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(54) Title: ANTAGONISTIC ANTI-TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY ANTIBODIES

(57) Abstract: The present invention relates to antagonistic TNFR2 polypeptides, such as antibodies and antigen-binding fragments thereof, and the use of these polypeptides to inhibit the proliferation of regulatory T cells (T-regs) and/or expand T effector cell populations or function. For example, antibodies of the invention include antagonistic TNFR2 antibodies and antigen-binding fragments thereof, and can be used to suppress the T-reg-mediated deactivation of tumor reactive T-lymphocytes, as well as to treat a wide variety of cancers and infectious diseases.



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**ANTAGONISTIC ANTI-TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY ANTIBODIES**

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**Field of the Invention**

The invention relates to polypeptides, such as antibodies and antigen-binding fragments thereof, capable of antagonizing tumor necrosis factor receptor 2. The polypeptides of the invention can be used to modulate the activity of regulatory T cells, as well as to upregulate the activity of T effector cells and to directly modulate surface oncogenes, such as in the field of immunotherapy for the treatment of cell proliferation disorders and infectious diseases.

**Background of the Invention**

The use of naturally-occurring and genetically engineered T-lymphocytes is a prominent paradigm for ameliorating various human pathologies. For instance, while traditional therapeutic platforms for the treatment of cancer include surgical removal of tumor mass, radiation therapy, and administration of chemotherapeutics (Shewach, Chem. Rev., 109:2859-2861, 2009), the last decade has witnessed a resurgence in the application of adoptive immunotherapy to cancer treatment regimens. With the advent of chimeric antigen receptor (CAR-T) therapy, new methods have emerged for the infusion of autologous and allogeneic tumor-reactive T cells to patients (June, J. Clin. Invest., 117:1466-1476, 2007). CAR-T therapies harness the resources of the adaptive immune response in order to promote cancer cell cytotoxicity and eradicate tumor material. A common motif in adoptive immunotherapy is the use of T cells that exhibit the ability to selectively potentiate cytotoxicity in cells that display distinct tumor antigens. Examples of this technique include the administration of tumor-infiltrating lymphocytes (Dudley et al., J. Immunother., 26:332-342, 2003), as well as autologous or allogeneic T cells that have been genetically re-engineered so as to exhibit reactivity with a tumor-specific antigen (Yee et al., PNAS., 99:16168-16173, 2002).

Despite the promise of T-lymphocyte-based cancer immunotherapy, the development of this therapeutic platform has been hindered by the natural propensity of the immune system to suppress immune attacks mounted on self cells. Cancer cells, like all nucleated human cells, express class I major histocompatibility complex (MHC) proteins that distinguish these cells from foreign cells. In order to prevent cell fratricide, regulatory T cells (T-reg cells) have evolved that suppress the activity of T cells that exhibit reactivity against "self" MHC antigens. T-reg cells represent a heterogeneous class of T cells that can be distinguished based on their unique surface protein presentation. The most well-understood populations of T-reg cells include CD4+, CD25+, FoxP3+ T-reg cells and CD17+ T-reg cells. The precise mechanisms by which these cells mediate suppression of autoreactive T cells is the subject of ongoing investigations, though it has been shown that certain classes of T-reg cells inhibit production of the proliferation-inducing cytokine IL-2 in target T cells and may additionally sequester IL-2 from autoreactive cells by virtue of the affinity of CD25 (a subdomain of the IL-2 receptor) for IL-2 (Josefowicz et al., Ann.

Rev. Immun., 30:531-564, 2012).

Although T-reg cells play an important role in maintaining peripheral tolerance, the same biochemical features that underlie the ability of these cells to modulate autoreactive T cell activity also serve to undermine adoptive immunotherapy and the natural immune response by suppressing the activity of tumor-reactive T lymphocytes. The development of chemical modulators of T-reg cell activity has been the subject of many pharmacological investigations, as access to an agent capable of inhibiting T-reg-mediated T cell suppression could vastly improve the scope and efficacy of adoptive cancer immunotherapy, as well as improve the ability of the immune system to eradicate pathogenic organisms that give rise to infectious diseases.

Tumor necrosis factor receptor (TNFR) subtypes 1 and 2 have been identified on the T-reg cell surface as signal transduction molecules that dictate cell fate. The activation of TNFR1, for instance, potentiates the caspase signaling cascade and terminates in T-reg apoptosis, while activation of TNFR2 induces signaling through the mitogen-activated protein kinase (MAPK) signaling pathway, which orchestrates signaling through TRAF2/3 and the NFκB-mediated transcription of genes that promote escape from apoptosis and cell proliferation. Due to its role in directing cell survival and growth, TNFR2 represents an attractive target for preventing immune detection of tumor-reactive T lymphocytes. As such, there is currently a need for therapies that can prevent T-reg cell survival and proliferation for use in treatments targeting cell proliferation disorders, such as cancer, and a wide array of infectious diseases.

### Summary of the Invention

The invention provides antagonistic tumor necrosis factor receptor 2 (TNFR2) polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof. Antagonistic TNFR2 polypeptides of the invention specifically bind epitopes within human TNFR2 that contain one or more residues of the KCRPG sequence (SEQ ID NO: 19) or equivalent epitopes in TNFR2 of non-human primates (e.g., bison or cattle, as described herein) and do not specifically bind residues of the KCSPG motif (SEQ ID NO: 12) within human TNFR2 or equivalent epitopes in TNFR2 of non-human primates. The polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) described herein can be used for the treatment of a variety of pathologies, including cancers and infectious diseases.

Antagonistic TNFR2 polypeptides of the invention are described as such since they exhibit the ability to inhibit the proliferation of, and/or promote the death of, T-reg cells. Antagonistic TNFR2 polypeptides of the invention may inhibit the proliferation of, and/or promote the death of, TNFR2- and oncogene-expressing cancer cells. Antagonistic TNFR2 polypeptides of the invention can permit the reciprocal expansion of T effector cells, such as cytotoxic CD8+ T cells. This may occur, for instance, due to the attenuation of T-reg cell proliferation and activity. Antagonistic TNFR2 polypeptides of the invention may directly expand T effector cells, such as CD8+ cytotoxic T cells. Therefore, the designation of TNFR2 polypeptides of the invention as antagonists refers to their capacity to attenuate the proliferation and activity of T-reg and TNFR2-expressing cancer cells and, for clarity, does not indicate antagonism of the T effector cell response.

Disclosed herein are polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof, capable of specifically binding human TNFR2 that contain a complementarity determining region-heavy chain 1 (CDR-H1) and a CDR-H2 derived from a TNFR2 antibody and a CDR-H3 having the amino acid sequence  $JZ^1JZ^2Z^4JZ^3JZ^5(J)_2Z^5Z^2Z^5$ ,  $JZ^1JZ^2Z^4Z^3Z^5(J)_2Z^5Z^2Z^5(J)_2$ ,

5 JRJDGJSJY(J)<sub>2</sub>FDJ (SEQ ID NO: 278), JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279),  
 QZ<sup>1</sup>VZ<sup>2</sup>Z<sup>4</sup>YZ<sup>3</sup>SZ<sup>5</sup>WYZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup> (SEQ ID NO: 265), or AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266),  
 wherein

each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid containing a cationic side-chain at  
 10 physiological pH, such as lysine, arginine, and histidine;

each Z<sup>2</sup> is independently a naturally occurring amino acid containing an anionic side-chain at  
 physiological pH, such as aspartic acid and glutamic acid;

each Z<sup>3</sup> is independently a naturally occurring amino acid containing a polar, uncharged side-  
 chain at physiological pH, such as serine, threonine, asparagine, and glutamine;

15 each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid containing a hydrophobic side-chain,  
 such as alanine, valine, leucine, isoleucine, proline, and methionine, tryptophan, phenylalanine, and  
 tyrosine. As used herein in the context of a polypeptide formula, numeric characters in subscript notation  
 designate the quantity of the preceding amino acid present in the formula, and numeric characters in  
 20 superscript notation designate the type of the preceding amino acid present in the formula.

In a first aspect, the invention features a polypeptide, such as a single-chain polypeptide,  
 antibody, or antigen-binding fragment thereof capable of specifically binding human tumor necrosis factor  
 receptor 2 (TNFR2), wherein the single-chain polypeptide, antibody, or antigen-binding fragment thereof  
 contains a CDR-H3 having the amino acid sequence of:

25 (a) JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279);

(b) AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266); or

(c) ARDDGSYSPFDYWG (SEQ ID NO: 259) or an amino acid sequence having up to two  
 amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

30 each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at  
 physiological pH, such as lysine, arginine, and histidine;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at  
 physiological pH, such as aspartic acid and glutamic acid;

35 each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-  
 chain at physiological pH, such as serine, threonine, asparagine, and glutamine;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain,  
 such as alanine, valine, leucine, isoleucine, proline, and methionine, tryptophan, phenylalanine, and  
 tyrosine.



In some embodiments, in the presence of the above CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding a peptide comprising the amino acid sequence of LRKCRPGFGVA (SEQ ID NO: 285) or VVCKPCAPGTFSN (SEQ ID NO: 286). In some embodiments, in the presence of the above CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding an epitope within amino acids 142-149 (KCRPGFGV) or amino acids 161-169 (CKPCAPGTF) of SEQ ID NO: 7.

In some embodiments, the CDR-H3 has the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259). In some embodiments, the CDR-H3 has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277);
- (b) a CDR-H2 having the amino acid sequence (J)<sub>5</sub>GSJ;
- (c) a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y;
- (d) a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and
- (e) a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T.

wherein each J is independently a naturally occurring amino acid.

In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X;
- (b) a CDR-H2 having the amino acid sequence VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264);
- (c) a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268);
- (d) a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and
- (e) a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271);

wherein each Z<sup>1</sup> is independently an amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently an amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently an amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine;

each Z<sup>5</sup> is independently an amino acid comprising a hydrophobic side-chain; and

each X is independently leucine or isoleucine.

In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257) or an amino acid sequence having up to two amino acid substitutions relative to the sequence;
- (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258) or an amino acid sequence having up to two amino acid substitutions relative to the sequence;

(c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260) or an amino acid sequence having up to two amino acid substitutions relative to the sequence;

(d) a CDR-L2 having the amino acid sequence TYS or YTS; and

5 (e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261) or an amino acid sequence having up to two amino acid substitutions relative to the sequence; wherein each X is independently leucine or isoleucine.

In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains one or more, or all, of the following regions (CDRs):

(a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257);

10 (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258);

(c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260);

(d) a CDR-L2 having the amino acid sequence TYS or YTS; and

(e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261).

wherein each X is independently leucine or isoleucine.

15 In some embodiments, the CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274). In some embodiments, the CDR-H1 has the amino acid sequence GYTFTDYI (SEQ ID NO: 275).

In some embodiments, the CDR-L2 has the amino acid sequence TYS. In some embodiments, the CDR-L2 has the amino acid sequence YTS.

20 In some embodiments, the CDR-L3 has the amino acid sequence CLQYVLLT (SEQ ID NO: 272). In some embodiments, the CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

In some embodiments, the CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274) and the CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

25 In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains a framework region that contains the amino acid sequence LLIR (SEQ ID NO: 262) bound to the N-terminus of the CDR-L2. In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof contains a framework region that contains the amino acid sequence TLE bound to the C-terminus of the CDR-L2.

In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment does not include one or more of the following CDRs:

30 (a) a CDR-H1 having the amino acid sequence GFTFSSY (SEQ ID NO: 23);

(b) a CDR-H2 having the amino acid sequence SSGGSY (SEQ ID NO: 24); and

(c) a CDR-L1 having the amino acid sequence SASSSVYYMY (SEQ ID NO: 26);

(d) a CDR-L2 having the amino acid sequence STSNLAS (SEQ ID NO: 27);

(e) a CDR-L3 having the amino acid sequence QRRNYPYT (SEQ ID NO: 28);

35 (f) a CDR-L1 containing the amino acid sequence RASKSVSTSGYSYMH (SEQ ID NO: 29);

(g) a CDR-L2 containing the amino acid sequence LASNLES (SEQ ID NO: 30); and

(h) a CDR-L3 containing the amino acid sequence QHSRELPRT (SEQ ID NO: 31).

In some embodiments, the antibody or antigen-binding fragment thereof contains a non-native constant region, such as a human constant region, lacks all or a portion of an Fc domain, lacks all or a portion of a native Fc domain, or lacks an Fc domain altogether.

In another aspect, the invention provides constructs containing a first polypeptide domain and a second polypeptide domain, each of which contains a single-chain polypeptide of the invention. The first and second polypeptide domains may be the same. In some embodiments, the first and second polypeptide domains may be different. The first and second polypeptide domains may be bound by a linker, such as a linker containing an amide bond or a disulfide bridge. The constructs may lack a murine Fc domain.

Polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may specifically bind to a peptide containing the amino acid sequence of any one of SEQ ID NOs: 11, 19, 20, and 34-117 with a  $K_D$  of less than about 100 nM and do not bind peptides containing amino acids 56-60 (KCSPG) of SEQ ID NO: 7. Similarly, polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may specifically bind a peptide containing one or more of amino acids 142-146 of SEQ ID NO: 7 (KCRPG) and do not bind peptides containing amino acids 56-60 of SEQ ID NO: 7 (KCSPG).

Polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may inhibit TNFR2 signaling. In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof reduces or inhibits the expression of one or more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3. In some embodiments, the single-chain polypeptide, antibody, or antigen-binding fragment thereof inhibits NF $\kappa$ B activation. For instance, antagonistic TNFR2 single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may reduce or inhibit the expression or post-translational modification (e.g., phosphorylation) of one or more of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, or cIAP2/BIRC3, e.g., by 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% relative to the expression or post-translational modification (e.g., phosphorylation) of one or more of these molecules isolated from a sample not treated with an antagonistic TNFR2 single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention. Exemplary assays that can be used to determine expression level and phosphorylation state are known in the art and include Western blot assays to determine protein content and quantitative reverse transcription polymerase chain reaction (RT-PCR) experiments to determine mRNA content. In preferred embodiments, anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) are dominant TNFR2 antagonists and are thus capable of inhibiting TNFR2 activation even in the presence of a TNFR2 agonist (such as TNF $\alpha$ ) or a growth-promoting agent, such as IL-2.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, antigen-binding fragments thereof, and constructs of the invention) may exhibit one or more, or all, of the following properties:

- a. Suppression of T-reg cell proliferation, for instance, by binding and inactivating TNFR2 on the T-reg cell surface;
- b. Suppression of MDSC proliferation, for instance, by binding and inactivating TNFR2 on the MDSC surface;
- 5 c. Promotion of the expansion of T effector cells, such as CD8+ T cells; and/or
- d. Suppression of the proliferation of TNFR2-expressing cancer cells, such as T cell lymphoma cells (e.g., Hodgkin's lymphoma cells and cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, and renal cell carcinoma cells.

For example, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may reduce the total quantity of T-reg or cancer cells in a patient (such as a human patient) or within a sample (e.g., a sample isolated from a patient, such as a human patient undergoing treatment for cancer or an infectious disease as described herein, relative to a patient or sample not treated with the antagonist).

In some embodiments, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, or antigen-binding fragment thereof) reduces expression of TNFR2, e.g., by a T-reg cell or a cancer cell (such as a T cell lymphoma cell (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cell), ovarian cancer cell, colon cancer cell, multiple myeloma cell, or renal cell carcinoma cell), and/or the secretion of soluble TNFR2 by these cells.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may inhibit the proliferation or reduce the total quantity of T-reg cells in a patient (e.g., a human patient) or in a sample (e.g., a sample isolated from a human patient undergoing treatment for cancer or an infectious disease as described herein).

Polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may be capable of reducing or inhibiting the proliferation of T-reg cells and/or cancer cells that express TNFR2. For instance, the cancer cells may be selected from the group consisting of T cell lymphoma cells (e.g., Hodgkin's and cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, and renal cell carcinoma cells. Binding of TNFR2 on the cancer cell may inhibit or reduce proliferation of the cancer cell or may promote the apoptosis of the cancer cell.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention may bind TNFR2 on the surface of a myeloid-derived suppressor cell (MDSC; e.g., a cell that expresses all or a subset of proteins and small molecules selected from the group consisting of B7-1 (CD80), B7-H1 (PD-L1), CCR2, CD1d, CD1d1, CD2, CD31 (PECAM-1), CD43, CD44, complement component C5a R1, F4/80 (EMR1), Fcγ RIII (CD16), Fcγ RII (CD32), Fcγ RIIA (CD32a), Fcγ RIIIB (CD32b), Fcγ RIIIB/C (CD32b/c), Fcγ RIIC (CD32c), Fcγ RIIIA (CD16A), Fcγ RIIIB (CD16b), galectin-3, GP130, Gr-1 (Ly-6G), ICAM-1 (CD54), IL-1RI, IL-4Rα, IL-6Rα, integrin α4 (CD49d), integrin αL (CD11a), integrin αM (CD11b), M-CSFR, MGL1 (CD301a), MGL1/2 (CD301a/b), MGL2 (CD301b), nitric oxide, PSGL-1 (CD162), L-selectin (CD62L), siglec-3 (CD33), transferrin receptor (TfR), VEGFR1 (Flt-1), and VEGFR2 (KDR or Flk-1). Particularly, MDSCs do not express proteins selected from the group

consisting of B7-2 (CD86), B7-H4, CD11c, CD14, CD21, CD23 (FcεRII), CD34, CD35, CD40 (TNFRSF5), CD117 (c-kit), HLA-DR, and Sca-1 (Ly6). Binding of TNFR2 on the MDSC may inhibit or reduce proliferation of the MDSC or may promote the apoptosis of the MDSC. Polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention do not require TNFα to reduce or inhibit the proliferation of T-reg cells, cancer cells (e.g., TNFR2-expressing cancer cells), and/or MDSCs.

In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, reduce or inhibit the proliferation of T-reg cells with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, reduce or inhibit the proliferation of T-reg cells with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer.

For example, in some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, reduce or inhibit the proliferation of T-reg cells with a potency that is greater in the microenvironment of a tumor than in a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer. For instance, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may exhibit an IC<sub>50</sub> for inhibiting the proliferation of T-reg cells in a tumor microenvironment that is less than the IC<sub>50</sub> of the polypeptides for inhibiting the proliferation of T-reg cells in a site that is free of cancer cells by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. The polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of T-reg cells with a potency that is greater in the microenvironment of a tumor containing T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or more of the foregoing cancers or in a subject without cancer.

In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, reduce or inhibit the proliferation of MDSCs with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, reduce or inhibit the proliferation of MDSCs with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or a in a subject without cancer.

For example, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention may bind TNFR2 on the surface of a MDSC present within the microenvironment of a tumor, and may inhibit or reduce proliferation of the MDSC or may

promote the apoptosis of the MDSC with a potency that is greater in the microenvironment of a tumor than at a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer. For instance, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may exhibit an  $IC_{50}$  for inhibiting the proliferation of MDSCs in a tumor microenvironment that is less than the  $IC_{50}$  of the polypeptides for inhibiting the proliferation of MDSCs in a site that is free of cancer cells by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. The polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of MDSCs or may promote the apoptosis of MDSCs with a potency that is greater in the microenvironment of a tumor containing T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or more of the foregoing cancers or in a subject without cancer.

In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, expand T effector cells, such as CD8+ cytotoxic T cells, with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, expand T effector cells, such as CD8+ cytotoxic T cells, with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer.

For instance, in some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, directly expand T effector cells, such as CD8+ cytotoxic T cells, with a potency that is greater in the microenvironment of a tumor than in a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer. For instance, the polypeptides of the invention may have an  $EC_{50}$  for expanding T effector cells in a cancer patient that is less than the  $EC_{50}$  of the polypeptides for expanding T effector cells in a subject without cancer by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. The polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may directly expand T effector cells, such as CD8+ cytotoxic T cells, with a potency that is greater in the microenvironment of a tumor containing T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or more of the foregoing cancers or in a subject without cancer. In some embodiments, the T effector cells (e.g., CD8+ cytotoxic T cells) specifically react with an antigen present on one or more cancer cells, such as Hodgkin's lymphoma cells, cutaneous non-Hodgkin's

lymphoma cells, T cell lymphoma cells, ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells.

In another aspect, the invention features a method of identifying a TNFR2 antagonist antibody or antigen-binding fragment thereof by:

5 (a) exposing a heterogeneous mixture of antibodies or fragments thereof to a peptide having the amino acid sequence of ID NO: 285 or 286, or an amino acid sequence having up to two amino acid substitutions relative to said sequences; and

(b) retaining antibodies or fragments thereof that specifically bind the peptide and removing antibodies or fragments thereof that do not specifically bind the peptide, thereby producing an enriched antibody mixture containing at least one the TNFR2 antagonist antibody or antigen-binding fragment thereof. In some embodiments, the method includes determining the amino acid sequence of one or more of the antibodies or antigen-binding fragments thereof in the enriched antibody mixture.

In some embodiments, the peptide is bound to a surface. The antibody or antigen-binding fragment thereof may be expressed on the surface of a viral particle or a cell, such as the surface of a phage, bacterial cell, or yeast cell. The antibody or antigen-binding fragment thereof may be expressed as one or more polypeptide chains non-covalently bound to ribosomes or covalently bound to mRNA or cDNA. In some embodiments, the peptide is conjugated to a detectable label, such as a detectable label selected from the group consisting of a fluorescent molecule (e.g., green fluorescent protein, cyan fluorescent protein, yellow fluorescent protein, red fluorescent protein, phycoerythrin, allophycocyanin, hoescht, 4',6-diamidino-2-phenylindole (DAPI), propidium iodide, fluorescein, coumarin, rhodamine, tetramethylrhoadmine, and cyanine), an epitope tag (e.g., maltose-binding protein, glutathione-S-transferase, a poly-histidine tag, a FLAG-tag, a myc-tag, human influenza hemagglutinin (HA) tag, biotin, and streptavidin), and a radiolabel. In some embodiments, steps (a) and (b) of the method are sequentially repeated one or more times.

25 In another aspect, the invention features a method of producing a TNFR2 antagonist antibody or antigen-binding fragment thereof by immunizing a non-human mammal with a peptide containing the sequence of SEQ ID NO: 285 or 286, or an amino acid sequence having up to two amino acid substitutions relative to said sequences, and collecting serum containing the TNFR2 antagonist antibody or antigen-binding fragment thereof. The non-human mammal may be selected from the group consisting of a rabbit, mouse, rat, goat, guinea pig, hamster, horse, and sheep.

In another aspect, the invention features an antibody or antigen-binding fragment thereof that is produced by the method of any of the above embodiments.

35 Antibodies or antigen-binding fragments thereof of the invention may be full-length antibodies or antibody fragments, such as a monoclonal antibody or antigen-binding fragment thereof, a polyclonal antibody or antigen-binding fragment thereof, a humanized antibody or antigen-binding fragment thereof, a primatized antibody or antigen-binding fragment thereof, a bispecific antibody or antigen-binding fragment thereof, a multi-specific antibody or antigen-binding fragment thereof, a dual-variable immunoglobulin domain, a monovalent antibody or antigen-binding fragment thereof, a chimeric antibody or antigen-binding fragment thereof, a single-chain Fv molecule (scFv), a diabody, a triabody, a

nanobody, an antibody-like protein scaffold, a domain antibody, a Fv fragment, a Fab fragment, a F(ab')<sub>2</sub> molecule, and a tandem scFv (taFv). In some embodiments, the antibody or antigen-binding fragment thereof contains two or more CDRs covalently bound to one another, e.g., by an amide bond, a thioether bond, a carbon-carbon bond, or a disulfide bridge, or by a linker, such as a linker described herein. In some embodiments, the antibody or antigen-binding fragment thereof has an isotype selected from the group consisting of IgG, IgA, IgM, IgD, and IgE. The antibody or antigen-binding fragment thereof may be conjugated, for example, to a therapeutic agent, such as a cytotoxic agent described herein.

The invention features a polynucleotide encoding a single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof of the invention, as well as a vector containing such a polynucleotide. The vector may be an expression vector, such as a eukaryotic expression vector, or a viral vector, such as an adenovirus (Ad, such as serotype 5, 26, 35, or 48 adenovirus), retrovirus (such as a  $\gamma$ -retrovirus or a lentivirus), poxvirus, adeno-associated virus, baculovirus, herpes simplex virus, or a vaccinia virus (such as a modified vaccinia Ankara (MVA)). The invention also features host cells, such as prokaryotic and eukaryotic (e.g., mammalian) cells containing a vector of the invention.

In another aspect, the invention features a pharmaceutical composition containing an antibody or antigen-binding fragment thereof, single-chain polypeptide, construct, polynucleotide, vector, or host cell of the invention (e.g., a TNFR2 antagonist antibody or antigen-binding fragment thereof) and a pharmaceutically acceptable carrier or excipient. The pharmaceutical composition may contain, for example, an additional therapeutic agent, such as an immunotherapy agent. In some embodiments, the immunotherapy agent is an anti-CTLA-4 agent, an anti-PD-1 agent, an anti-PD-L1 agent, an anti-PD-L2 agent, a TNF- $\alpha$  cross-linking agent, a TRAIL cross-linking agent, an anti-CD27 agent, an anti-CD30 agent, an anti-CD40 agent, an anti-4-1BB agent, an anti-GITR agent, an anti-OX40 agent, an anti-TRAILR1 agent, an anti-TRAILR2 agent, or an anti-TWEAKR agent. For example, the immunotherapy agent may be an anti-CTLA-4 antibody or antigen-binding fragment thereof, an anti-PD-1 antibody or antigen-binding fragment thereof, an anti-PD-L1 antibody or antigen-binding fragment thereof, an anti-PD-L2 antibody or antigen-binding fragment thereof, a TNF- $\alpha$  cross-linking antibody or antigen-binding fragment thereof, a TRAIL cross-linking antibody or antigen-binding fragment thereof, an anti-CD27 antibody or antigen-binding fragment thereof, an anti-CD30 antibody or antigen-binding fragment thereof, an anti-CD40 antibody or antigen-binding fragment thereof, an anti-4-1BB antibody or antigen-binding fragment thereof, an anti-GITR antibody or antigen-binding fragment thereof, an anti-OX40 antibody or antigen-binding fragment thereof, an anti-TRAILR1 antibody or antigen-binding fragment thereof, an anti-TRAILR2 antibody or antigen-binding fragment thereof, or an anti-TWEAKR antibody or antigen-binding fragment thereof. The immunotherapy agent may be capable of specifically binding one or more of the immunological targets described in Table 1 of Mahoney et al., *Cancer Immunotherapy*, 14:561-584 (2015), the disclosure of which is incorporated herein by reference in its entirety. For example, the immunotherapy agent may be an agent, such as an antibody or antigen-binding fragment thereof, that specifically binds one or more of OX40L, TL1A, CD40L, LIGHT, BTLA, LAG3, TIM3, Singlecs, ICOS, B7-H3, B7-H4, VISTA, TMIGD2, BTNL2, CD48, KIR, LIR, LIR antibody, ILT, NKG2D, NKG2A, MICA, MICB, CD244, CSF1R, IDO, TGF $\beta$ , CD39, CD73, CXCR4, CXCL12, SIRPA, CD47, VEGF, or neuropilin. In



particular, the pharmaceutical composition contains a TNFR2 antagonist antibody or antigen-binding fragment thereof and an anti-PD-1 or anti-PDL1 antibody. In some embodiments, the immunotherapy agent is Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, gabapentin, antibodies to lymphoid cell surface receptors and/or lymphokines, antibodies to surface cancer proteins, and/or small molecular therapies like Vorinostat.

In some embodiments, the additional therapeutic agent is a chemotherapeutic agent, such as a chemotherapeutic agent described herein. The antibody or antigen-binding fragment thereof, single-chain polypeptide, construct, polynucleotide, vector, or host cell of the invention (e.g., a TNFR2 antagonist antibody or antigen-binding fragment thereof) may be formulated for co-administration with a chemotherapeutic agent, for instance, by admixing the antibody or antigen-binding fragment thereof, single-chain polypeptide, construct, polynucleotide, vector, or host cell with the chemotherapeutic agent. In some embodiments, the antibody or antigen-binding fragment thereof, single-chain polypeptide, construct, polynucleotide, vector, or host cell is formulated for administration separately from the chemotherapeutic agent. In some embodiments, the chemotherapeutic agent is conjugated directly to the antibody or antigen-binding fragment thereof, single-chain polypeptide, construct, polynucleotide, vector, or host cell, for instance, using bond-forming techniques described herein or known in the art.

The invention also features a method of producing a polypeptide (e.g., single-chain polypeptide, construct, antibody, or antigen-binding fragment) of the invention by expressing a polynucleotide encoding the single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof in a host cell and recovering the single-chain polypeptide, antibody, or antigen-binding fragment thereof from host cell medium.

The invention additionally features a method of inhibiting an immune response mediated by a regulatory T cell, as well as a method of treating a cell proliferation disorder in a human, by administering a single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof, polynucleotide, vector, host cell, or pharmaceutical composition (e.g., a pharmaceutical composition containing a TNFR2 antagonist antibody or antigen-binding fragment thereof and, optionally, an immunotherapy agent, such as an anti-PD-1 or anti-PDL1 antibody) of the invention to the human in need of treatment. Additionally, the invention features a composition containing a single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof, polynucleotide, vector, or host cell of the invention for inhibiting an immune response mediated by a regulatory T cell, as well as for treating a cell proliferation disorder in a human.

In some embodiments, the cell proliferation disorder may be a cancer, such as leukemia, lymphoma, liver cancer, bone cancer, lung cancer, brain cancer, bladder cancer, gastrointestinal cancer, breast cancer, cardiac cancer, cervical cancer, uterine cancer, head and neck cancer, gallbladder cancer, laryngeal cancer, lip and oral cavity cancer, ocular cancer, melanoma, pancreatic cancer, prostate cancer, colorectal cancer, testicular cancer, or throat cancer. In particular cases, the cell proliferation disorder may be a cancer selected from the group consisting of acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia

(CML), adrenocortical carcinoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytoma, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, extrahepatic cancer, ewing sarcoma family, osteosarcoma and malignant fibrous histiocytoma, central nervous system embryonal tumors, central nervous system germ cell tumors, craniopharyngioma, 5 ependymoma, bronchial tumors, burkitt lymphoma, carcinoid tumor, primary lymphoma, chordoma, chronic myeloproliferative neoplasms, colon cancer, extrahepatic bile duct cancer, ductal carcinoma in situ (DCIS), endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, extracranial germ cell tumor, extragonadal germ cell tumor, fallopian tube cancer, fibrous histiocytoma of bone, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular germ cell tumor, 10 gestational trophoblastic disease, glioma, childhood brain stem glioma, hairy cell leukemia, hepatocellular cancer, langerhans cell histiocytosis, hodgkin lymphoma, hypopharyngeal cancer, islet cell tumors, pancreatic neuroendocrine tumors, wilms tumor and other childhood kidney tumors, langerhans cell histiocytosis, small cell lung cancer, cutaneous T cell lymphoma, intraocular melanoma, merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, multiple endocrine 15 neoplasia syndromes, multiple myeloma/plasma cell neoplasm, myelodysplastic syndromes, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-hodgkin lymphoma (NHL), non-small cell lung cancer (NSCLC), epithelial ovarian cancer, germ cell ovarian cancer, low malignant potential ovarian cancer, pancreatic neuroendocrine tumors, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, 20 pheochromocytoma, pituitary tumor, pleuropulmonary blastoma, primary peritoneal cancer, rectal cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, kaposi sarcoma, rhabdomyosarcoma, sézary syndrome, small intestine cancer, soft tissue sarcoma, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, urethral cancer, endometrial uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, and Waldenström macroglobulinemia.

25 The invention also features methods of treating T cell lymphoma (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer, colon cancer, multiple myeloma, or renal cell carcinoma by administration of an antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof), a polynucleotide, vector, or host cell of the invention to a patient (e.g., a mammalian patient, such as a human patient). For instance, the invention provides a 30 method of treating ovarian cancer by administration of an antagonistic TNFR2 antibody or antigen-binding fragment thereof of the invention to a patient (e.g., a mammalian patient, such as a human patient). The invention additionally features a composition containing a single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof, polynucleotide, vector, or host cell of the invention for treating Hodgkin's or cutaneous non-Hodgkin's lymphoma, T cell lymphoma, ovarian cancer, colon cancer, 35 multiple myeloma, or renal cell carcinoma in a patient (e.g., a human patient).

