leu 210	Gln	Met	Asn	Ser	Leu 215	Arg	Ala	Glu	Asp	Thr 220	Ala	Val	Tyr	Phe
Cys 225	Ala	Arg	Gly	Tyr	Ser 230	Thr	Tyr	Tyr	Arg	Asp 235	Phe	Asn	Ile	Trp	Gly 240
Gln	Gly	Thr	Leu	Val 245	Thr	Val	Ser	Ser	Ser 250	Glu	Pro	Lys	Ser	Ser 255	Asp
Lys	Thr	His	Thr 260	Cys	Pro	Pro	Cys	Pro 265	Ala	Pro	Glu	Ala	Ala 270	Gly	Ala
Pro	Ser	Val 275	Phe	Leu	Phe	Pro	Pro 280	Lys	Pro	Lys	Asp	Thr 285	Leu	Met	Ile
Ser	Arg 290	Thr	Pro	Glu	Val	Thr 295	Cys	Val	Val	Val	Asp 300	Val	Ser	His	Glu
Asp 305	Pro	Glu	Val	Lys	Phe 310	Asn	Trp	Tyr	Val	Asp 315	Gly	Val	Glu	Val	His 320
Asn	Ala	Lys	Thr	Lys 325	Pro	Arg	Glu	Glu	Gln 330	Tyr	Asn	Ser	Thr	Tyr 335	Arg
Val	Val	Ser	Val 340	Leu	Thr	Val	Leu	His 345	Gln	Asp	Trp	Leu	Asn 350	Gly	Lys
Glu	Tyr	Lys 355	Cys	Ala	Val	Ser	Asn 360	Lys	Ala	Leu	Pro	Ala 365	Pro	Ile	Glu
Lys	Thr 370	Ile	Ser	Lys	Ala	Lys 375	Gly	Gln	Pro	Arg	Glu 380	Pro	Gln	Val	Tyr
Thr 385	Leu	Pro	Pro	Ser	Arg 390	Asp	Glu	Leu	Thr	Lys 395	Asn	Gln	Val	Ser	Leu 400
Thr	Cys	Leu	Val	Lys 405	Gly	Phe	Tyr	Pro	Ser 410	Asp	Ile	Ala	Val	Glu 415	Trp
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val

SeqList.txt

420

425

430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
 500 505 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
 565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
 580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
 610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
 625 630 635 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 645 650 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
 675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser

690

695

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 115
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR191 Anti-ROR1 X anti-CD3 bispecific molecule

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atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180
ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240
cggttctccg gtcctggctc cggcaccgac ttcacctga ccatctctc cctgcagccc 300
gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360
ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcg aggtggatcc 420
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gccgtgtact tctgcgccg gggctactcc acctactacc gggacttcaa catctggggc 780
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ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140
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ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

SeqList.txt

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380
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 tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500
 ggttctggtg gaggcgggtc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560
 caggtccagc tgggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc 1620
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 tcaggtggag gcggttcagg cggaggtgga tccggcgggt gcggatcggg tggcggcgga 1980
 tctgacatcc agatgacca gtctccttcc accctgtctg catctgtagg agacagagtc 2040
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<210> 116

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR191 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 116

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

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

SeqList.txt

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Gly Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Thr Asp Ile Asn
 145 150 155 160
 Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365

SeqList.txt

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525
 Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540
 Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560
 Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 565 570 575
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 580 585 590
 Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605
 Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 625 630 635 640

SeqList.txt

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 117
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR182 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 117
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gacatccaga tgaccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120
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ggcgggtggcg gtcctgggtg cggcggatct gaggtgcagc tgggtggagtc cggcggcggc 480
ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540
gactaccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc 600
atcaactccg gcgggtccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660
cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720
gccgtgtact attgcgccg gggctactcc acctactacc gggacttcaa catctggggc 780
cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840
tgcccaccgt gccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca 900

SeqList.txt

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aatgccaaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc      1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac      1140
aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa      1200
ccacaggtgt acaccctgcc cccatcccg gatgagctga ccaagaacca ggtcagcctg      1260
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cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc      1380
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tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg      1500
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ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggcccca      1860
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agcgggtggcg gagggctctg ggggtggcgga tccggaggtg gtggctctgc acaagacatc      1980
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc      2040
tgcagtgcc a gctcaagtgt aagttacatg aactgggtacc agcagaagcc gggcaaggcc      2100
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt      2160
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc      2220
gccacttatt actgccagca gtggagtcgt aaccaccca cgttcgagg ggggaccaag      2280
ctacaaatta catcctccag ctaa      2304

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<210> 118

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR182 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 118

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

SeqList.txt

35

40

45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95
 Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160
 Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 165 170 175
 Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 Page 188