The invention also features a method of treating an infectious disease in a patient (e.g., a human patient) by administering a single-chain polypeptide, construct, antibody, or antigen-binding fragment thereof, polynucleotide, vector, or host cell of the invention to the human in need of treatment, as well as a composition containing a single-chain polypeptide, construct, antibody, or antigen-binding fragment

thereof, polynucleotide, vector, or host cell of the invention for treating an infectious disease in a patient (e.g., a human patient). In some embodiments, the infectious disease is caused by a virus, a bacterium, a fungus, or a parasite. For instance, viral infections that can be treated according to the methods of the invention include hepatitis C virus, Yellow fever virus, Kadam virus, Kyasanur Forest disease virus, 5 Langat virus, Omsk hemorrhagic fever virus, Powassan virus, Royal Farm virus, Karshi virus, tick-borne encephalitis virus, Neudoerfl virus, Sofjin virus, Louping ill virus, Negishi virus, Meaban virus, Saumarez Reef virus, Tyuleniy virus, Aroa virus, dengue virus, Kedougou virus, Cacipacore virus, Koutango virus, Japanese encephalitis virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey 10 meningoencephalo-myelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, Tamana bat virus, cell fusing agent virus, 15 Ippy virus, Lassa virus, lymphocytic choriomeningitis virus (LCMV), Mobala virus, Mopeia virus, Amapari virus, Flexal virus, Guanarito virus, Junin virus, Latino virus, Machupo virus, Oliveros virus, Paraná virus, Pichinde virus, Pirital virus, Sabiá virus, Tacaribe virus, Tamiami virus, Whitewater Arroyo virus, Chapare virus, Lujo virus, Hantaan virus, Sin Nombre virus, Dugbe virus, Bunyamwera virus, Rift Valley fever virus, La Crosse virus, California encephalitis virus, Crimean-Congo hemorrhagic fever (CCHF) virus, 20 Ebola virus, Marburg virus, Venezuelan equine encephalitis virus (VEE), Eastern equine encephalitis virus (EEE), Western equine encephalitis virus (WEE), Sindbis virus, rubella virus, Semliki Forest virus, Ross River virus, Barmah Forest virus, O'nyong'nyong virus, and the chikungunya virus, smallpox virus, monkeypox virus, vaccinia virus, herpes simplex virus, human herpes virus, cytomegalovirus (CMV), Epstein-Barr virus (EBV), Varicella-Zoster virus, Kaposi's sarcoma associated-herpesvirus (KSHV), 25 influenza virus, severe acute respiratory syndrome (SARS) virus, rabies virus, vesicular stomatitis virus (VSV), human respiratory syncytial virus (RSV), Newcastle disease virus, hendravirus, nipahvirus, measles virus, rinderpest virus, canine distemper virus, Sendai virus, human parainfluenza virus (e.g., 1, 2, 3, and 4), rhinovirus, mumps virus, poliovirus, human enterovirus (A, B, C, and D), hepatitis A virus, coxsackievirus, hepatitis B virus, human papilloma virus, adeno-associated virus, astrovirus, JC virus, BK 30 virus, SV40 virus, Norwalk virus, rotavirus, human immunodeficiency virus (HIV), human T-lymphotropic virus Types I and II, and transmissible spongiform encephalopathy, such as chronic wasting disease.

In some embodiments, bacterial infections that can be treated according to the methods of the invention include those caused by a bacterium belonging to a genus selected from the group consisting of *Salmonella*, *Streptococcus*, *Bacillus*, *Listeria*, *Corynebacterium*, *Nocardia*, *Neisseria*, *Actinobacter*, 35 *Moraxella*, *Enterobacteriaceae* (e.g., *E. coli*, such as O157:H7), *Pseudomonas*, *Escherichia*, *Klebsiella*, *Serratia*, *Enterobacter*, *Proteus*, *Salmonella*, *Shigella*, *Yersinia*, *Haemophilus*, *Bordatella*, *Legionella*, *Pasturella*, *Francisella*, *Brucella*, *Bartonella*, *Clostridium*, *Vibrio*, *Campylobacter*, and *Staphylococcus*. In addition, parasitic infections that can be treated according to the methods of the invention include those caused by *Entamoeba histolytica*, *Giardia lamblia*, *Cryptosporidium muris*, *Trypanosomatida gambiense*,

*Trypanosomatida rhodesiense*, *Trypanosomatida cruzi*, *Leishmania mexicana*, *Leishmania braziliensis*, *Leishmania tropica*, *Leishmania donovani*, *Toxoplasma gondii*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium falciparum*, *Trichomonas vaginalis*, and *Histomonas meleagridis*. Exemplary helminthic parasites include *richuris trichiura*, *Ascaris lumbricoides*, *Enterobius vermicularis*,  
5 *Ancylostoma duodenale*, *Necator americanus*, *Strongyloides stercoralis*, *Wuchereria bancrofti*, and *Dracunculus medinensis*, *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Fasciola hepatica*, *Fasciola gigantica*, *Heterophyes*, *Paragonimus westermani*, *Taenia solium*, *Taenia saginata*, *Hymenolepis nana*, or *Echinococcus granulosus*.

The invention also features kits, such as a kit that contains a single-chain polypeptide, construct,  
10 antibody, or antigen-binding fragment of the invention (e.g., an antagonist TNFR2 antibody), a polynucleotide of the invention, a vector of the invention, or a host cell of the invention. In some cases, kits of the invention may contain instructions for transfecting a vector of the invention into a host cell of the invention. Optionally, kits may contain instructions for (and optionally, a reagent that can be used for) expressing a single-chain polypeptide, antibody, or antigen-binding fragment of the invention in a host cell  
15 of the invention. A kit of the invention may also contain instructions for administering a single-chain polypeptide, construct, antibody or antigen-binding fragment of the invention, a polynucleotide of the invention, a vector of the invention, or a host cell of the invention to a human patient. Optionally a kit may contain instructions for making or using an antibody or antigen-binding fragment of the invention, a polynucleotide of the invention, a vector of the invention, or a host cell of the invention.

#### 20 Definitions

As used herein, the term "about" refers to a value that is no more than 10% above or below the value being described. For example, the term "about 5 nM" indicates a range of from 4.5 nM to 5.5 nM.

As used herein, the term "antibody" (Ab) refers to an immunoglobulin molecule that specifically binds to, or is immunologically reactive with, a particular antigen, and includes polyclonal, monoclonal,  
25 genetically engineered and otherwise modified forms of antibodies, including but not limited to chimeric antibodies, humanized antibodies, heteroconjugate antibodies (e.g., bi- tri- and quad-specific antibodies, diabodies, triabodies, and tetrabodies), and antigen-binding fragments of antibodies, including e.g., Fab', F(ab')<sub>2</sub>, Fab, Fv, rIgG, and scFv fragments. Moreover, unless otherwise indicated, the term "monoclonal antibody" (mAb) is meant to include both intact molecules, as well as, antibody fragments (such as, for  
30 example, Fab and F(ab')<sub>2</sub> fragments) that are capable of specifically binding to a target protein. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of an intact antibody, clear more rapidly from the circulation of the animal, and may have less non-specific tissue binding than an intact antibody (see Wahl et al., J. Nucl. Med. 24:316, 1983; incorporated herein by reference).

The term "antigen-binding fragment," as used herein, refers to one or more fragments of an  
35 antibody that retain the ability to specifically bind to a target antigen. The antigen-binding function of an antibody can be performed by fragments of a full-length antibody. The antibody fragments can be a Fab, F(ab')<sub>2</sub>, scFv, SMIP, diabody, a triabody, an affibody, a nanobody, an aptamer, or a domain antibody. Examples of binding fragments encompassed of the term "antigen-binding fragment" of an antibody include, but are not limited to: (i) a Fab fragment, a monovalent fragment consisting of the V<sub>L</sub>, V<sub>H</sub>, C<sub>L</sub>, and

C<sub>H</sub>1 domains; (ii) a F(ab')<sub>2</sub> fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V<sub>H</sub> and C<sub>H</sub>1 domains; (iv) a Fv fragment consisting of the V<sub>L</sub> and V<sub>H</sub> domains of a single arm of an antibody, (v) a dAb including V<sub>H</sub> and V<sub>L</sub> domains; (vi) a dAb fragment (Ward et al., Nature 341:544-546, 1989), which consists of a V<sub>H</sub> domain; 5 (vii) a dAb which consists of a V<sub>H</sub> or a V<sub>L</sub> domain; (viii) an isolated complementarity determining region (CDR); and (ix) a combination of two or more isolated CDRs which may optionally be joined by a synthetic linker. Furthermore, although the two domains of the Fv fragment, V<sub>L</sub> and V<sub>H</sub>, are coded for by separate genes, they can be joined, using recombinant methods, by a linker that enables them to be made as a single protein chain in which the V<sub>L</sub> and V<sub>H</sub> regions pair to form monovalent molecules (known as single-chain Fv (scFv); see, e.g., Bird et al., Science 242:423-426, 1988, and Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883, 1988). These antibody fragments can be obtained using conventional techniques known to those of skill in the art, and the fragments can be screened for utility in the same manner as intact antibodies. Antigen-binding fragments can be produced by recombinant DNA techniques, enzymatic or chemical cleavage of intact immunoglobulins, or, in some embodiments, by 10 chemical peptide synthesis procedures known in the art.

As used herein, the terms “anti-tumor necrosis factor receptor 2 antibody,” “TNFR2 antibody,” “anti-TNFR2 antibody portion,” and/or “anti-TNFR2 antibody fragment” and the like include any protein or peptide-containing molecule that includes at least a portion of an immunoglobulin molecule, such as but not limited to at least one complementarity determining region (CDR) of a heavy or light chain or a ligand binding portion thereof, a heavy chain or light chain variable region, a heavy chain or light chain constant region, a framework region, or any portion thereof, that is capable of specifically binding to TNFR2. For instance, two or more portions of an immunoglobulin molecule may be covalently bound to one another, e.g., via an amide bond, a thioether bond, a carbon-carbon bond, a disulfide bridge, or by a linker, such as a linker described herein or known in the art. TNFR2 antibodies also include antibody-like protein 20 scaffolds, such as the tenth fibronectin type III domain (<sup>10</sup>Fn3), which contains BC, DE, and FG structural loops similar in structure and solvent accessibility to antibody CDRs. The tertiary structure of the <sup>10</sup>Fn3 domain resembles that of the variable region of the IgG heavy chain, and one of skill in the art can graft, e.g., the CDRs of a TNFR2 monoclonal antibody onto the fibronectin scaffold by replacing residues of the BC, DE, and FG loops of <sup>10</sup>Fn3 with residues from the CDR-H1, CDR-H2, or CDR-H3 regions of a TNFR2 monoclonal antibody. 30

As used herein, the terms “antagonist TNFR2 antibody” and “antagonistic TNFR2 antibody” refer to TNFR2 antibodies that are capable of inhibiting or reducing activation of TNFR2 and/or attenuating one or more signal transduction pathways mediated by TNFR2. For example, antagonistic TNFR2 antibodies can inhibit or reduce the growth and proliferation of regulatory T cells. Antagonistic TNFR2 antibodies may inhibit or reduce TNFR2 activation by blocking TNFR2 from binding TNF $\alpha$ . In this way, antagonistic TNFR2 antibodies may block the trimerization of TNFR2 that would otherwise be induced by interacting with TNF $\alpha$ , thus resulting in suppression of TNFR2 activity. 35

As used herein, the term “bispecific antibodies” refers to monoclonal, often human or humanized antibodies that have binding specificities for at least two different antigens. In the invention, one of the

binding specificities can be directed towards TNFR2, the other can be for any other antigen, e.g., for a cell-surface protein, receptor, receptor subunit, tissue-specific antigen, virally derived protein, virally encoded envelope protein, bacterially derived protein, or bacterial surface protein, etc.

As used herein, the phrase "chemotherapeutic agent" refers to any chemical agent with therapeutic usefulness in the treatment of cancer, such as a cancer described herein. Chemotherapeutic agents encompass both chemical and biological agents. These agents can function to inhibit a cellular activity upon which a cancer cell depends for continued survival. Categories of chemotherapeutic agents include alkylating/alkaloid agents, antimetabolites, hormones, hormone analogs, and antineoplastic drugs. Exemplary chemotherapeutic agents suitable for use in conjunction with the compositions and methods described herein include, without limitation, those set forth in Slapak and Kufe, Principles of Cancer Therapy, Chapter 86 in Harrison's Principles of Internal medicine, 14<sup>th</sup> edition; Perry et al., Chemotherapeutic, Chapter 17 in Abeloff, Clinical Oncology 2<sup>nd</sup> ed., 2000; Baltzer L. and Berkery R. (eds): Oncology Pocket Guide to Chemotherapeutic, 2<sup>nd</sup> ed. St. Louis, mosby-Year Book, 1995; Fischer D. S., Knobf M. F., Durivage H.J. (eds): The Cancer Chemotherapeutic Handbook, 4<sup>th</sup> ed. St. Louis, Mosby-Year Handbook, the disclosures of each of which are incorporated herein by reference as they pertain to chemotherapeutic agents.

As used herein, the term "chimeric" antibody refers to an antibody having variable domain sequences (e.g., CDR sequences) derived from an immunoglobulin of one source organism, such as rat or mouse, and constant regions derived from an immunoglobulin of a different organism (e.g., a human, another primate, pig, goat, rabbit, hamster, cat, dog, guinea pig, member of the bovidae family (such as cattle, bison, buffalo, elk, and yaks, among others), cow, sheep, horse, or bison, among others). Methods for producing chimeric antibodies are known in the art. See, e.g., Morrison, 1985, Science 229(4719): 1202-7; Oi et al, 1986, BioTechniques 4:214-221; Gillies et al, 1985, J. Immunol. Methods 125:191-202; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397; incorporated herein by reference.

As used herein, the term "complementarity determining region" (CDR) refers to a hypervariable region found both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). As is appreciated in the art, the amino acid positions that delineate a hypervariable region of an antibody can vary, depending on the context and the various definitions known in the art. Some positions within a variable domain may be viewed as hybrid hypervariable positions in that these positions can be deemed to be within a hypervariable region under one set of criteria while being deemed to be outside a hypervariable region under a different set of criteria. One or more of these positions can also be found in extended hypervariable regions. The invention includes antibodies comprising modifications in these hybrid hypervariable positions. The variable domains of native heavy and light chains each comprise four framework regions that primarily adopt a  $\beta$ -sheet configuration, connected by three CDRs, which form loops that connect, and in some cases form part of, the  $\beta$ -sheet structure. The CDRs in each chain are held together in close proximity by the FR regions in the order FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4 and, with the CDRs from the other antibody chains, contribute to the formation of the target binding site of antibodies (see Kabat et al, Sequences of Proteins of Immunological Interest (National Institute of Health,

Bethesda, Md. 1987; incorporated herein by reference). As used herein, numbering of immunoglobulin amino acid residues is done according to the immunoglobulin amino acid residue numbering system of Kabat et al, unless otherwise indicated.

As used herein, the terms “conservative mutation,” “conservative substitution,” or “conservative amino acid substitution” refer to a substitution of one or more amino acids for one or more different amino acids that exhibit similar physicochemical properties, such as polarity, electrostatic charge, and steric volume. These properties are summarized for each of the twenty naturally-occurring amino acids in table 1 below.

Table 1. Representative physicochemical properties of naturally-occurring amino acids

Amino Acid	3 Letter Code	1 Letter Code	Side-chain Polarity	Electrostatic character at physiological pH (7.4)	Steric Volume <sup>†</sup>
Alanine	Ala	A	nonpolar	neutral	small
Arginine	Arg	R	polar	cationic	large
Asparagine	Asn	N	polar	neutral	intermediate
Aspartic acid	Asp	D	polar	anionic	intermediate
Cysteine	Cys	C	nonpolar	neutral	intermediate
Glutamic acid	Glu	E	polar	anionic	intermediate
Glutamine	Gln	Q	polar	neutral	intermediate
Glycine	Gly	G	nonpolar	neutral	small
Histidine	His	H	polar	Both neutral and cationic forms in equilibrium at pH 7.4	large
Isoleucine	Ile	I	nonpolar	neutral	large
Leucine	Leu	L	nonpolar	neutral	large
Lysine	Lys	K	polar	cationic	large
Methionine	Met	M	nonpolar	neutral	large
Phenylalanine	Phe	F	nonpolar	neutral	large
Proline	Pro	P	non-polar	neutral	intermediate
Serine	Ser	S	polar	neutral	small
Threonine	Thr	T	polar	neutral	intermediate
Tryptophan	Trp	W	nonpolar	neutral	bulky
Tyrosine	Tyr	Y	polar	neutral	large
Valine	Val	V	nonpolar	neutral	intermediate

<sup>†</sup>based on volume in Å<sup>3</sup>: 50-100 is small, 100-150 is intermediate, 150-200 is large, and >200 is bulky

From this table it is appreciated that the conservative amino acid families include, e.g., (i) G, A, V, L, I, P, and M; (ii) D and E; (iii) C, S and T; (iv) H, K and R; (v) N and Q; and (vi) F, Y and W. A conservative mutation or substitution is therefore one that substitutes one amino acid for a member of the same amino acid family (e.g., a substitution of Ser for Thr or Lys for Arg).

As used herein, the term “conjugate” refers to a compound formed by the chemical bonding of a reactive functional group of one molecule with an appropriately reactive functional group of another molecule.

As used herein in the context of a TNFR2 antagonist, the term “construct” refers to a fusion protein containing a first polypeptide domain bound to a second polypeptide domain. The polypeptide domains may each independently be antagonistic TNFR2 single chain polypeptides, for instance, as described herein. The first polypeptide domain may be covalently bound to the second polypeptide domain, for instance, by way of a linker, such as a peptide linker or a disulfide bridge, among others. Exemplary linkers that may be used to join the polypeptide domains of an antagonistic TNFR2 construct include, without limitation, those that are described in Leriche et al., *Bioorg. Med. Chem.*, 20:571-582 (2012), the disclosure of which is incorporated herein by reference in its entirety.

As used herein, the term “derivatized antibodies” refers to antibodies that are modified by a chemical reaction so as to cleave residues or add chemical moieties not native to an isolated antibody. Derivatized antibodies can be obtained by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by addition of known chemical protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein. Any of a variety of chemical modifications can be carried out by known techniques, including, without limitation, specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. using established procedures. Additionally, the derivative can contain one or more non-natural amino acids, e.g., using amber suppression technology (see, e.g., US Patent No. 6,964,859; incorporated herein by reference).

As used herein, the term “diabodies” refers to bivalent antibodies comprising two polypeptide chains, in which each polypeptide chain includes V<sub>H</sub> and V<sub>L</sub> domains joined by a linker that is too short (e.g., a linker composed of five amino acids) to allow for intramolecular association of V<sub>H</sub> and V<sub>L</sub> domains on the same peptide chain. This configuration forces each domain to pair with a complementary domain on another polypeptide chain so as to form a homodimeric structure. Accordingly, the term “triabodies” refers to trivalent antibodies comprising three peptide chains, each of which contains one V<sub>H</sub> domain and one V<sub>L</sub> domain joined by a linker that is exceedingly short (e.g., a linker composed of 1-2 amino acids) to permit intramolecular association of V<sub>H</sub> and V<sub>L</sub> domains within the same peptide chain. In order to fold into their native structure, peptides configured in this way typically trimerize so as to position the V<sub>H</sub> and V<sub>L</sub> domains of neighboring peptide chains spatially proximal to one another to permit proper folding (see Holliger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-48, 1993; incorporated herein by reference).

As used herein, a “dominant antagonist” of TNFR2 is an antagonist (e.g., an antagonistic polypeptide, such as a single-chain polypeptide, antibody, or antigen-binding fragment thereof) that is capable of inhibiting TNFR2 activation even in the presence of a TNFR2 agonist, such as TNF $\alpha$ , or IL-2. For example, a TNFR2 antagonist is a dominant antagonist if the IC<sub>50</sub> of the antagonist increases by less than 200% (e.g., less than 200%, 100%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, 1%, or less) in the presence of a TNFR2 agonist (e.g., TNF $\alpha$ ) or IL-2 relative to the IC<sub>50</sub> of the antagonist as measured in the same assay in the absence of a TNFR2 agonist, such as TNF $\alpha$ , or IL-2. Inhibition of TNFR2 activation can be assessed, for instance, by measuring the inhibition of proliferation of TNFR2+ cells, such as T-reg cells, cancer cells that express TNFR2, or myeloid-derived suppressor cells, as well as by measuring the inhibition of NF $\kappa$ B signaling (e.g., by monitoring the reduction in expression of one or



more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3 in a conventional gene expression assay). Cell proliferation assays and gene expression assays that can be used to monitor TNFR2 activation are described herein, for instance, in Examples 9 and 12, respectively.

5 As used herein, a “dual variable domain immunoglobulin” (“DVD-Ig”) refers to an antibody that combines the target-binding variable domains of two monoclonal antibodies via linkers to create a tetravalent, dual-targeting single agent. (Gu et al., Meth. Enzymol., 502:25-41, 2012; incorporated by reference herein). Suitable linkers for use in the light chains of the DVDs of the invention include those identified on Table 2.1 on page 30 of Gu et al.: the short K chain linkers ADAAP (SEQ ID NO: 118)  
10 (murine) and TVAAP (SEQ ID NO: 119) (human); the long κ chain linkers ADAAPTVSIFP (SEQ ID NO: 120) (murine) and TVAAPSVFIFPP (SEQ ID NO: 121) (human); the short λ chain linker QPKAAP (SEQ ID NO: 122) (human); the long λ chain linker QPKAAPSVTLFPP (SEQ ID NO: 123) (human); the GS-short linker GGSGG (SEQ ID NO: 124), the GS-medium linker GGSGGGSG (SEQ ID NO: 125), and the GS-long linker GGSGGGSGGGGS (SEQ ID NO: 126) (all GS linkers are murine and human).  
15 Suitable linkers for use in the heavy chains of the DVDs include those identified on Table 2.1 on page 30 of Gu & Ghayur, 2012, Methods in Enzymology 502:25-41, incorporated by reference herein: the short linkers AKTTAP (SEQ ID NO: 127) (murine) and ASTKGP (SEQ ID NO: 128) (human); the long linkers AKTTAPSVYPLAP (SEQ ID NO: 129) (murine) and ASTKGPSVFPLAP (SEQ ID NO: 130) (human); the GS-short linker GGGGSG (SEQ ID NO: 131), the GS-medium linker GGGGSGGGGS (SEQ ID NO: 132),  
20 and the GS-long linker GGGGSGGGSGGGG (SEQ ID NO: 133) (all GS linkers are murine and human).

As used herein, the term “endogenous” describes a molecule (e.g., a polypeptide, nucleic acid, or cofactor) that is found naturally in a particular organism (e.g., a human) or in a particular location within an organism (e.g., an organ, a tissue, or a cell, such as a human cell).

As used herein, the term “exogenous” describes a molecule (e.g., a polypeptide, nucleic acid, or cofactor) that is not found naturally in a particular organism (e.g., a human) or in a particular location within an organism (e.g., an organ, a tissue, or a cell, such as a human cell). Exogenous materials include those that are provided from an external source to an organism or to cultured matter extracted there from.

As used herein, the term “framework region” or “FW region” includes amino acid residues that are adjacent to the CDRs. FW region residues may be present in, for example, human antibodies, rodent-derived antibodies (e.g., murine antibodies), humanized antibodies, primatized antibodies, chimeric antibodies, antibody fragments (e.g., Fab fragments), single-chain antibody fragments (e.g., scFv fragments), antibody domains, and bispecific antibodies, among others.

As used herein, the term “fusion protein” refers to a protein that is joined via a covalent bond to another molecule. A fusion protein can be chemically synthesized by, e.g., an amide-bond forming reaction between the N-terminus of one protein to the C-terminus of another protein. Alternatively, a fusion protein containing one protein covalently bound to another protein can be expressed recombinantly in a cell (e.g., a eukaryotic cell or prokaryotic cell) by expression of a polynucleotide encoding the fusion protein, for example, from a vector or the genome of the cell. A fusion protein may contain one protein that is covalently bound to a

linker, which in turn is covalently bound to another molecule. Examples of linkers that can be used for the formation of a fusion protein include peptide-containing linkers, such as those that contain naturally occurring or non-naturally occurring amino acids. In some embodiments, it may be desirable to include D-amino acids in the linker, as these residues are not present in naturally-occurring proteins and are thus more resistant to degradation by endogenous proteases. Linkers can be prepared using a variety of strategies that are well known in the art, and depending on the reactive components of the linker, can be cleaved by enzymatic hydrolysis, photolysis, hydrolysis under acidic conditions, hydrolysis under basic conditions, oxidation, disulfide reduction, nucleophilic cleavage, or organometallic cleavage (Leriche et al., *Bioorg. Med. Chem.*, 20:571-582, 2012).

As used herein, the term "heterospecific antibodies" refers to monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. Traditionally, the recombinant production of heterospecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two heavy chains have different specificities (Milstein et al., *Nature* 305:537, 1983). Similar procedures are disclosed, e.g., in WO 93/08829, U.S. Pat. Nos. 6,210,668; 6,193,967; 6,132,992; 6,106,833; 6,060,285; 6,037,453; 6,010,902; 5,989,530; 5,959,084; 5,959,083; 5,932,448; 5,833,985; 5,821,333; 5,807,706; 5,643,759, 5,601,819; 5,582,996, 5,496,549, 4,676,980, WO 91/00360, WO 92/00373, EP 03089, Traunecker et al., *EMBO J.* 10:3655 (1991), Suresh et al., *Methods in Enzymology* 121:210 (1986); incorporated herein by reference. Heterospecific antibodies can include Fc mutations that enforce correct chain association in multi-specific antibodies, as described by Klein et al, *mAbs* 4(6):653-663, 2012; incorporated herein by reference.

As used herein, the term "human antibody" refers to an antibody in which substantially every part of the protein (e.g., CDR, framework, C<sub>L</sub>, C<sub>H</sub> domains (e.g., C<sub>H</sub>1, C<sub>H</sub>2, C<sub>H</sub>3), hinge, (V<sub>L</sub>, V<sub>H</sub>)) is substantially non-immunogenic in humans, with only minor sequence changes or variations. A human antibody can be produced in a human cell (e.g., by recombinant expression), or by a non-human animal or a prokaryotic or eukaryotic cell that is capable of expressing functionally rearranged human immunoglobulin (e.g., heavy chain and/or light chain) genes. Further, when a human antibody is a single-chain antibody, it can include a linker peptide that is not found in native human antibodies. For example, an Fv can comprise a linker peptide, such as two to about eight glycine or other amino acid residues, which connects the variable region of the heavy chain and the variable region of the light chain. Such linker peptides are considered to be of human origin. Human antibodies can be made by a variety of methods known in the art including phage display methods using antibody libraries derived from human immunoglobulin sequences. See U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 1998/46645; WO 1998/50433; WO 1998/24893; WO 1998/16654; WO 1996/34096; WO 1996/33735; and WO 1991/10741; incorporated herein by reference. Human antibodies can also be produced using transgenic mice that are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. See, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; U.S. Patent Nos. 5,413,923; 5,625, 126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598; incorporated by reference herein.

As used herein, the term “humanized” antibodies refers to forms of non-human (e.g., murine) antibodies that are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other target-binding subdomains of antibodies) which contain minimal sequences derived from non-human immunoglobulin. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin. All or substantially all of the FR regions may also be those of a human immunoglobulin sequence. The humanized antibody can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin consensus sequence. Methods of antibody humanization are known in the art. See, e.g., Riechmann et al., Nature 332:323-7, 1988; U.S. Patent Nos: 5,530,101; 5,585,089; 5,693,761; 5,693,762; and 6,180,370 to Queen et al; EP239400; PCT publication WO 91/09967; U.S. Patent No. 5,225,539; EP592106; and EP519596; incorporated herein by reference.

As used herein, the term “hydrophobic side-chain” refers to an amino acid side-chain that exhibits low solubility in water relative due to, e.g., the steric or electronic properties of the chemical moieties present within the side-chain. Examples of amino acids containing hydrophobic side-chains include those containing unsaturated aliphatic hydrocarbons, such as alanine, valine, leucine, isoleucine, proline, and methionine, as well as amino acids containing aromatic ring systems that are electrostatically neutral at physiological pH, such as tryptophan, phenylalanine, and tyrosine.

As used herein, the term “immunotherapy agent” refers to a compound, such as an antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct as described herein, that specifically binds an immune checkpoint receptor or ligand and exerts an antagonistic effect on the receptor or ligand, thereby reducing or inhibiting the signal transduction of the receptor or ligand that would otherwise lead to a downregulation of the immune response. Immunotherapy agents include compounds, such as antibodies, antigen-binding fragments, single-chain polypeptides, and constructs capable of specifically binding receptors expressed on the surfaces of hematopoietic cells, such as lymphocytes (e.g., T cells), and suppressing the signaling induced by the receptor or ligand that would otherwise lead to tolerance towards an endogenous (“self”) antigen, such as a tumor-associated antigen. Immunotherapy agents may reduce the signaling induced by the receptor or ligand by, for example, 1%, 2%, 3%, 4%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, or 100% relative to the signaling induced by the receptor or ligand exhibited in the absence of the immunotherapy agent. Exemplary assays that can be used to measure the extent of receptor or ligand signaling include, for example, enzyme-linked immunosorbant assay (ELISA) techniques to measure protein expression alterations that are associated with a particular signal transduction pathway, as well as polymerase chain reaction (PCR)-based techniques, such as quantitative PCR, reverse-transcription PCR, and real-time PCR experiments useful for determining changes in gene expression associated with a particular signal transduction pathway, among others. Exemplary methods that can be used to determine whether an agent is an “immunotherapy agent” include the assays described in Mahoney et al., Cancer Immunotherapy, 14:561-584 (2015), the disclosure of which is incorporated herein by reference in its entirety. Examples of immunotherapy agents include, e.g., antibodies or antigen-binding fragments

thereof that specifically bind one or more of OX40L, TL1A, CD40L, LIGHT, BTLA, LAG3, TIM3, Singlecs, ICOS, B7-H3, B7-H4, VISTA, TMIGD2, BTNL2, CD48, KIR, LIR, LIR antibody, ILT, NKG2D, NKG2A, MICA, MICB, CD244, CSF1R, IDO, TGF $\beta$ , CD39, CD73, CXCR4, CXCL12, SIRPA, CD47, VEGF, and neuropilin. Additional example of immunotherapy agents include Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, gabapentin, antibodies to lymphoid cell surface receptors and/or lymphokines, antibodies to surface cancer proteins, and/or small molecular therapies like Vorinostat.

As used herein, the term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

As used herein, the term "multi-specific antibodies" refers to antibodies that exhibit affinity for more than one target antigen. Multi-specific antibodies can have structures similar to full immunoglobulin molecules and include Fc regions, for example IgG Fc regions. Such structures can include, but not limited to, IgG-Fv, IgG-(scFv)<sub>2</sub>, DVD-Ig, (scFv)<sub>2</sub>-(scFv)<sub>2</sub>-Fc and (scFv)<sub>2</sub>-Fc-(scFv)<sub>2</sub>. In case of IgG-(scFv)<sub>2</sub>, the scFv can be attached to either the N-terminal or the C-terminal end of either the heavy chain or the light chain. Exemplary multi-specific molecules that include Fc regions and into which anti-TNFR2 antibodies or antigen-binding fragments thereof can be incorporated have been reviewed by Kontermann, 2012, *mAbs* 4(2):182-197, Yazaki et al, 2013, *Protein Engineering, Design & Selection* 26(3):187- 193, and Grote et al, 2012, in Proetzl & Ebersbach (eds.), *Antibody Methods and Protocols, Methods in Molecular Biology* vol. 901, chapter 16:247-263; incorporated herein by reference. In some embodiments, antibody fragments can be components of multi-specific molecules without Fc regions, based on fragments of IgG or DVD or scFv. Exemplary multi-specific molecules that lack Fc regions and into which antibodies or antibody fragments can be incorporated include scFv dimers (diabodies), trimers (triabodies) and tetramers (tetrabodies), Fab dimers (conjugates by adhesive polypeptide or protein domains) and Fab trimers (chemically conjugated), are described by Hudson and Souriau, 2003, *Nature Medicine* 9:129-134; incorporated herein by reference.