305 310 315 320

305				310				315				320			
Asn	Ala	Lys	Thr	Lys 325	Pro	Arg	Glu	Glu	Gln 330	Tyr	Asn	Ser	Thr	Tyr 335	Arg
Val	Val	Ser	Val 340	Leu	Thr	Val	Leu	His 345	Gln	Asp	Trp	Leu	Asn 350	Gly	Lys
Glu	Tyr	Lys 355	Cys	Ala	Val	Ser	Asn 360	Lys	Ala	Leu	Pro	Ala 365	Pro	Ile	Glu
Lys	Thr 370	Ile	Ser	Lys	Ala	Lys 375	Gly	Gln	Pro	Arg	Glu 380	Pro	Gln	Val	Tyr
Thr 385	Leu	Pro	Pro	Ser	Arg 390	Asp	Glu	Leu	Thr	Lys 395	Asn	Gln	Val	Ser	Leu 400
Thr	Cys	Leu	Val 405	Lys	Gly	Phe	Tyr	Pro	Ser 410	Asp	Ile	Ala	Val	Glu 415	Trp
Glu	Ser	Asn	Gly 420	Gln	Pro	Glu	Asn	Asn 425	Tyr	Lys	Thr	Thr	Pro 430	Pro	Val
Leu	Asp	Ser 435	Asp	Gly	Ser	Phe	Phe 440	Leu	Tyr	Ser	Lys	Leu 445	Thr	Val	Asp
Lys	Ser 450	Arg	Trp	Gln	Gln	Gly 455	Asn	Val	Phe	Ser	Cys 460	Ser	Val	Met	His
Glu 465	Ala	Leu	His	Asn	His 470	Tyr	Thr	Gln	Lys	Ser 475	Leu	Ser	Leu	Ser	Pro 480
Gly	Ser	Gly	Gly	Gly 485	Gly	Ser	Gly	Gly	Gly 490	Gly	Ser	Gly	Gly	Gly 495	Gly
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Gln	Pro	Gly 515	Arg	Ser	Leu	Arg	Leu 520	Ser	Cys	Lys	Ala	Ser 525	Gly	Tyr	Thr
Phe	Thr 530	Arg	Ser	Thr	Met	His 535	Trp	Val	Arg	Gln	Ala 540	Pro	Gly	Gln	Gly
Leu 545	Glu	Trp	Ile	Gly	Tyr 550	Ile	Asn	Pro	Ser	Ser 555	Ala	Tyr	Thr	Asn	Tyr 560
Asn	Gln	Lys	Phe	Lys 565	Asp	Arg	Phe	Thr	Ile 570	Ser	Ala	Asp	Lys	Ser 575	Lys
Ser	Thr	Ala	Phe	Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly

580

585

590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
 610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
 625 630 635 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 645 650 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
 660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
 675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
 690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
 705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
 725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
 740 745

<210> 119
 <211> 2316
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR192 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 119
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 ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420
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SeqList.txt

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SeqList.txt

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
 85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255

SeqList.txt

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525

SeqList.txt

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
 545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 565 570 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 580 585 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
 595 600 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 625 630 635 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
 660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
 675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
 725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
 740 745 750

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<220>
 <223> sss(s)-hIgG1 hinge

<400> 121

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 Page 194

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1                5                10                15

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<400> 122
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
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<210> 123
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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
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<210> 124
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<400> 124
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1                5                10                15

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<400> 126

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SeqList.txt

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1 5 10 15

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 <211> 15
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<400> 127

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1 5 10 15

<210> 128
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<400> 128

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1 5 10 15

<210> 129
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<400> 129

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1 5 10 15

<210> 130
 <211> 15
 <212> PRT
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<220>
 <223> csc(p)-hIgG1 hinge

<400> 130

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1 5 10 15

<210> 131
 <211> 15
 <212> PRT
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<220>
 <223> ssc(p)-hIgG1 hinge

SeqList.txt

<400> 131

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Cys	Pro
1				5					10					15

<210> 132

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> scc(p)-hIgG1 hinge

<400> 132

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
1				5					10					15

<210> 133

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> css(p)-hIgG1 hinge

<400> 133

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
1				5					10					15

<210> 134

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> scs(p)-hIgG1 hinge

<400> 134

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Ser	Pro
1				5					10					15

<210> 135

<211> 6

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<223> Scppcp linker

<400> 135

Ser	Cys	Pro	Pro	Cys	Pro
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<210> 136

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SeqList.txt

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<223> STD1 linker

<400> 136

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

Ser Gly Asn Ser
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<211> 38

<212> PRT

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<220>

<223> STD2 linker

<400> 137

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Asn Ser
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<210> 138

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<223> H1 linker

<400> 138

Asn Ser
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<210> 139

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> H2 linker

<400> 139

Gly Gly Gly Gly Ser Gly Asn Ser
 1 5

<210> 140

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<212> PRT

<213> Artificial Sequence

SeqList.txt

<220>

<223> H3 linker

<400> 140

Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
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<210> 141

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> H4 linker

<400> 141

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1 5 10

<210> 142

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H5 linker

<400> 142

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1 5 10 15

<210> 143

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> H6 linker

<400> 143

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Asn Ser

<210> 144

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> H7 linker

<400> 144

Gly Cys Pro Pro Cys Pro Asn Ser
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SeqList.txt

<210> 145
 <211> 15
 <212> PRT
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<220>
 <223> (G4S)3 linker

<400> 145

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 146
 <211> 16
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<220>
 <223> H105 linker

<400> 146

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 147
 <211> 20
 <212> PRT
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<220>
 <223> (G4S)4 linker

<400> 147

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 148
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H75 (NKG2A quadruple mutant) linker

<400> 148

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1 5 10 15

His Ser Pro Asn Ser
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<210> 149
 <211> 16
 <212> PRT

<213> Artificial Sequence

<220>

<223> H83 (NKG2A derived) linker

<400> 149

Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 150

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> H106 (NKG2A derived) linker

<400> 150

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15

His Ser

<210> 151

<211> 14

<212> PRT

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<220>

<223> H81 (NKG2D derived) linker

<400> 151

Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
1 5 10

<210> 152

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> H91 (NKG2D derived) linker