As used herein, the term "myeloid-derived suppressor cell" or "MDSC" refers to a cell of the immune system that modulates the activity of a variety of effector cells and antigen-presenting cells, such as T cells, NK cells, dendritic cells, and macrophages, among others. Myeloid derived suppressor cells are distinguished by their gene expression profile, and express all or a subset of proteins and small molecules selected from the group consisting of B7-1 (CD80), B7-H1 (PD-L1), CCR2, CD1d, CD1d1, CD2, CD31 (PECAM-1), CD43, CD44, complement component C5a R1, F4/80 (EMR1), Fc $\gamma$  RIII (CD16), Fc $\gamma$  RII (CD32), Fc $\gamma$  RIIA (CD32a), Fc $\gamma$  RIIIB (CD32b), Fc $\gamma$  RIIIB/C (CD32b/c), Fc $\gamma$  RIIIC (CD32c), Fc $\gamma$  RIIIA (CD16A), Fc $\gamma$  RIIIB (CD16b), galectin-3, GP130, Gr-1 (Ly-6G), ICAM-1 (CD54), IL-1RI, IL-4R $\alpha$ , IL-6R $\alpha$ , integrin  $\alpha$ 4 (CD49d), integrin  $\alpha$ L (CD11a), integrin  $\alpha$ M (CD11b), M-CSFR, MGL1 (CD301a), MGL1/2 (CD301a/b), MGL2 (CD301b), nitric oxide, PSGL-1 (CD162), L-selectin (CD62L), siglec-3 (CD33), transferrin receptor (TfR), VEGFR1 (Flt-1), and VEGFR2 (KDR or Flk-1). Particularly, MDSCs do not express proteins selected from the group consisting of B7-2 (CD86), B7-H4, CD11c, CD14, CD21, CD23 (Fc $\epsilon$ RII), CD34, CD35, CD40 (TNFRSF5), CD117 (c-kit), HLA-DR, and Sca-1 (Ly6).

As used herein, the terms “neutral TNFR2 polypeptide” and “phenotype-neutral TNFR2 polypeptide” refer to a polypeptide (such as a single-chain polypeptide, an antibody, or an antibody fragment) that binds TNFR2 and does not exert an antagonistic or an agonistic effect on TNFR2 activation. For instance, a TNFR2 polypeptide is a neutral TNFR2 polypeptide if the polypeptide binds TNFR2 and neither potentiates nor suppresses TNFR2 activation, for instance, as assessed by measuring the proliferation of TNFR2-expressing cells (e.g., T-reg cells, TNFR2+ cancer cells, and/or MDSCs) and/or by measuring the expression of one or more NFκB target genes, such as CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and/or cIAP2/BIRC3. Exemplary assays for measuring cell proliferation and gene expression are described, e.g., in Examples 9 and 12, respectively.

As used herein, the term “non-native constant region” refers to an antibody constant region that is derived from a source that is different from the antibody variable region or that is a human-generated synthetic polypeptide having an amino sequence that is different from the native antibody constant region sequence. For instance, an antibody containing a non-native constant region may have a variable region derived from a non-human source (e.g., a mouse, rat, or rabbit) and a constant region derived from a human source (e.g., a human antibody constant region), or a constant region derived from another primate, pig, goat, rabbit, hamster, cat, dog, guinea pig, member of the bovidae family (such as cattle, bison, buffalo, elk, and yaks, among others), cow, sheep, horse, or bison, among others).

As used herein, the term “percent (%) sequence identity” refers to the percentage of amino acid (or nucleic acid) residues of a candidate sequence that are identical to the amino acid (or nucleic acid) residues of a reference sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity (e.g., gaps can be introduced in one or both of the candidate and reference sequences for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software, such as BLAST, ALIGN, or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For example, a reference sequence aligned for comparison with a candidate sequence may show that the candidate sequence exhibits from 50% to 100% sequence identity across the full length of the candidate sequence or a selected portion of contiguous amino acid (or nucleic acid) residues of the candidate sequence. The length of the candidate sequence aligned for comparison purposes may be, for example, at least 30%, (e.g., 30%, 40, 50%, 60%, 70%, 80%, 90%, or 100%) of the length of the reference sequence. When a position in the candidate sequence is occupied by the same amino acid residue as the corresponding position in the reference sequence, then the molecules are identical at that position.

As used herein, the term “primatized antibody” refers to an antibody comprising framework regions from primate-derived antibodies and other regions, such as CDRs and/or constant regions, from antibodies of a non-primate source. Methods for producing primatized antibodies are known in the art. See e.g., U.S. Patent Nos. 5,658,570; 5,681,722; and 5,693,780; incorporated herein by reference. For instance, a primatized antibody or antigen-binding fragment thereof of the invention can be produced by

inserting the CDRs of a non-primate antibody or antigen-binding fragment thereof into an antibody or antigen-binding fragment thereof that contains one or more framework regions of a primate.

As used herein, the term “operatively linked” in the context of a polynucleotide fragment is intended to mean that the two polynucleotide fragments are joined such that the amino acid sequences  
5 encoded by the two polynucleotide fragments remain in-frame.

As used herein, the term “pharmacokinetic profile” refers to the absorption, distribution, metabolism, and clearance of a drug over time following administration of the drug to a patient.

As used herein, a “recessive antagonist” of TNFR2 is an antagonist (e.g., an antagonistic polypeptide, such as a single-chain polypeptide, antibody, or antigen-binding fragment thereof) that  
10 inhibits TNFR2 activation to a significantly lesser extent in the presence of a TNFR2 agonist, such as TNF $\alpha$ , or IL-2 relative to the extent of inhibition of the same antagonist as measured in the absence of a TNFR2 agonist, such as TNF $\alpha$ , or IL-2. For example, a TNFR2 antagonist is a recessive antagonist if the IC<sub>50</sub> of the antagonist increases by, e.g., 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 60-fold, 70-fold, 80-fold,  
15 90-fold, 100-fold, or more in the presence of a TNFR2 agonist (e.g., TNF $\alpha$ ) or IL-2 relative to the IC<sub>50</sub> of the antagonist as measured in the same assay the absence of a TNFR2 agonist, such as TNF $\alpha$ , or IL-2. Inhibition of TNFR2 activation can be assessed, for instance, by measuring the inhibition of proliferation of TNFR2+ cells, such as T-reg cells, cancer cells that express TNFR2, or myeloid-derived suppressor cells, as well as by measuring the inhibition of NF $\kappa$ B signaling (e.g., by monitoring the reduction in  
20 expression of one or more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3 in a conventional gene expression assay). Cell proliferation assays and gene expression assays that can be used to monitor TNFR2 activation are described herein, for instance, in Examples 9 and 12, respectively.

As used herein, the term “regulatory sequence” includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals) that control the transcription or translation of  
25 the antibody chain genes. Such regulatory sequences are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185 (Academic Press, San Diego, CA, 1990); incorporated herein by reference.

As used herein, the term “scFv” refers to a single-chain Fv antibody in which the variable domains of the heavy chain and the light chain from an antibody have been joined to form one chain. scFv  
30 fragments contain a single polypeptide chain that includes the variable region of an antibody light chain (VL) (e.g., CDR-L1, CDR-L2, and/or CDR-L3) and the variable region of an antibody heavy chain (VH) (e.g., CDR-H1, CDR-H2, and/or CDR-H3) separated by a linker. The linker that joins the VL and VH regions of a scFv fragment can be a peptide linker composed of proteinogenic amino acids. Alternative linkers can be used to so as to increase the resistance of the scFv fragment to proteolytic degradation  
35 (e.g., linkers containing D-amino acids), in order to enhance the solubility of the scFv fragment (e.g., hydrophilic linkers such as polyethylene glycol-containing linkers or polypeptides containing repeating glycine and serine residues), to improve the biophysical stability of the molecule (e.g., a linker containing cysteine residues that form intramolecular or intermolecular disulfide bonds), or to attenuate the immunogenicity of the scFv fragment (e.g., linkers containing glycosylation sites). scFv molecules are

known in the art and are described, e.g., in US patent 5,892,019, Flo et al., (Gene 77:51, 1989); Bird et al., (Science 242:423, 1988); Pantoliano et al., (Biochemistry 30:10117, 1991); Milenic et al., (Cancer Research 51:6363, 1991); and Takkinen et al., (Protein Engineering 4:837, 1991). The VL and VH domains of a scFv molecule can be derived from one or more antibody molecules. It will also be understood by one of ordinary skill in the art that the variable regions of the scFv molecules of the invention can be modified such that they vary in amino acid sequence from the antibody molecule from which they were derived. For example, in one embodiment, nucleotide or amino acid substitutions leading to conservative substitutions or changes at amino acid residues can be made (e.g., in CDR and/or framework residues). Alternatively or in addition, mutations are made to CDR amino acid residues to optimize antigen binding using art recognized techniques. scFv fragments are described, for example, in WO 2011/084714; incorporated herein by reference.

As used herein, the phrase "specifically binds" refers to a binding reaction which is determinative of the presence of an antigen in a heterogeneous population of proteins and other biological molecules that is recognized, e.g., by an antibody or antigen-binding fragment thereof, with particularity. An antibody or antigen-binding fragment thereof that specifically binds to an antigen will bind to the antigen with a  $K_D$  of less than 100 nM. For example, an antibody or antigen-binding fragment thereof that specifically binds to an antigen will bind to the antigen with a  $K_D$  of up to 100 nM (e.g., between 1 pM and 100 nM). An antibody or antigen-binding fragment thereof that does not exhibit specific binding to a particular antigen or epitope thereof will exhibit a  $K_D$  of greater than 100 nM (e.g., greater than 500 nm, 1  $\mu$ M, 100  $\mu$ M, 500  $\mu$ M, or 1 mM) for that particular antigen or epitope thereof. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein or carbohydrate. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein or carbohydrate. See, Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988) and Harlow & Lane, *Using Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1999), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

As used herein, the terms "subject" and "patient" refer to an organism that receives treatment for a particular disease or condition as described herein (such as cancer or an infectious disease). Examples of subjects and patients include mammals, such as humans, primates, pigs, goats, rabbits, hamsters, cats, dogs, guinea pigs, members of the bovidae family (such as cattle, bison, buffalo, elk, and yaks, among others), cows, sheep, horses, and bison, among others, receiving treatment for diseases or conditions, for example, cell proliferation disorders, such as cancer or infectious diseases.

As used herein, the term "transfection" refers to any of a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, e.g., electroporation, lipofection, calcium-phosphate precipitation, DEAE-dextran transfection and the like.

As used herein, the terms "treat" or "treatment" refer to therapeutic treatment, in which the object is to prevent or slow down (lessen) an undesired physiological change or disorder, such as the progression of a cell proliferation disorder, such as cancer, or an infectious disease. Beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease,

stabilized (i.e. , not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. Those in need of treatment include those already with the condition or disorder, as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

As used herein, the term "tumor microenvironment" refers to cancer cells that form a tumor and the population of non-cancer cells, molecules, and/or blood vessels within the tumor or that border or surround the cancer cells.

As used herein, the terms "tumor necrosis factor receptor superfamily," "TNFR superfamily," or "TNFRS" refer to a group of type I transmembrane proteins with a carboxy-terminal intracellular domain and an amino-terminal extracellular domain characterized by a common cysteine rich domain (CRD). The TNFR superfamily includes receptors that mediate cellular signaling as a consequence of binding to one or more ligands in the TNF superfamily. The TNFR superfamily can be divided into two subgroups: receptors containing the intracellular death domain and those lacking this domain. The death domain is an 80 amino acid motif that propagates apoptotic signal transduction cascades following receptor activation. Exemplary TNFR super family members that contain the intracellular death domain include TNFR1, while TNFR2 represents a TNFR super family protein that does not contain this domain. Members of the TNFR superfamily include TNFR1, TNFR2, RANK, CD30, CD40, Lymphotoxin beta receptor (LT- $\beta$ R), OX40, Fas receptor, Decoy receptor 3 (DCR3), CD27, 4-1BB, Death receptor 4 (DR4), Death receptor 5 (DR5), Decoy receptor 1 (DCR1), Decoy receptor 2 (DCR2), Osteoprotegerin, TWEAK receptor, TACI, BAFF receptor, Herpesvirus entry mediator, Nerve growth factor receptor, B cell maturation antigen, Glucocorticoid-induced TNFR-related, TROY, Death receptor 6 (DR6), Death receptor 3 (DR3), and Ectodysplasin A2 receptor.

As used herein the term "variable region CDR" includes amino acids in a CDR or complementarity determining region as identified using sequence or structure based methods. As used herein, the term "CDR" or "complementarity determining region" refers to the noncontiguous antigen-binding sites found within the variable regions of both heavy and light chain polypeptides. These particular regions have been described by Kabat et al., J. Biol. Chem. 252:6609-6616, 1977 and Kabat, et al., Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91 -3242, 1991; by Chothia et al., (J. Mol. Biol. 196:901-917, 1987), and by MacCallum et al., (J. Mol. Biol. 262:732-745, 1996) where the definitions include overlapping or subsets of amino acid residues when compared against each other. In certain embodiments, the term "CDR" is a CDR as defined by Kabat based on sequence comparisons.

As used herein, the term "vector" includes a nucleic acid vector, e.g., a DNA vector, such as a plasmid, a RNA vector, virus or other suitable replicon (e.g., viral vector). A variety of vectors have been developed for the delivery of polynucleotides encoding exogenous proteins into a prokaryotic or eukaryotic cell. Examples of such expression vectors are disclosed in, e.g., WO 1994/11026; incorporated herein by reference. Expression vectors of the invention contain a polynucleotide sequence as well as, e.g., additional sequence elements used for the expression of proteins and/or the integration



of these polynucleotide sequences into the genome of a mammalian cell. Certain vectors that can be used for the expression of antibodies and antibody fragments of the invention include plasmids that contain regulatory sequences, such as promoter and enhancer regions, which direct gene transcription. Other useful vectors for expression of antibodies and antibody fragments contain polynucleotide sequences that enhance the rate of translation of these genes or improve the stability or nuclear export of the mRNA that results from gene transcription. These sequence elements include, e.g., 5' and 3' untranslated regions, an internal ribosomal entry site (IRES), and polyadenylation signal site in order to direct efficient transcription of the gene carried on the expression vector. The expression vectors of the invention may also contain a polynucleotide encoding a marker for selection of cells that contain such a vector. Examples of a suitable marker include genes that encode resistance to antibiotics, such as ampicillin, chloramphenicol, kanamycin, or nourseothricin.

As used herein, the term "VH" refers to the variable region of an immunoglobulin heavy chain of an antibody, including the heavy chain of an Fv, scFv, or Fab. References to "VL" refer to the variable region of an immunoglobulin light chain, including the light chain of an Fv, scFv, dsFv or Fab. Antibodies (Abs) and immunoglobulins (Igs) are glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific target, immunoglobulins include both antibodies and other antibody-like molecules which lack target specificity. Native antibodies and immunoglobulins are usually heterotetrameric glycoproteins of about 150,000 Daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each heavy chain of a native antibody has at the amino terminus a variable domain (VH) followed by a number of constant domains. Each light chain of a native antibody has a variable domain at the amino terminus (VL) and a constant domain at the carboxy terminus.

### Brief Description of the Figures

**Figures 1A and 1B** show the DNA and amino acid sequences of the heavy and light chains of the antagonistic TNFR2 antibody TNFRAB1. **Figure 1A** shows the DNA sequence that encodes the heavy chain of TNFRAB1 (top) and amino acid sequence of the heavy chain (bottom). The amino acid sequences of the three complementarity-determining regions (CDRs) are shown in bold. **Figure 1B** shows the DNA sequence that encodes the light chain of TNFRAB1 (top) and amino acid sequence of the light chain (bottom). The amino acid sequences of the three CDRs are shown in bold.