<400> 152

Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15

Ser Pro Asn Ser
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<210> 153

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> H94 linker

SeqList.txt

<400> 153

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Pro Asn Ser

<210> 154

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H16 hinge

<400> 154

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1 5 10 15

<210> 155

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> H17 hinge

<400> 155

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Cys Pro Pro
 1 5 10 15

Cys Pro Asn Ser
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<210> 156

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H18 hinge

<400> 156

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1 5 10 15

<210> 157

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> H19 hinge

<400> 157

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro
 Page 202

1 5 10 15

Cys Pro Asn Ser
20

<210> 158
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H20 hinge

<400> 158

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
1 5 10 15

<210> 159
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H21 hinge

<400> 159

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Cys Pro Pro
1 5 10 15

Cys Pro Asn Ser
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<210> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H22 hinge

<400> 160

Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
1 5 10 15

<210> 161
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H23 hinge

<400> 161

Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Ser Cys Pro
1 5 10 15

Pro Cys Pro Asn Ser

20

<210> 162
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H24 hinge

<400> 162

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
 1 5 10 15

<210> 163
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H25 hinge

<400> 163

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Cys Pro Pro
 1 5 10 15

Cys Pro Asn Ser
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<210> 164
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 164

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1 5 10 15

<210> 165
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H27 hinge

<400> 165

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Cys Pro Pro
 1 5 10 15

Cys Pro Asn Ser
 20

<210> 166

SeqList.txt

<211> 15
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<220>
 <223> H28 hinge

<400> 166

Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
 1 5 10 15

<210> 167
 <211> 15
 <212> PRT
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<220>
 <223> H30 hinge

<400> 167

Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
 1 5 10 15

<210> 168
 <211> 15
 <212> PRT
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<220>
 <223> H32 hinge

<400> 168

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1 5 10 15

<210> 169
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H33 hinge

<400> 169

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Cys Pro Pro
 1 5 10 15

Cys Pro Asn Ser
 20

<210> 170
 <211> 13
 <212> PRT
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<220>
 <223> H36 hinge

<400> 170

SeqList.txt

Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1 5 10

<210> 171
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H40 hinge
 <400> 171

Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1 5

<210> 172
 <211> 9
 <212> PRT
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<220>
 <223> H41 hinge
 <400> 172

Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1 5

<210> 173
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H42 hinge
 <400> 173

Gly Cys Pro Pro Cys Pro Asn Ser
 1 5

<210> 174
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H44 hinge
 <400> 174

Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1 5 10

<210> 175
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H45 hinge

SeqList.txt

<400> 175

Gly	Gly	Gly	Ala	Ser	Cys	Pro	Pro	Cys	Ala	Gly	Asn	Ser
1				5					10			

<210> 176

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> H46 hinge

<400> 176

Gly	Gly	Gly	Ala	Ser	Cys	Pro	Pro	Cys	Ala	Asn	Ser
1				5					10		

<210> 177

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H47 hinge

<400> 177

Leu	Ser	Val	Lys	Ala	Asp	Phe	Leu	Thr	Pro	Ser	Ile	Gly	Asn	Ser
1				5					10					15

<210> 178

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> H48 hinge

<400> 178

Ala	Asp	Phe	Leu	Thr	Pro	Ser	Ile	Gly	Asn	Ser
1				5					10	

<210> 179

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H50 hinge

<400> 179

Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Gly	Asn	Ser
1				5					10					15

<210> 180

<211> 15

<212> PRT

<213> Artificial Sequence

SeqList.txt

<220>

<223> H51 hinge

<400> 180

Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Gly	Asn	Ser
1				5					10					15

<210> 181

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> H52 hinge

<400> 181

Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ser
1				5					10	

<210> 182

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> H53 hinge

<400> 182

Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Cys	Pro	Pro	Cys	Pro	Asn	Ser
1				5					10					15	

<210> 183

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> H54 hinge

<400> 183

Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Ser	Cys	Pro	Pro	Cys
1				5					10					15	

Pro Asn Ser

<210> 184

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> H55 hinge

<400> 184

Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala	Asn	Ser
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SeqList.txt

<210> 185
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H56 hinge

<400> 185

Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1 5 10

<210> 186
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H57 hinge

<400> 186

Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1 5 10

<210> 187
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H58 hinge

<400> 187

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1 5 10 15

<210> 188
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H59 hinge

<400> 188

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1 5 10 15

<210> 189
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H60 hinge

<400> 189

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
 Page 209

```

1                5                10                15

<210>  190
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  H61 hinge

<400>  190
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
1                5                10                15

Asp Cys Pro Asn Ser
                20

<210>  191
<211>  21
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  H62 hinge

<400>  191
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
1                5                10                15

His Cys Pro Asn Ser
                20

<210>  192
<211>  20
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  H63 hinge

<400>  192
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1                5                10                15

Cys Pro Asn Ser
                20

<210>  193
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  ((Gly4Ser)3) linker

<400>  193
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

```

1 5 10 15

<210> 194
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (Gly4Ser)n linker

<220>
 <221> MISC_FEATURE
 <222> (6)..(25)
 <223> amino acid residues may be absent

<400> 194

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 195
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> secretory signal sequence

<400> 195

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly
 20

<210> 196
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H111 linker

<400> 196

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

Pro Gly Ser

<210> 197
 <211> 751
 <212> PRT
 <213> Artificial Sequence

SeqList.txt

<220>

<223> Chimeric bispecific anti-CD123 (VLVH) x anti-CD3 (TSC456)
scFv-Fc-scFv CD3-binding domain

<400> 197

Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15Glu Lys Phe Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe Phe Gly
20 25 30Ser Thr Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ala
65 70 75 80Ile Ser Ser Val Met Pro Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95Tyr Tyr Asn Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125Gly Gly Gly Gly Ser Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
130 135 140Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Asp Tyr Ser
145 150 155 160Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
165 170 175Lys Leu Glu Trp Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr
180 185 190Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
195 200 205Asn Gln Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala
210 215 220Thr Tyr Tyr Cys Ser Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly
225 230 235 240Gln Gly Thr Thr Leu Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

SeqList.txt

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350
 Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495
 Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
 500 505 510
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 515 520 525

SeqList.txt

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
565 570 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
580 585 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625 630 635 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 198

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric bispecific anti-CD123 (VHVL) x anti-CD3 (TSC456)
scFv-Fc-scFv CD3-binding domain

<400> 198

SeqList.txt

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser
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 Leu Ser Leu Thr Cys Ser Val Thr Asp Tyr Ser Ile Thr Ser Gly Tyr
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 Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met
 35 40 45
 Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ser
 85 90 95
 Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly Gln Gly Thr Thr Leu
 100 105 110
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Met Met Ser Gln Ser Pro
 130 135 140
 Ser Ser Leu Ala Val Ser Val Gly Glu Lys Phe Thr Met Thr Cys Lys
 145 150 155 160
 Ser Ser Gln Ser Leu Phe Phe Gly Ser Thr Gln Lys Asn Tyr Leu Ala
 165 170 175
 Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
 180 185 190
 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
 195 200 205
 Ser Gly Thr Asp Phe Thr Leu Ala Ile Ser Ser Val Met Pro Glu Asp
 210 215 220
 Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp Thr Phe
 225 230 235 240
 Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser
 245 250 255
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 260 265 270

SeqList.txt

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 275 280 285
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 290 295 300
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 305 310 315 320
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 325 330 335
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 340 345 350
 Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
 355 360 365
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 370 375 380
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 385 390 395 400
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 405 410 415
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 420 425 430
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 435 440 445
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 450 455 460
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 465 470 475 480
 Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 485 490 495
 Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu
 500 505 510
 Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 515 520 525
 Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
 530 535 540

SeqList.txt

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
 545 550 555 560

Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
 565 570 575

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
 580 585 590

Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
 595 600 605

Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 625 630 635 640

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
 645 650 655

Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val
 660 665 670

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
 675 680 685

Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
 690 695 700

Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu
 705 710 715 720

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn
 725 730 735

Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser
 740 745 750

Ser

<210> 199
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VH CDR1 (IMGT) CD3-binding domain

<400> 199

Gly Tyr Thr Phe Thr Arg Ser Thr

1

5

<210> 200
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VH CDR2 (IMGT) CD3-binding domain
 <400> 200

Ile Asn Pro Ser Ser Ala Tyr Thr
 1 5

<210> 201
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VH CDR3 (IMGT) CD3-binding domain
 <400> 201

Gln Gln Trp Ser Arg Asn Pro Pro Thr
 1 5

<210> 202
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VL CDR1 (IMGT) CD3-binding domain
 <400> 202

Ala Ser Ser Ser Val Ser Tyr
 1 5

<210> 203
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VL CDR2 (IMGT) CD3-binding domain
 <400> 203

Asp Ser Ser
 1

<210> 204
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cris7 and DRA222 VL CDR3 (IMGT) CD3-binding domain
 <400> 204

SeqList.txt

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1 5

<210> 205
<211> 2286
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC471 Anti-PSMA X anti-CD3 bispecific molecule

<400> 205
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atcacttgcc gggcgagtaa gagcattagc aaatatattag cctggtttca gcagaaacca 180
gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240
cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300
gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360
gggaccaagg tggaaatcaa acgaggtggc ggaggggtctg ggggtggcgg atccggagggt 420
ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480
gtgaaggctc cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540
cgacaggccc ctggacaagg gcttgagtggt atgggatatt ttaatcctta taatgattat 600
actagatacg cacagaagtt ccagggcaga gtcacatga ccagggacac gtctatcagc 660
acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720
agatcggatg gttactacga tgctatggac tactgggggtc aaggaaccac agtcaccgtc 780
tcctcgagtg agcccaaadc ttctgacaaa actcacacat gccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 900
atctcccggg cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080
tggtgaatg gcaaggaata caagtgcgcg gtctccaaca aagccctccc agccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gtcaccgtg 1380
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttccggagg tggcggttcg 1500
ggaggtggcg ggtcaggagg tgggggctct ccttcacagg tgcagctggt gcagtctggt 1560
cctgaggtga aaaagcctgg ctccagcgtg aagggtgtcct gcaaggccag cggatacacc 1620

SeqList.txt

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ttagccggt ccaccatgca ttgggtgagg caggctcctg gacagggcct ggagtggatc 1680
ggctacatca accccagcag cgcttatacc aactacaatc agaagtttaa ggaccgggtg 1740
accatcaccg ccgataagtc caccagcacc gcctacatgg agctgtccag cctgaggagc 1800
gaggataccg ccgtgtacta ttgcgcccgg cccaggtcc attacgacta caacggcttc 1860
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tacgactcca gcaagctggc ctctggtgtc ccagcaggt tctctggtag cggcagcggc 2160
acagactaca ccctgacat ctctccctg cagcccgacg atttcgccac ctactattgc 2220
cagcagtggg cccggaatcc ccctacctt ggcggcggca ccaaggtgga gatcaagagg 2280
agctaa 2286

```