**Figures 2A and 2B** show the amino acid sequence of human TNFR2 (SEQ ID NO: 7). Notably, human TNFR2 is numbered herein starting with an N-terminal methionine at position 1 and concluding with a C-terminal serine at position 461 (SEQ ID NO: 7). All references to amino acid positions within TNFR2 are made in the context of the TNFR2 numbering scheme shown in Figures 2A and 2B. **(Figure 2A)** Shaded residues KCRPGFGV (SEQ ID NO: 20) define an epitope that is specifically bound by the antagonistic TNFR2 antibody TNFRAB1. Significantly, the ability of TNFRAB1 to selectively bind residues within this region without binding underlined residues KCSPG (SEQ ID NO: 12) promotes antagonism of TNFR2 signaling. The poor (or lack of) affinity of the antibodies of the invention for residues within the region of, or near, the underlined residues is consistent with the antagonistic activity of these antibodies,

as binding to epitopes containing the underlined residues has been correlated with attenuation of the inhibitory activity among TNFR2 antibodies. TNFRAB1 additionally binds an epitope that includes shaded residues CKPCAPGTF (SEQ ID NO: 21). Though these residues are not consecutive in primary sequence with the KCRPG motif, they are likely spatially proximal in the three dimensional tertiary structure of TNFR2 and may be appropriately positioned for interaction with an antagonistic TNFR2 antibody of the invention (see Figure 4). **(Figure 2B)** Shaded residues CAPLRKRCR (SEQ ID NO: 11) define an epitope that is specifically bound by the antagonistic TNFR2 antibody TNFRAB2. TNFRAB2 may additionally bind one or more regions that include the residues DSTYTQL (SEQ ID NO: 8), PECLSCGS (SEQ ID NO: 9), and RICTCRPG (SEQ ID NO: 10), which may be part of a discontinuous epitope. Though these residues are not consecutive in primary sequence, they are likely spatially proximal in the three dimensional tertiary structure of TNFR2 and may be appropriately positioned for interaction with an antagonistic TNFR2 antibody of the invention.

**Figures 3A and 3B** are tables showing the raw data obtained from enzyme-linked immunosorbant assay (ELISA) experiments that were conducted to determine the affinity of TNFRAB1 and TNFRAB2 for various continuous and discontinuous epitopes within TNFR2 (see Example 1). Raw luminescence values are shown in the fourth column of the tables (right). The peptide sequences shown represent those that contain a portion of the conformational epitope within TNFR2 that interacts with TNFRAB1 **(Figure 3A)** or TNFRAB2 **(Figure 3B)**. Amino acid residues with the single-digit code "2" designate cysteine residues that were chemically protected at the thiol position with an acetamidomethyl (ACM) moiety during peptide synthesis. These residues are not reactive with bromomethyl-containing electrophiles and were therefore not cross-linked during the cyclization and bicyclization phases of peptide synthesis. The third column in the tables indicates the general structure of the peptide scaffold. "CYS.S" indicates a 27-residue peptide in which positions 1-11 and 17-27 of the peptide represent 11-residue peptides derived from TNFR2 that contain cysteine residues that form disulfide bridges in the native protein based on information available for UniProt entry P20333. The sequence Gly-Gly-Ser-Gly-Gly was incorporated into positions 12-16 of peptides of this group. Native Cys residues that do not form disulfide bridges were protected with acetamidomethyl (ACM) protecting groups and are designated with the single-digit code "2".

**Figure 4** is a schematic illustrating the conformational epitopes within TNFR2 that may interact with antagonist TNFR2 antibodies, such as TNFRAB1 and TNFRAB2, as well as residues that do not interact with antagonist TNFR2 antibodies. The KCSPG motif is shown in the expansion at the top left of the figure; the KCRPG motif is shown in the expansion at the right of the figure. Exterior surface of the protein designates the van der Waals surface of TNFR2. Figure 4 is a rendering of a monomer of TNFR2 isolated from the X-ray crystal structure of TNFR2 (PDB ID: 3ALQ, Mukai, et al., Sci. Signal., 3:ra83, 2010).

**Figure 5** is a graph showing that TNFRAB1 suppresses the growth of cultured T-reg cells *in vitro*. Values represent the fraction of viable T-reg cells relative to untreated control cells that remained in culture after exposure of the cells to a particular condition. Bars shown on the far left represent T-reg cells treated with either IL-2 at 200 U/ml (control), TNF $\alpha$  (20 ng/ml), TNFR2 agonist (2.5  $\mu$ g/ml), antagonistic

TNFR2 antibody TNFRAB1 (2.5 µg/ml), or antagonistic TNFR2 antibody TNFRAB2 (2.5 µg/ml). Bars shown second from the left demonstrate the dose-dependent variation in T-reg viability upon treatment of cells with TNFRAB1. Bars shown second from the right show the ability of TNFRAB1 to inhibit the growth-promoting activity of TNFα. T-reg cells were treated with a constant concentration of TNFα (20 ng/ml) and varying concentrations of TNFRAB1 (from 0.0008 to 25 µg/ml). TNFRAB1 was capable of suppressing TNFα-induced proliferation in a concentration-dependent manner, indicating that TNFRAB1 antagonizes TNFR2. Bars shown on the far right demonstrate the effect of TNFα on the growth of T-reg cells. Incubation of T-reg cells with 20 ng/ml TNFα resulted in approximately 130% proliferation relative to untreated cells.

**Figure 6A** is a graph showing the ability of TNFα to induce aT-reg cell proliferation in a dose-dependent manner.

**Figure 6B** is a graph showing the ability of IL-2 to induce aT-reg cell proliferation in a dose-dependent manner. Incubation of freshly isolated human CD4+ cells for up to 48 hours with TNFα and IL-2 (200 U/ml) induces T-reg cell expansion in a dose-dependent manner and the presence of IL-2 is important for promoting T-reg expansion.

**Figure 6C** is a graph showing the effect of TNFα and dominant antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 on T-reg cell proliferation. Values on the x-axis represent the percent change in the quantity of T-reg cells relative to a sample treated with IL-2.

**Figures 6D and 6E** are graphs showing the results of duplicate experiments conducted in order to determine the effect of TNFRAB2 on T-reg cell proliferation.

**Figures 6F and 6G** are graphs showing the results of duplicate experiments conducted in order to determine the effect of TNFRAB1 on T-reg cell proliferation.

**Figure 7A** is a graph showing the effect of TNFα on the proliferation of CD4+ T-reg cells. Values on the x-axis indicate the percent change in the quantity of T-reg cells upon treatment with TNFα relative to treatment with IL-2.

**Figure 7B** is a graph showing the ability of TNFRAB1 to dominantly inhibit T-reg cell proliferation in the presence and absence of TNFα.

**Figure 7C** is a graph showing the ability of TNFRAB2 to inhibit T-reg cell proliferation in the presence and absence of TNFα.

**Figures 7D and 7E** are graphs showing the effect of TNFR2 dominant antagonists on proliferation of T-reg cells in the presence and absence of TNFα.

**Figure 8A** is a graph showing the ability of TNFRAB1 and TNFRAB2 to inhibit the proliferation of T-reg cells generally.

**Figure 8B** is a graph showing the effect of TNFRAB1 and TNFRAB2 on T-reg cell proliferation relative to the effect induced by treatment with IL-2.

**Figure 8C** is a graph showing the effect of TNFRAB1 and TNFRAB2 on total T-reg quantity.

**Figure 8D** is a graph showing the effect of TNFRAB1 and TNFRAB2 on total T-reg quantity relative to the effect induced by treatment with IL-2.

**Figure 8E** is a graph demonstrating the effect of TNFRAB1 and TNFRAB2 on activated T-reg

cells (aT-reg cells) that express CD25 in a high-affinity state (CD25<sup>Hi</sup>) and CD45RA in a low-affinity state (CD45RA<sup>Low</sup>).

**Figure 8F** is a graph showing the effect of TNFRAB1 and TNFRAB2 on a population of T-reg cells that express CD45RO<sup>Hi</sup> and CD25<sup>Hi</sup>.

5 **Figure 8G** is a graph showing the effect of TNFRAB2 on CD25<sup>Hi</sup>-expressing CD4<sup>+</sup> T cells.

**Figure 8H** is a graph demonstrating the effect of TNFRAB2 on CD25<sup>Hi</sup>-expressing T-reg cells. These data demonstrate that, while the proliferation of both activated (aT-reg) and resting (rT-reg) cells is inhibited upon treatment with TNFRAB1 or TNFRAB2, antagonistic TNFR2 antibodies preferentially inhibit the proliferation of aT-reg cells.

10 **Figure 9A** is a series of 2-dimensional flow cytometry plots demonstrating the effect of agents that direct the growth of T-reg cells (e.g., TNF $\alpha$ , IL-2, and TNFR2 agonists) as well as a TNFR2 antagonist, TNFRAB2, on the proliferation of T-reg cells of various phenotypes. Treatment with a TNFR2 antagonist antibody preferentially inhibits the proliferation of CD25<sup>Hi</sup>-expressing T-reg cells. The proportion of CD4<sup>+</sup>, CD25<sup>Hi</sup>+ cells expressing TNFR2 after up to 48 hours of incubation with either IL-2  
15 (200 U/ml) alone, with TNF $\alpha$  (20 ng/ml), or with TNFR2 antagonist antibodies (12.5  $\mu$ g/ml) is shown.

**Figure 9B** is a graph showing the effect of TNFRAB1 on the secretion of TNFR2, shown in units of pg/ml.

**Figure 9C** is a series of 1-dimensional flow cytometry plots showing the effect of TNFRAB2 on CD8<sup>+</sup> T cell count as measured by carboxyfluorescein (CFSE) labeling.

20 **Figure 10A** is a graph showing the ability of full-length TNFRAB1 (IgG) as well as F(ab)<sub>2</sub> fragment of TNFRAB1 to inhibit the proliferation of T-reg cells.

**Figure 10B** is a graph showing the ability of full-length TNFRAB2 (IgG), as well as a F(ab)<sub>2</sub> fragment of TNFRAB2, to inhibit the proliferation of T-reg cells. These data demonstrate that specific binding of the Fab regions of these antagonistic TNFR2 antibodies to TNFR2 is likely responsible for  
25 modulating T-reg cell growth, rather than non-specific binding of the Fc regions of these antibodies. Incubation of freshly isolated CD4<sup>+</sup> cells for up to 48 hrs with IL-2 (200 U/ml) plus either the full antibody or F(ab)<sub>2</sub> fragment of TNFRAB1 or TNFRAB2 produces similar dose-dependent inhibition of T-reg cells in the presence or absence of TNF $\alpha$  (20 ng/ml).

30 **Figure 10C** is a graph showing the results of a dose-response assay in which T-reg cells were treated with TNFRAB1 in the presence of anti-IgG antibodies.

**Figure 10D** is a graph showing the results of a dose-response assay in which T-reg cells were treated with TNFRAB2 in the presence of anti-IgG antibodies. The dose-dependent suppression of T-reg cell growth induced by TNFR2 antagonist antibodies was unaffected by the presence of anti-IgG molecules, indicating that non-specific cross-linking mediated by TNFRAB1 or TNFRAB2 is not  
35 responsible for the inhibitory effect of these antibodies on T-reg cell proliferation. Co-incubation of crosslinking antibody (2.5  $\mu$ g/ml) with TNFR2 antagonist antibodies (0.02 – 25  $\mu$ g/ml) does not affect the ability of the antibodies to inhibit T-reg proliferation in a dose-dependent manner. Data are presented as a single representative example.

**Figure 11A** is an image of a polyacrylamide gel showing the results of SDS-PAGE analysis

conducted following the expression of TNFRAB1.

**Figure 11B** is an image of a polyacrylamide gel showing the results of SDS-PAGE analysis conducted following the expression of TNFRAB2. Analysis of reduced and non-reduced TNFR2 antagonist antibodies (2.5  $\mu\text{g}$ ) is shown.

5 **Figure 11C** is an image of a polyacrylamide gel showing the results of a SDS-PAGE analysis conducted following the expression of  $\text{F(ab')}_2$  fragments of TNFRAB1.

**Figure 11D** is an image of a polyacrylamide gel showing the results of a SDS-PAGE analysis conducted following the expression of  $\text{F(ab')}_2$  fragments of TNFRAB2. Analysis of TNFR2 antagonist antibodies before and after digestion in  $\text{F(ab')}_2$  fragment preparation is shown.

10 **Figure 12A** is a graph showing the effect of TNFR2 antagonist antibodies on the expression of  $\text{TNF}\alpha$  and lymphotoxin.

**Figure 12B** is a graph showing the effect of TNFR2 antagonist antibodies on the expression of FoxP3 and CD25.

15 **Figure 12C** is a graph showing the effect of TNFR2 antagonist antibodies on the expression of genes that promote  $\text{NF}\kappa\text{B}$  activation: conserved helix-loop-helix ubiquitous kinase (CHUK), nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor epsilon ( $\text{NF}\kappa\text{BIE}$ ), nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor alpha ( $\text{NF}\kappa\text{BIA}$ ), mitogen-activated protein kinase 11 (MAP3K11),  $\text{TNF}\alpha$  receptor-associated factor 2 (TRAF2),  $\text{TNF}\alpha$  receptor-associated factor 3 (TRAF3), transcription factor  $\text{relB}$ , and baculoviral IAP repeat containing 3 protein ( $\text{cIAP2/BIRC3}$ ). Real-time PCR analysis was used to detect RNA isolated from fresh  $\text{CD4}^+$  cells after incubation with IL-2 (50 U/ml) in combination with either  $\text{TNF}\alpha$  (20 ng/ml) or the TNFR2 antagonist (2.5  $\mu\text{g}/\text{ml}$ ) for 3 hours.

20 **Figure 12D** is a graph showing the ability of TNFRAB1 to suppress  $\text{NF}\kappa\text{B}$  activation as measured using a cell-based ELISA assay.

25 **Figure 12E** is a graph showing the ability of TNFRAB2 to suppress  $\text{NF}\kappa\text{B}$  activation as measured using a cell-based ELISA assay. Phosphorylated  $\text{RelA/NF}\kappa\text{B p65}$  was used as a marker of  $\text{NF}\kappa\text{B}$  activity. Treatment of T-reg cells with antagonistic TNFR2 antibodies resulted in attenuated  $\text{NF}\kappa\text{B}$  activation relative to treatment with  $\text{TNF}\alpha$ . Using a cell-based ELISA, the phosphorylation  $\text{RelA/NF}\kappa\text{B p65}$  was measured after 10 minute incubation of fresh  $\text{CD4}^+$  cells with IL-2 (200 U/ml) and various concentrations of  $\text{TNF}\alpha$  (0.2 – 20 ng/ml) or TNFR2 antagonist antibodies (0.02 – 25  $\mu\text{g}/\text{ml}$ ). Phosphorylation of  $\text{RelA/NF}\kappa\text{B p65}$  is induced by  $\text{TNF}\alpha$  and inhibited by the TNFR2 antagonist mAbs in a dose-dependent manner.

30 **Figure 13A** is a table showing the kinetic and thermodynamic parameters of the binding of TNFRAB1 and TNFRAB2 to TNFR2. Association rate constants are shown in units of  $\text{M}^{-1}\text{s}^{-1}$ , dissociation rate constants are shown in units of  $\text{s}^{-1}$ , and equilibrium constants are shown in units of M.

35 **Figure 13B** is a table showing the affinity of TNFRAB1 and TNFRAB2 for various linear peptide sequences within human TNFR2. Relative affinity is indicated as a series of “+” symbols, such that higher quantities of this symbol represent elevated affinity values. Raw data derived from ELISA binding experiments are provided in the “Reading” column.

**Figure 13C** is a table showing the effect of  $\text{TNF}\alpha$  on the affinity of TNFRAB1 and TNFRAB2 for

various linear peptide sequences within human TNFR2. Relative affinity is indicated as a series of "+" symbols, such that higher quantities of this symbol represent elevated affinity values. Raw data derived from ELISA binding experiments are provided in the "Reading" column.

**Figures 14A and 14B** are graphs showing the results of duplicate experiments conducted in order to determine the effect of a recessive-TNFR2 antagonist antibody that mildly inhibits TNFR2 activity (recessive-antagonist TNFR2 antibody A) on the proliferation of T-reg cells.