```

<210> 206
<211> 741
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TSC471 Anti-PSMA X anti-CD3 bispecific molecule

```

```

<400> 206

```

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
1           5           10          15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20          25          30

```

```

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Arg Ile
35          40          45

```

```

His Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85          90          95

```

```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100         105         110

```

```

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu Val
115         120         125

```

```

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
Page 220

```

SeqList.txt
140

130

135

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
260 265 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
275 280 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
Page 221

SeqList.txt

405

410

415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Pro Ser Gln Val Gln Leu
 485 490 495

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
 500 505 510

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
 515 520 525

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 530 535 540

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
 545 550 555 560

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
 565 570 575

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
 580 585 590

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
 595 600 605

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 625 630 635 640

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 645 650 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 660 665 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 Page 222

675

680

685

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
 705 710 715 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 725 730 735

Glu Ile Lys Arg Ser
 740

<210> 207
 <211> 2307
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR243 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 207
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 agggacgact ccaagtccat tgcctacctg cagatgaact ccctgaagac cgaggacacc 720
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 aaaccaagg acacctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960
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SeqList.txt

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 ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
 tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500
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<210> 208
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR243 Anti-ROR1 X anti-CD3 bispecific molecule
 <400> 208

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
 20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
 65 70 75 80

SeqList.txt

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 Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
 100 105 110
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 115 120 125
 Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
 145 150 155 160
 Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 165 170 175
 Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
 180 185 190
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
 195 200 205
 Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
 210 215 220
 Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
 245 250 255
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
 260 265 270
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 275 280 285
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 290 295 300
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 305 310 315 320
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 325 330 335
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 340 345 350

SeqList.txt

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 370 375 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 485 490 495

Ser Pro Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
 500 505 510

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 515 520 525

Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 530 535 540

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn
 545 550 555 560

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
 565 570 575

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 580 585 590

Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro
 595 600 605

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 610 615 620

SeqList.txt

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625 630 635 640

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
645 650 655

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
660 665 670

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
675 680 685

Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
690 695 700

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
705 710 715 720

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
725 730 735

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745

<210> 209
<211> 2289
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC266 Anti-PSMA X anti-CD3 bispecific molecule

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SeqList.txt

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tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg     1560
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tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg     2160
accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc     2220
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<210> 210

<211> 742

<212> PRT

<213> Artificial Sequence

<220>

<223> TSC266 Anti-PSMA X anti-CD3 bispecific molecule

<400> 210

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
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Page 228

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30

SeqList.txt
300

290

295

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Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465 470 475 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
485 490 495

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
500 505 510

Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
515 520 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
530 535 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545 550 555 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
Page 230

SeqList.txt

565

570

575

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
 580 585 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
 595 600 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 610 615 620

Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
 625 630 635 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
 645 650 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 660 665 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
 675 680 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
 690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 705 710 715 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 725 730 735

Gln Ile Thr Ser Ser Ser
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<210> 211
 <211> 2301
 <212> DNA
 <213> Artificial Sequence

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 <223> ROR206 Anti-ROR1 X anti-CD3 bispecific molecule

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 ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240
 cgtttctccg gtcctggctc cggcaccgac ttcacctga ccatctctc cctgcagccc 300
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SeqList.txt

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atcaactccg	gcggctccac	ctggtacgcc	tcctgggtga	agggccggtt	caccatctcc	660
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gccgtgtact	attgcgccc	gggtactcc	acctactacc	gggacttcaa	catctggggc	780
cagggcaccc	tgggtgaccgt	gtcctcgagt	gagcccaa	cttctgacaa	aactcacaca	840
tgcccaccgt	gccagacacc	tgaagccg	ggtgcaccgt	cagtcttcct	cttccccca	900
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SeqList.txt

<211> 767
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR206 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 212

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Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
 35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
 50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
 100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 145 150 155 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
 165 170 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
 180 185 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
 195 200 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 210 215 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 225 230 235 240

SeqList.txt

Ala Val Tyr Tyr Cys₂₄₅ Ala Arg Gly Tyr Ser₂₅₀ Thr Tyr Tyr Arg Asp₂₅₅ Phe
 Asn Ile Trp Gly₂₆₀ Gln Gly Thr Leu Val₂₆₅ Thr Val Ser Ser Ser₂₇₀ Glu Pro
 Lys Ser Ser₂₇₅ Asp Lys Thr His Thr₂₈₀ Cys Pro Pro Cys Pro₂₈₅ Ala Pro Glu
 Ala Ala Gly Ala Pro Ser Val₂₉₅ Phe Leu Phe Pro Pro₃₀₀ Lys Pro Lys Asp
 Thr₃₀₅ Leu Met Ile Ser Arg₃₁₀ Thr Pro Glu Val Thr₃₁₅ Cys Val Val Val Asp₃₂₀
 Val Ser His Glu Asp₃₂₅ Pro Glu Val Lys Phe₃₃₀ Asn Trp Tyr Val Asp₃₃₅ Gly
 Val Glu Val His₃₄₀ Asn Ala Lys Thr Lys₃₄₅ Pro Arg Glu Glu Gln₃₅₀ Tyr Asn
 Ser Thr Tyr₃₅₅ Arg Val Val Ser Val₃₆₀ Leu Thr Val Leu His₃₆₅ Gln Asp Trp
 Leu Asn Gly Lys Glu Tyr Lys₃₇₅ Cys Ala Val Ser Asn₃₈₀ Lys Ala Leu Pro
 Ala Pro Ile Glu Lys Thr₃₉₀ Ile Ser Lys Ala Lys₃₉₅ Gly Gln Pro Arg Glu₄₀₀
 Pro Gln Val Tyr Thr₄₀₅ Leu Pro Pro Ser Arg₄₁₀ Asp Glu Leu Thr Lys₄₁₅ Asn
 Gln Val Ser Leu₄₂₀ Thr Cys Leu Val Lys₄₂₅ Gly Phe Tyr Pro Ser₄₃₀ Asp Ile
 Ala Val Glu₄₃₅ Trp Glu Ser Asn Gly₄₄₀ Gln Pro Glu Asn Asn₄₄₅ Tyr Lys Thr
 Thr Pro₄₅₀ Pro Val Leu Asp Ser₄₅₅ Asp Gly Ser Phe Phe₄₆₀ Leu Tyr Ser Lys
 Leu Thr Val Asp Lys Ser₄₇₀ Arg Trp Gln Gln Gly₄₇₅ Asn Val Phe Ser Cys₄₈₀
 Ser Val Met His Glu₄₈₅ Ala Leu His Asn His₄₉₀ Tyr Thr Gln Lys Ser₄₉₅ Leu
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SeqList.txt

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 545 550 555 560
 Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
 565 570 575
 Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
 580 585 590
 Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
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 Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
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 Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
 625 630 635 640
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 645 650 655
 Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 660 665 670
 Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
 675 680 685
 Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
 690 695 700
 Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 705 710 715 720
 Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
 725 730 735
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 <211> 2313
 <212> DNA

<213> Artificial Sequence

<220>

<223> ROR207 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 213

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acctgcctgg	tcaaaggctt	ctatccaagc	gacatcgccg	tggagtggga	gagcaatggg	1320
cagccggaga	acaactacaa	gaccacgcct	cccgtgctgg	actccgacgg	ctccttcttc	1380
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tcctgcaagg	cttctggata	taccttcagc	agatctacga	tgcactgggt	gcgacaggcc	1680
cctggacaag	ggcttgagtg	gataggatac	attaatccta	gcagtgctta	tactaattac	1740
aatcagaaat	tcaaggacag	agtcacgatt	accgcggaca	aatccacgag	cacagcctac	1800
atggagctga	gcagcctgag	atctgaggac	acggccgtgt	attactgtgc	gagaccccaa	1860

SeqList.txt

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gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920
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tctgacatcc agatgacca gtctccttcc accctgtctg catctgtagg agacagagtc 2040
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gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160
aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220
gatgattttg caacttatta ctgccaacag tggagtcgta acccaccac tttcggcgga 2280
gggaccaagg tggagatcaa acggtcctcc agc 2313

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<210> 214
 <211> 771
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR207 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 214

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1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145 150 155 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly

SeqList.txt

165

170

175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
 180 185 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
 195 200 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 210 215 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 225 230 235 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
 245 250 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
 260 265 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 Page 238

SeqList.txt

435

440

445

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Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
  450      455      460
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
  465      470      475      480
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
      485      490      495
Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
      500      505      510
Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
      515      520      525
Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
      530      535      540
Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
      545      550      555      560
Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
      565      570      575
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
      580      585      590
Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
      595      600      605
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
      610      615      620
Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
      625      630      635      640
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
      645      650      655
Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
      660      665      670
Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
      675      680      685
Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
      690      695      700
Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser

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Ser Ser Ser
770

<220>
<223> ROR208 Anti-ROR1 X anti-CD3 bispecific molecule

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cggttctccg	gctccggctc	cggcaccgac	ttcacctga	ccatctcctc	cctggaggcc	300
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ttcggcgggc	gcaccaaggt	ggagatcaag	ggtggaggcg	gttcaggcgg	aggtggatcc	420
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gactacccca	tcacctgggt	gcggcaggcc	cccggccagg	gcctggagt	gatcggcttc	600
atcaactccg	gcggctccac	ctggtacgcc	tcctgggtga	agggccgggt	caccatctcc	660
cgggacgact	ccaagtccat	cgcctacctg	cagatgaact	ccctgaagac	cgaggacacc	720
gccgtgtact	attgcgccc	gggctactcc	acctactacc	gggacttcaa	catctggggc	780
cagggcacc	tggtgaccgt	gtcctcgagt	gagcccaa	cttctgacaa	aactcacaca	840
tgcccaccgt	gcccagcacc	tgaagccgcg	ggtgcaccgt	cagtcttcct	cttcccccca	900
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gtgagccacg	aagaccctga	ggtcaagttc	aactggtacg	tggacggcgt	ggagggtgat	1020
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ctcaccgtcc	tgcaccagga	ctggctgaat	ggcaaggaat	acaagtgcgc	ggtctccaac	1140
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SeqList.txt

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 cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttctc 1380
 ctctacagca agctcacctg ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
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<210> 216
 <211> 767
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR208 Anti-ROR1 X anti-CD3 bispecific molecule
 <400> 216

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Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp
65 70 75 80

SeqList.txt

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
 100 105 110
 Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125
 Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 145 150 155 160
 Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
 165 170 175
 Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
 180 185 190
 Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
 195 200 205
 Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 210 215 220
 Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 225 230 235 240
 Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
 245 250 255
 Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
 260 265 270
 Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285
 Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

SeqList.txt

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365
 Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495
 Ser Leu Ser Pro Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510
 Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly
 515 520 525
 Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
 530 535 540
 Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
 545 550 555 560
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 565 570 575
 Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
 580 585 590
 Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
 595 600 605
 Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
 610 615 620