**Figures 14C and 14D** are graphs showing the results of duplicate experiments conducted in order to determine the effect of a second recessive-TNFR2 antagonist that mildly inhibits TNFR2 activity (recessive-antagonist TNFR2 antibody B) on the proliferation of T-reg cells. These recessive-antagonist antibodies were raised against the exterior region of TNFR2 in order to prevent TNFR2 trimerization that leads to NF $\kappa$ B activation.

**Figure 15A** is a structural model showing a three-dimensional structure of the anti-parallel dimer and parallel dimer of human TNFR2.

**Figure 15B** is a structural model showing the three-dimensional structure of the TNF $\alpha$ -TNFR2 complex. Shaded residues represent amino acids within human TNFR2 that are bound by TNFRAB1. Proteins are portrayed in ribbon form beneath a Van der Waals surface. The data described herein clearly shows that for the full antibody or the F(ab')<sub>2</sub> fragment thereof to bind to TNFR2 in an anti-parallel conformation, the TNFR2 receptor would bind the antibody or fragment thereof at the indicated amino acid motifs. The binding sites of the parallel dimer are too close to one another and would thus preclude antibody binding. Moreover, the trimeric TNF $\alpha$ -TNFR2 complex masks the epitopes bound by antagonistic TNFR2 antibodies, as these residues are located within the interior of the trimeric structure.

**Figure 15C** is an image showing the known and published trimeric structural model of TNFR2 as a trimer with contained trimer TNF. Also shown in this structure are shaded residues that represent amino acids within human TNFR2 that are bound by the recessive-antagonist TNFR2 antibodies A and B.

**Figure 16A** is a graph showing the effect of TNFRAB1 on the proliferation of T-reg cells isolated from a patient presenting with ovarian cancer (grey shade) and of T-reg cells isolated from a subject not presenting with ovarian cancer (black shade).

**Figure 16B** is a graph showing the effect of TNFRAB2 on the proliferation of T-reg cells isolated from a patient presenting with ovarian cancer (grey shade) and of T-reg cells isolated from a subject not presenting with ovarian cancer (black shade).

**Figure 17A** is a graph showing the effect of TNFRAB1 on the proliferation of T-reg cells isolated from a subject not presenting with ovarian cancer.

**Figure 17B** is a graph showing the effect of TNFRAB2 on the proliferation of T-reg cells isolated from a subject not presenting with ovarian cancer.

**Figure 17C** is a graph showing the effect of TNFRAB1 on the proliferation of T-reg cells isolated from a subject presenting with ovarian cancer.

**Figure 17D** is a graph showing the effect of TNFRAB2 on the proliferation of T-reg cells isolated from a subject presenting with ovarian cancer.

**Figure 17E** is a graph showing the effect of TNFRAB1 on the proliferation of T-reg cells isolated

from a subject not presenting with ovarian cancer (duplicate data set relative to Figure 17A).

**Figure 17F** is a graph showing the effect of TNFRAB2 on the proliferation of T-reg cells isolated from a subject not presenting with ovarian cancer (duplicate data set relative to Figure 17B).

5 **Figure 17G** is a graph showing the effect of TNFRAB1 on the proliferation of T-reg cells isolated from a subject presenting with ovarian cancer (duplicate data set relative to Figure 17C).

**Figure 17H** is a graph showing the effect of TNFRAB2 on the proliferation of T-reg cells isolated from a subject presenting with ovarian cancer (duplicate data set relative to Figure 17D).

10 **Figure 18A** is a table showing the fluorescence values obtained from an ELISA-based binding assay to determine the TNFR2 binding affinity of twelve murine antibodies. The twelve antibodies were arrayed from columns 1 through 12 of a 96-well microtiter plate and were serially diluted from rows A through F of the plate.

15 **Figure 18B** is a table showing the fluorescence values obtained from an ELISA-based binding assay to determine the affinity of twelve murine antibodies for target peptide 1 having the amino acid sequence LRKCRPGFGVA (SEQ ID NO: 285) bound to bovine serum albumin (BSA) at the N-terminus. The twelve antibodies were arrayed from columns 1 through 12 of a 96-well microtiter plate and were serially diluted from rows A through F of the plate.

20 **Figure 18C** is a table showing the fluorescence values obtained from an ELISA-based binding assay to determine the binding affinity of twelve murine antibodies for target peptide 2 having the amino acid sequence VVCKPCAPGTFSN (SEQ ID NO: 286) bound to BSA at the C-terminus. The twelve antibodies were arrayed from columns 1 through 12 of a 96-well microtiter plate and were serially diluted from rows A through F of the plate.

25 **Figure 19** is a table showing the fluorescence values obtained from an ELISA-based binding assay to determine the binding affinity of twelve murine antibodies for an unrelated TNFR2 epitope. The twelve antibodies were arrayed from columns 1 through 12 of a 96-well microtiter plate were serially diluted from rows A through F of the plate

**Figure 20** is a table showing the fluorescence values obtained from an ELISA-based binding assay to determine the affinity of BSA conjugates of target peptide 1 (LRKCRPGFGVA, SEQ ID NO: 285) and target peptide 2 (VVCKPCAPGTFSN, SEQ ID NO: 286) for TNFR2A3.

30 **Figure 21A** is a graph showing the percent change in a population of cultured T-reg cells following incubation with IL-2, TNF $\alpha$ , a TNFR2 agonist, and varying concentrations of the antagonistic TNFR2 antibody TNFRAB2. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 21B** is a graph showing the percent change in a population of cultured T-reg cells following incubation with IL-2, TNF $\alpha$ , a TNFR2 agonist, and varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

35 **Figure 21C** is a graph showing the percent change in a population of cultured T effector cells following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1 and TNFRAB2. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 21D** is a graph showing the percent change in a population of cultured OVCAR3 cells, a TNFR2-expressing ovarian cell cancer line, following incubation with varying concentrations of the

antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 22A** is a graph showing the percent change in a population of T-reg cells in a sample isolated from a patient suffering from ovarian cancer or a human subject without cancer following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 22B** is a graph showing the percent change in a population T effector cells in a sample isolated from a patient suffering from ovarian cancer or a human subject without cancer following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 23A** is a graph showing the percent change in a population of T effector cells in a sample isolated from a patient suffering from cutaneous T cell lymphoma and that is undergoing treatment with an immunotherapy agent or a human subject without cancer following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 23B** is a graph showing the percent change in a population T-reg cells in a sample isolated from a patient suffering from cutaneous T cell lymphoma and that is undergoing treatment with an immunotherapy agent or a human subject without cancer following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

**Figure 23C** is a graph showing the percent change in a population TNFR2+ CD26- cells in a sample isolated from a patient suffering from cutaneous T cell lymphoma and that is undergoing treatment with an immunotherapy agent or a human subject without cancer following incubation with varying concentrations of the antagonistic TNFR2 antibody TNFRAB1. Numerical values shown along the X-axis are in units of  $\mu\text{g/ml}$ .

### Detailed Description

Antagonistic TNFR2 polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments inhibit the activation of TNFR2 on TNFR2-expressing cells by binding this receptor (e.g., on the exterior surface of a T-reg cell, a cancer cell that expresses TNFR2, or a myeloid-derived suppressor cell (MDSC) and thus prevent the protein from recruiting its cognate ligand, TNF $\alpha$ . TNF $\alpha$  potentiates TNFR2 signaling by nucleating a trimer of TNFR2 proteins. It is this trimerization event that brings individual TNFR2 proteins into close proximity and initiates signaling via the MAPK/NF $\kappa$ B/TRAF2/3 pathway, which ultimately leads to cell growth and escape from apoptosis. TNFR2 antibodies can antagonize this interaction by binding the receptor and preventing TNF $\alpha$  from triggering this structural change. For instance, one mechanism by which this may occur is through the formation of an anti-parallel TNFR2 dimer, which is an inactive structural form of the receptor.

The invention is based in part on the discovery of epitopes within TNFR2 that promote receptor antagonism, as well as on the finding that the binding specificity of an antagonistic TNFR2 antibody or antigen-binding fragment thereof is dictated primarily by the CDR-H3 sequence of the antibody or



fragment thereof. It has been discovered that binding of distinct residues within TNFR2 promote receptor antagonism, such as residues containing the KCRPG motif (SEQ ID NO: 19) within TNFR2, as well as downstream amino acids (for instance, the LRKCRPGFGVA (SEQ ID NO: 285) and VVCKPCAPGTFNS (SEQ ID NO: 286) epitopes). Additionally, it has been found that replacement of the CDR-H3 sequence of a neutral anti-TNFR2 antibody (i.e., an antibody that is neither antagonistic nor agonistic in function) with the CDR-H3 of an antagonistic TNFR2 antibody converts the phenotype-neutral antibody to an antagonistic TNFR2 antibody, such as a dominant antagonistic TNFR2 antibody. Collectively, these discoveries enable the production of TNFR2-binding polypeptides (e.g., single-chain polypeptides containing a CDR-H3 region optionally bound to one or more additional CDRs, antibodies, and antigen-binding fragments thereof), such as dominant antagonist polypeptides that bind TNFR2 and suppress receptor activation.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, antigen-binding fragments thereof, and constructs described herein) may exhibit one or more, or all, of the following properties:

- a. Suppression of T-reg cell proliferation, for instance, by binding and inactivating TNFR2 on the T-reg cell surface;
- b. Suppression of MDSC proliferation, for instance, by binding and inactivating TNFR2 on the MDSC surface;
- c. Promotion of the expansion of T effector cells, such as CD8+ T cells; and/or
- d. Suppression of the proliferation of TNFR2-expressing cancer cells, such as T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, and renal cell carcinoma cells.

In some embodiments, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, antigen-binding fragments thereof, and constructs described herein) exert one or more, or all, of the above characteristics with a greater potency in the microenvironment of a tumor than in a site that is free of cancer cells. For instance, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, antigen-binding fragments thereof, and constructs described herein) may exert one or more, or all, of properties (a), (b), and (c) preferentially in a patient (such as a mammalian patient, e.g., a human) suffering from cancer relative to a subject (such as a mammalian subject, e.g., a human) that does not have cancer.

The sections that follow provide a description of exemplary characteristics of antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, antigen-binding fragments thereof, and constructs of the invention, and their use in therapeutic methods.

### **Antagonistic TNFR2 polypeptides**

#### *Effects on TNFR2/MAPK/TRAF2/3 signal transduction cascades*

Anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention are capable of interacting with and inhibiting the activity of TNFR2. Thus, the anti-TNFR2 polypeptides of the invention can selectively antagonize the TNF $\alpha$ -TNFR2

interaction rather than promote TNFR2 signaling. This is particularly important for therapeutic applications, such as cancer immunotherapy, as TNFR2 activation upon association with TNF $\alpha$  leads to propagation of the MAPK and TRAF2/3 signal cascade and activation of NF $\kappa$ B-mediated transcription of genes involved in T-reg cell growth and escape from apoptosis (Faustman, et al., Nat. Rev. Drug Disc., 5 9:482-493, 2010). The TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may bind TNFR2 with high affinity and may sterically sequester the receptor from TNF $\alpha$  rather than allow TNF $\alpha$  binding to TNFR2 initiate TNFR2 signaling, e.g., by binding TNFR2 in an anti-parallel dimer conformation in which TNF $\alpha$  binding sites are sterically inaccessible. This, in turn, prevents TNF $\alpha$  from nucleating an activated trimer of TNFR2, which triggers 10 TNFR2 signal transduction. The antibodies of the invention can therefore be used to suppress T-reg cell growth and proliferation, thereby allowing, for example, the proliferation of T effector cells that can mount an immune response against, e.g., a cancer cell or foreign pathogen. Thus, antagonistic TNFR2 polypeptides described herein can be administered to a mammalian subject, such as a human patient with a cell proliferation disorder or an infectious disease, in order to enhance the effectiveness of an 15 immune response (e.g., an immune response against cancer cells or pathogenic organisms) in the patient.

#### *Effects on T-reg cell proliferation*

Antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention can be used to attenuate the activity (e.g., proliferation) of T-reg 20 cells that typically accompanies T cell-mediated cytotoxicity against self cells, such as the attack of a tumor cell by a T-lymphocyte. Antagonistic TNFR2 antibodies can be administered to a mammalian subject, such as a human (e.g., by any of a variety of routes of administration described herein) in order to prolong the duration of an adaptive immune response, such as a response against a cancer cell or a 25 pathogenic organism. In this way, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may synergize with existing techniques to enhance T-lymphocyte-based therapy for cancer and for infectious diseases. For instance, TNFR2 antagonists of the invention may be administered to suppress T-reg cell activity, thereby enhancing the cytotoxic effect of tumor reactive T cells. TNFR2 antagonists may also synergize with existing strategies 30 to promote tumor-reactive T cell survival, such as lymphodepletion and growth factor therapy, and in turn prolong the duration of anti-tumor reactivity *in vivo*.

Antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof can also be used to treat a broad array of infectious diseases in a mammalian subject (e.g., a human), as inhibition of T-reg proliferation promotes the activity of CD8+ T-lymphocytes 35 capable of mounting an attack on pathogenic organisms. Additionally, antagonistic TNFR2 antibodies and antigen-binding fragments thereof of the invention can be used to treat a wide variety of infectious diseases, such as *Mycobacterium tuberculosis*, in a human or an agricultural farm animal (e.g., a bovine mammal, pig, cow, horse, sheep, goat, cat, dog, rabbit, hamster, guinea pig, or other non-human mammal).

*Direct effects on TNFR2+ cancer cells*

Antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may bind and inactivate TNFR2 on the surface of a cancer cell, such as a TNFR2+ tumor cell. For instance, antagonistic TNFR2 antibodies and antigen-binding fragments thereof described herein may bind TNFR2 on the surface a T cell lymphoma cell (e.g., a Hodgkin's or cutaneous non-Hodgkin's lymphoma cell), ovarian cancer cell, colon cancer cell, multiple myeloma cell, or renal cell carcinoma cell, among others. The ability of antagonistic TNFR2 antibodies and antigen-binding fragments thereof of the invention to bind TNFR2 directly on a cancer cell provides another pathway by which these molecules may attenuate cancer cell survival and proliferation. For instance, an antagonistic TNFR2 antibody or antigen-binding fragment thereof of the invention, such as an antibody or antigen-binding fragment thereof that contains the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3, may bind TNFR2 directly on the surface of a cancer cell (e.g., a cutaneous T cell lymphoma cell, ovarian cancer cell, colon cancer cell, or multiple myeloma cell, such as an ovarian cancer cell) in order to suppress the ability of the cell to proliferate and/or to promote apoptosis of the cell.

*TNFR2 antagonist polypeptides are not reliant on additional TNFR2-binding agents for activity*

Significantly, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention are capable of binding TNFR2 and suppressing TNFR2-mediated signalling without the need for an endogenous TNFR2-binding agent, such as TNF $\alpha$ . Antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention do not require TNF $\alpha$  to attenuate T-reg and/or cancer cell proliferation. Without being limited by mechanism, antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may exhibit this property due to the ability of these antibodies or antigen-binding fragments thereof to bind TNFR2 and stabilize the anti-parallel dimer conformation of this receptor. This structural configuration is not capable of potentiating NF $\kappa$ B signaling. By maintaining TNFR2 in an inactive structural state, antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may prevent TNFR2 agonists from restoring cell growth.

For instance, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may bind TNFR2 on the surface of a TNFR2+ cell, such as a T-reg cell, cancer cell, or myeloid-derived suppressor cell (MDSC) and inhibit the proliferation of such cells in the presence or absence of TNF $\alpha$ . For example, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may inhibit the proliferation of such cells by, e.g., 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, or more, relative to such cells that are not treated with the TNFR2 antagonist polypeptide. The antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or antigen-binding fragment thereof) may exhibit an IC<sub>50</sub> value in such a cell proliferation assay that is largely unchanged by the presence or absence of TNF $\alpha$  (e.g., an IC<sub>50</sub> value in the presence of TNF $\alpha$  that is changed by less than 50%, 45%,

40%, 35%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or less than 1% relative to the IC<sub>50</sub> value of the antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or antigen-binding fragment thereof) in the same cell proliferation assay in the absence of TNF $\alpha$ ). Examples of cell death assays that can be used to measure the antagonistic effects of TNFR2 antibodies are described herein, e.g., in Example 9, below. Similarly, antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention may inhibit TNFR2 signaling as assessed by measuring the expression of one or more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3 by, e.g., 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, or more, relative to such cells that are not treated with the TNFR2 antagonist polypeptide. The antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or antigen-binding fragment thereof) may exhibit an IC<sub>50</sub> value in such a gene expression assay that is largely unchanged by the presence or absence of TNF $\alpha$  (e.g., an IC<sub>50</sub> value in the presence of TNF $\alpha$  that is changed by less than 50%, 45%, 40%, 35%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or less than 1% relative to the IC<sub>50</sub> value of the antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or antigen-binding fragment thereof) in the same gene expression assay in the absence of TNF $\alpha$ ). Examples of gene expression assays that can be used to measure the antagonistic effects of TNFR2 antibodies are described herein, e.g., in Example 12, below.