SeqList.txt

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
660 665 670

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
675 680 685

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
690 695 700

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
705 710 715 720

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
725 730 735

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
740 745 750

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
755 760 765

<210> 217
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR209 Anti-ROR1 X anti-CD3 bispecific molecule

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atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

SeqList.txt

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tgcccaccgt	gcccagcacc	tgaagccg	ggtgcaccgt	cagtcttct	cttcccccca	900
aaacccaagg	acaccctcat	gatctccc	accctgagg	tcacatgcgt	ggtggtggac	960
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ctcaccgtcc	tgcaccagga	ctggctgaat	ggcaaggaat	acaagtgcgc	ggtctccaac	1140
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ccacaggtgt	acaccctgcc	cccatccc	gatgagctga	ccaagaacca	ggtcagcctg	1260
acctgcctgg	tcaaaggctt	ctatccaagc	gacatcgccg	tggagtggga	gagcaatggg	1320
cagccggaga	acaactacaa	gaccacgcct	cccgtgctgg	actccgacgg	ctccttcttc	1380
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aatcagaaat	tcaaggacag	agtcacgatt	accgcggaca	aatccacgag	cacagcctac	1800
atggagctga	gcagcctgag	atctgaggac	acggccgtgt	attactgtgc	gagaccccaa	1860
gtccactatg	attacaacgg	gtttccttac	tggggccaag	gaaccctggt	caccgtctcc	1920
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accatgactt	gcagtgccag	ctcaagtgt	agttacatga	actggtatca	gcagaaacca	2100
gggaaagccc	ctaagagatg	gatttatgac	tcatccaaac	tggcttcttg	ggtcccatca	2160
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gatgattttg	caacttatta	ctgccaacag	tggagtcgta	accacccac	tttcggcgga	2280
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<210> 218

<211> 771

<212> PRT

<213> Artificial Sequence

<220>

<223> ROR209 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 218

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro

SeqList.txt

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						Ser	Pro
						Ser	Ser
						Leu	Ser
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						40	Ile
						Asn	Cys
						Gln	Ala
						45	Ser
						Gln	Ser
Ile	Asp 50	Ser	Asn	Leu	Ala	Trp 55	Phe
						Gln	Gln
						Lys	Pro
						60	Gly
						Gln	Pro
						Pro	Pro
Lys 65	Leu	Leu	Ile	Tyr	Arg 70	Ala	Ser
						75	Gly
						Val	Pro
						80	Asp
Arg	Phe	Ser	Gly	Ser 85	Gly	Ser	Gly
						Thr	Asp
						90	Phe
						Thr	Leu
						Thr	Ile
						95	Ser
Ser	Leu	Glu	Ala 100	Glu	Asp	Val	Ala
						105	Thr
						Tyr	Tyr
						Cys	Leu
						110	Gly
						Gly	Val
Gly	Ala	Val 115	Ser	Tyr	Arg	Thr	Ser
						120	Phe
						Gly	Gly
						Gly	Gly
						125	Thr
						Lys	Val
						Glu	Gly
Ile	Lys 130	Gly	Gly	Gly	Gly	Ser 135	Gly
						Gly	Gly
						Gly	Gly
						140	Ser
						Gly	Gly
						Gly	Gly
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						Gln	Leu
						155	Val
						Glu	Ser
						Gly	Gly
						160	Gly
Leu	Val	Gln	Pro	Gly 165	Arg	Ser	Leu
						Arg	Leu
						170	Ser
						Cys	Thr
						Ala	Ser
						175	Gly
Ser	Asp	Ile	Asn 180	Asp	Tyr	Pro	Ile
						Thr 185	Trp
						Val	Arg
						Gln	Ala
						190	Pro
						Gly	Gly
Gln	Gly	Leu 195	Glu	Trp	Ile	Gly	Phe
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						Asn	Ser
						Gly	Gly
						205	Ser
						Thr	Trp
Tyr	Ala 210	Ser	Trp	Val	Lys	Gly 215	Arg
						Phe	Thr
						Ile	Ser
						220	Arg
						Asp	Asp
						Ser	Ser
Lys 225	Ser	Ile	Ala	Tyr	Leu 230	Gln	Met
						Asn	Ser
						Leu 235	Lys
						Thr	Glu
						Asp	Thr
						240	Thr
Ala	Val	Tyr	Tyr	Cys 245	Ala	Arg	Gly
						Tyr	Ser
						250	Thr
						Tyr	Tyr
						Arg	Asp
						255	Phe
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						Val 265	Thr
						Val	Ser
						Ser	Ser
						270	Ser
						Glu	Pro
Lys	Ser	Ser	Asp	Lys	Thr	His	Thr
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						Pro	Pro
						Cys	Pro
						Ala	Pro
						Glu	Glu

SeqList.txt

275

280

285

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 290 295 300

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 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
 515 520 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
 530 535 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
 Page 247

SeqList.txt

545 550 555 560
 Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
 565 570 575
 Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
 580 585 590
 Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 595 600 605
 Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
 610 615 620
 Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 625 630 635 640
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 645 650 655
 Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
 660 665 670
 Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
 675 680 685
 Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 690 695 700
 Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
 705 710 715 720
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 725 730 735
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
 740 745 750
 Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 755 760 765
 Ser Ser Ser
 770

<210> 219
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR231 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 219

SeqList.txt

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gacatccaga	tgaccaatc	cccttctagt	ctctccgcta	gcgtcggaga	ccgcgtgacc	120
atcaattgtc	aagcatctca	gagtattgac	agcaatctcg	cctggtttca	gcagaagcca	180
ggaaagccac	ccaagctcct	gatttatagg	gctagcaacc	tggcttcttg	tgtccctagt	240
aggttcagcg	gctctgggag	tggcacagac	ttcacctga	ccattagtag	tctgcagccc	300
gaagatgtcg	ctacctatta	ctgcctcgga	ggagtgggtg	ccgtttctta	tcgcacctca	360
tttggaggtg	gcaccaaagt	ggagatcaaa	ggtggtggcg	gctccggggg	tggcgggtca	420
ggggggggag	ggtctggagg	cggcggatca	gaagttcagc	tggtggaatc	tggaggaggt	480
ctggtgcagc	caggcaggtc	cctccggctg	agctgcactg	catccggctc	tgacattaat	540
gactacccta	tcacctgggt	gaggcaggcc	cccggtaaag	gcctggagtg	gatcgggttc	600
atcaattctg	gtggatctac	ttggtacgca	agctgggtga	aaggacgctt	cacaattagt	660
agagacgact	ctaagtctat	cgcatactctg	cagatgaata	gcttgaagac	agaggacacc	720
gccgtgtact	attgtgcaag	aggatactcc	acttactacc	gcgatttcaa	tatctggggc	780
cagggaaacc	tgggtgacagt	gtcctcgagt	gagcccaa	cttctgacaa	aactcacaca	840
tgcccaccgt	gcccgacc	tgaagccg	ggtgcaccgt	cagtcttcct	cttccccca	900
aaaccaagg	acacctcat	gatctccc	accctgagg	tcacatgct	ggtggtggac	960
gtgagccacg	aagacctga	ggtcaagttc	aactggtacg	tggacggcgt	ggaggtgcat	1020
aatgccaaga	caaagccg	ggaggagcag	tacaacagca	cgtaccgtgt	ggtcagcgctc	1080
ctcaccgtcc	tgcaccagga	ctggctgaat	ggcaaggaat	acaagtgcgc	ggtctccaac	1140
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cctggacagg	gcctggagtg	gatcggctac	atcaacccca	gcagcgctta	taccaactac	1740
aatcagaagt	ttaaggaccg	ggtgaccatc	accgccgata	agtcaccag	caccgcctac	1800
atggagctgt	ccagcctgag	gagcgaggat	accgccgtgt	actattgcgc	ccggccccag	1860
gtccattacg	actacaacgg	cttcccctat	tggggccagg	gaaccctggt	gaccgtgtcc	1920
agcggaggcg	gcggcagcgg	cggcggcg	agcggcggag	gaggcagcgg	cggaggaggc	1980
tccgacattc	agatgacca	gtccccctcc	accctgtccg	ctagcgtggg	cgatcgggtg	2040

SeqList.txt

accatgacct gcagcgccag cagctccgtg tcctacatga actggtacca gcagaagccc 2100
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 aggttctctg gtagcggcag cggcacagac tacaccctga ccatctcctc cctgcagccc 2220
 gacgatttcg ccacctacta ttgccagcag tgggtcccga atccccctac ctttggcggc 2280
 ggcaccaagg tggagatcaa gaggagctcc agc 2313

<210> 220
 <211> 771
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR231 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 220

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
 35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
 50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
 100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 145 150 155 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
 165 170 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
 180 185 190

SeqList.txt

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
 195 200 205
 Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 210 215 220
 Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 225 230 235 240
 Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
 245 250 255
 Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
 260 265 270
 Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285
 Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365
 Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

SeqList.txt

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495
 Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510
 Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
 515 520 525
 Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
 530 535 540
 Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
 545 550 555 560
 Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
 565 570 575
 Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
 580 585 590
 Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
 595 600 605
 Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
 610 615 620
 Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 625 630 635 640
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 645 650 655
 Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
 660 665 670
 Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
 675 680 685
 Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 690 695 700
 Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
 705 710 715 720
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 725 730 735

SeqList.txt

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
 740 745 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 755 760 765

Ser Ser Ser
 770

<210> 221
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ROR233 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 221
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 atcaactgcc aggcctccca gtccattgac tccaatctgg cctgggttcca gcagaagccc 180
 ggacagcccc ccaagctgct gatttacagg gcctccaacc tggcttccgg cgtgcctgac 240
 aggttctccg gatccggcag cggcaccgac ttcaccctga ccatctcctc cctggaggcc 300
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 ggcggcggag gctccggcgg cggcggcagc gaggtgcagc tgggtgaaag cggaggaggc 480
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 aatgccaaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080
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 acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320
 cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

SeqList.txt

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 ggttccggag gcggcggctc cggcggcggc ggcagcggcg gcggcggcag ccccgatcc 1560
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 aatcagaagt ttaaggaccg ggtgaccatc accgccgata agtccaccag caccgcctac 1800
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 ggcaccaagg tggagatcaa gaggagctcc agc 2313

<210> 222
 <211> 771
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ROR233 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 222

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
 35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
 Page 254

SeqList.txt

100

105

110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 145 150 155 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
 165 170 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
 180 185 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
 195 200 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 210 215 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
 225 230 235 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
 245 250 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
 260 265 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 Page 255

SeqList.txt
380

370

375

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
515 520 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
530 535 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
565 570 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
580 585 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
595 600 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
610 615 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
Page 256

SeqList.txt

645

650

655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
 660 665 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
 675 680 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 690 695 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
 705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 725 730 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
 740 745 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 755 760 765

Ser Ser Ser
 770