#### 20 *Direct killing of T-reg cells, TNFR2+ cancer cells, and MDSCs*

Antagonistic TNFR2 polypeptides disclosed herein, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof, can not only reduce T-reg cell, TNFR2+ cancer cell, and/or MDSC proliferation, but can also induce the death of T-reg cells, TNFR2+ cancer cells, and/or MDSCs within a sample (e.g., within a patient, such as a human patient). Antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may be capable of reducing the total quantity of T-reg cells, cancer cells (such as cutaneous T cell lymphoma cells, ovarian cancer cells, colon cancer cells, renal cell carcinoma cells or multiple myeloma cells, among others), and/or MDSCs in a sample treated with an antagonist TNFR2 antibody or antigen-binding fragment thereof (such as a sample isolated from a human patient undergoing treatment for cancer or an infectious disease as described herein) by, e.g., 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, or more, relative to a sample not treated with an antagonist TNFR2 antibody or antigen-binding fragment thereof.

The ability of antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention to attenuate T-reg, MDSC, and/or cancer cell growth may be due in part to the ability of these antibodies or antigen-binding fragments to diminish the quantity of soluble TNFR2 within a sample (e.g., a sample isolated from a human patient undergoing treatment for cancer or an infectious disease as described herein). In the absence of this beneficial activity, soluble TNFR2 can be secreted by, e.g., T-reg cells, and could otherwise interfere with the ability of TNFR2 antagonists to localize to TNFR2 at the surface of a T-reg cell, TNFR2+ cancer cell, or MDSC by binding

and sequestering such antagonists in the extracellular environment. By reducing TNFR2 secretion, antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may render T-reg cells, TNFR2+ cancer cells, and/or MDSCs increasingly susceptible to therapeutic molecules, such as an antagonistic TNFR2 antibody or antigen-binding fragment thereof, and/or additional anti-cancer agents described herein or known in the art that may be used in conjunction with the compositions and methods of the invention.

*Selective modulation of active (CD25<sup>Hi</sup> and CD45RA<sup>Low</sup>) T-reg cells*

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may be capable of inhibiting the proliferation or reducing the total quantity of T-reg cells in a sample (e.g., a sample isolated from a human patient undergoing treatment for cancer or an infectious disease as described herein) and may act selectively on T-reg cells in an actively-dividing state. Antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may selectively target active T-reg cells that express CD25<sup>Hi</sup> and CD45RA<sup>Low</sup>, e.g., over resting T-reg cells that express CD25<sup>Med</sup> and CD45RA<sup>Hi</sup>. For instance, antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may be capable of reducing the proliferation of T-reg cells expressing CD25<sup>Hi</sup> and CD45RA<sup>Low</sup> by, e.g., 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, or more relative to T-reg cells that do not express the CD25<sup>Hi</sup> and CD45RA<sup>Low</sup> proteins, such as T-reg cells that express CD25<sup>Med</sup> and CD45RA<sup>Hi</sup> proteins.

*Modulation of T-reg cells, MDSCs, and T effector cells in the tumor microenvironment*

Antagonist TNFR2 polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of T-reg cells with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. The antagonist TNFR2 polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of T-reg cells with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer. This effect may be determined using, for example, a cell death assay as described herein. For instance, the polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may exhibit an IC<sub>50</sub> for reducing or inhibiting the proliferation of T-reg cells in the microenvironment of a tumor that is less than the IC<sub>50</sub> of the polypeptides for reducing or inhibiting the proliferation of T-reg cells in a site that is free of cancer cells by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. Examples of cell death assays that can be used to measure the antagonistic effects of anti-TNFR2 polypeptides are described herein, e.g., in Example 9, below. The polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of T-reg cells

with a potency that is greater in the microenvironment of a tumor containing T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or more of the foregoing cancers or in a subject

5 without cancer.

Additionally or alternatively, the polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of MDSCs with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. The polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-

10 binding fragments thereof, may reduce or inhibit the proliferation of MDSCs with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without cancer. This effect may be determined using, for example, a cell death assay described herein. For instance, the polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may have an  $IC_{50}$

15 for reducing or inhibiting the proliferation of MDSCs in the microenvironment of a tumor that is less than the  $IC_{50}$  of the polypeptides for reducing or inhibiting the proliferation of MDSCs in a site that is free of cancer cells by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold, 1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. Examples of cell death assays

20 that can be used to measure the antagonistic effects of anti-TNFR2 polypeptides are described herein, e.g., in Example 9, below. The polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may reduce or inhibit the proliferation of MDSCs or may promote the apoptosis of MDSCs with a potency that is greater in the microenvironment of a tumor containing Hodgkin's lymphoma cells, cutaneous non-Hodgkin's lymphoma cells, T cell lymphoma cells,

25 ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or more of the foregoing cancers or in a subject without cancer.

Additionally or alternatively, the polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may expand T effector cells, such as

30 CD8+ cytotoxic T cells, with a greater potency in a patient suffering from cancer relative to a subject that does not have cancer. In some embodiments, the polypeptides of the invention, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, expand T effector cells, such as CD8+ cytotoxic T cells, with a greater potency in the microenvironment of a tumor relative to a site that is free of cancer cells, such as a site distal from a tumor in a patient suffering from cancer or in a subject without

35 cancer. This effect may be determined using, for example, a cell proliferation assay described herein. For instance, the polypeptides described herein, such as single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may have an  $EC_{50}$  for the expansion of T effector cells in the microenvironment of a tumor that is less than the  $EC_{50}$  of the polypeptides for expanding T effector cells in a site that is free of cancer cells by, for example, 1.1-fold, 1.2-fold, 1.3-fold, 1.4-fold, 1.5-fold, 1.6-fold,

1.7-fold, 1.8-fold, 1.9-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 35-fold, 40-fold, 45-fold, 50-fold, 100-fold, 1,000-fold, 10,000-fold, or more. Examples of cell proliferation assays that can be used to measure the effects of anti-TNFR2 polypeptides on T effector cells are described herein, e.g., in Example 18, below. The polypeptides described herein, such as  
5 single-chain polypeptides, antibodies, and antigen-binding fragments thereof, may directly expand T effector cells, such as CD8+ cytotoxic T cells, with a potency that is greater in the microenvironment of a tumor containing T cell lymphoma cells (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells than in a site that is free of such cancer cells, such as a site distal from a tumor in a patient suffering from one or  
10 more of the foregoing cancers or in a subject without cancer. The T effector cells (e.g., CD8+ cytotoxic T cells) may, for example, specifically react with an antigen present on one or more cancer cells, such as Hodgkin's lymphoma cells, cutaneous non-Hodgkin's lymphoma cells, T cell lymphoma cells, ovarian cancer cells, colon cancer cells, multiple myeloma cells, or renal cell carcinoma cells, among cells of other cancers described herein.

15 *Activity of antigen-binding fragments of full-length TNFR2 antagonist antibodies*

Antagonistic TNFR2 antibodies of the invention may inhibit, e.g., T-reg, cancer cell, and/or MDSC growth, or promote T effector cell growth, with a similar potency as that exhibited by antigen-binding fragments of such antibodies. For instance, removal of the Fc region of an antagonistic TNFR2 antibody  
20 of the invention may not alter the ability of the molecule to attenuate the proliferation or reduce the total quantity of T-reg cells, MDSCs, and/or cancer cells in a sample (e.g., a sample isolated from a human patient undergoing treatment for cancer or an infectious disease as described herein). Antagonistic TNFR2 antibodies and antigen-binding fragments thereof of the invention may function by a pathway distinct from antibody-dependent cellular cytotoxicity (ADCC), in which a Fc region is required to recruit  
25 effector proteins in order to induce cell death. Additionally, antagonistic TNFR2 antibodies or antigen-binding fragments thereof may not be susceptible to a loss of inhibitory capacity in the presence of cross-linking agents. Antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may therefore exhibit therapeutic activity in a variety of isotypes, such as IgG, IgA, IgM, IgD, or IgE, or in a variety of forms, such as a single-chain polypeptide (e.g., a single-chain polypeptide one or more CDRs  
30 covalently bound to one another, for instance, by an amide bond, a thioether bond, a carbon-carbon bond, or a disulfide bridge), a monoclonal antibody or antigen-binding fragment thereof, a polyclonal antibody or antigen-binding fragment thereof, a humanized antibody or antigen-binding fragment thereof, a primatized antibody or antigen-binding fragment thereof, a bispecific antibody or antigen-binding fragment thereof, a multi-specific antibody or antigen-binding fragment thereof, a dual-variable  
35 immunoglobulin domain, a monovalent antibody or antigen-binding fragment thereof, a chimeric antibody or antigen-binding fragment thereof, a single-chain Fv molecule (scFv), a diabody, a triabody, a nanobody, an antibody-like protein scaffold, a domain antibody, a Fv fragment, a Fab fragment, a F(ab')<sub>2</sub> molecule, and a tandem scFv (taFv).

*Specific binding properties of antagonistic TNFR2 polypeptides*

The specific binding of a polypeptide, such as a single-chain polypeptide, antibody, or antibody fragment of the invention, to human TNFR2 can be determined by any of a variety of established methods. The affinity can be represented quantitatively by various measurements, including the concentration of antibody needed to achieve half-maximal inhibition of the TNF $\alpha$ -TNFR2 interaction *in vitro* (IC<sub>50</sub>) and the equilibrium constant (K<sub>D</sub>) of the antibody-TNFR2 complex dissociation. The equilibrium constant, K<sub>D</sub>, that describes the interaction of TNFR2 with an antibody of the invention is the chemical equilibrium constant for the dissociation reaction of a TNFR2-antibody complex into solvent-separated TNFR2 and antibody molecules that do not interact with one another.

Polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention include those that specifically bind to TNFR2 with a K<sub>D</sub> value of less than 100 nM (e.g., 95 nM, 90 nM, 85 nM, 80 nM, 75 nM, 70 nM, 65 nM, 60 nM, 55 nM, 50 nM, 45 nM, 40 nM, 35 nM, 30 nM, 25 nM, 20 nM, 15 nM, 10 nM, 5 nM, 4 nM, 3 nM, 2 nM, or 1 nM). In some embodiments, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention are those that specifically bind to TNFR2 with a K<sub>D</sub> value of less than 1 nM (e.g., 990 pM, 980 pM, 970 pM, 960 pM, 950 pM, 940 pM, 930 pM, 920 pM, 910 pM, 900 pM, 890 pM, 880 pM, 870 pM, 860 pM, 850 pM, 840 pM, 830 pM, 820 pM, 810 pM, 800 pM, 790 pM, 780 pM, 770 pM, 760 pM, 750 pM, 740 pM, 730 pM, 720 pM, 710 pM, 700 pM, 690 pM, 680 pM, 670 pM, 660 pM, 650 pM, 640 pM, 630 pM, 620 pM, 610 pM, 600 pM, 590 pM, 580 pM, 570 pM, 560 pM, 550 pM, 540 pM, 530 pM, 520 pM, 510 pM, 500 pM, 490 pM, 480 pM, 470 pM, 460 pM, 450 pM, 440 pM, 430 pM, 420 pM, 410 pM, 400 pM, 390 pM, 380 pM, 370 pM, 360 pM, 350 pM, 340 pM, 330 pM, 320 pM, 310 pM, 300 pM, 290 pM, 280 pM, 270 pM, 260 pM, 250 pM, 240 pM, 230 pM, 220 pM, 210 pM, 200 pM, 190 pM, 180 pM, 170 pM, 160 pM, 150 pM, 140 pM, 130 pM, 120 pM, 110 pM, 100 pM, 90 pM, 80 pM, 70 pM, 60 pM, 50 pM, 40 pM, 30 pM, 20 pM, 10 pM, 5 pM, or 1 pM).

Polypeptides of the invention can also be characterized by a variety of *in vitro* binding assays. Examples of experiments that can be used to determine the K<sub>D</sub> or IC<sub>50</sub> of an anti-TNFR2 polypeptide include, e.g., surface plasmon resonance, isothermal titration calorimetry, fluorescence anisotropy, and ELISA-based assays, among others. ELISA represents a particularly useful method for analyzing antibody activity, as such assays typically require minimal concentrations of antibodies. A common signal that is analyzed in a typical ELISA assay is luminescence, which is typically the result of the activity of a peroxidase conjugated to a secondary antibody that specifically binds a primary antibody (e.g., a TNFR2 antibody of the invention). Polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention are capable of binding TNFR2 and epitopes derived thereof, such as epitopes containing one or more of residues 142-146 of SEQ ID NO: 7 within human TNFR2 (KCRPG, as shown in Figures 2A and 2B), as well as isolated peptides derived from TNFR2 that structurally pre-organize various residues in a manner that may simulate the conformation of these amino acids in the native protein. For instance, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may bind peptides containing the amino acid sequence of any one of SEQ ID NOs: 11, 19, 20, 34-117, 285, or 286, or a peptide containing between about 10 and about 30 continuous or discontinuous amino acids between positions 80 and 130 of SEQ ID NO: 7. In a direct ELISA



experiment, this binding can be quantified, e.g., by analyzing the luminescence that occurs upon incubation of an HRP substrate (e.g., 2,2'-azino-di-3-ethylbenzthiazoline sulfonate) with an antigen-antibody complex bound to a HRP-conjugated secondary antibody. For instance, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may induce a luminescence response of about 400 absorbance units or more when incubated with surface-immobilized antigen and a HRP-conjugated secondary antibody in the presence of an HRP substrate (see, e.g., Example 3). In some embodiments, the luminescence observed can be from about 400 to about 900 absorbance units (e.g., 400-900 absorbance units, 500-800 absorbance units, or 600-700 absorbance units). In some embodiments, the luminescence observed can be from about 600 to about 900 absorbance units (e.g., 600-900 absorbance units or 700-800 absorbance units).

#### *Kinetic properties of antagonistic TNFR2 polypeptides*

In addition to the thermodynamic parameters of a TNFR2-polypeptide interaction, it is also possible to quantitatively characterize the kinetic association and dissociation of a polypeptide of the invention with TNFR2. This can be done, e.g., by monitoring the rate of antibody-antigen complex formation according to established procedures. For example, one can use surface plasmon resonance (SPR) to determine the rate constants for the formation ( $k_{on}$ ) and dissociation ( $k_{off}$ ) of an antibody-TNFR2 complex. These data also enable calculation of the equilibrium constant of ( $K_D$ ) of antibody-TNFR2 complex dissociation, since the equilibrium constant of this unimolecular dissociation can be expressed as the ratio of the  $k_{off}$  to  $k_{on}$  values. SPR is a technique that is particularly advantageous for determining kinetic and thermodynamic parameters of receptor-antibody interactions since the experiment does not require that one component be modified by attachment of a chemical label. Rather, the receptor is typically immobilized on a solid metallic surface which is treated in pulses with solutions of increasing concentrations of antibody. Antibody-receptor binding induces distortion in the angle of reflection of incident light at the metallic surface, and this change in refractive index over time as antibody is introduced to the system can be fit to established regression models in order to calculate the association and dissociation rate constants of an antibody-receptor interaction.

Polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may exhibit high  $k_{on}$  and low  $k_{off}$  values upon interaction with TNFR2, consistent with high-affinity receptor binding. For example, antibodies of the invention may exhibit  $k_{on}$  values in the presence of TNFR2 of greater than  $10^4 \text{ M}^{-1}\text{s}^{-1}$  (e.g.,  $1.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $1.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $2.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $2.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $3.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $3.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $4.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $4.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $5.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $5.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $6.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $6.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $7.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $7.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $8.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $8.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $9.0 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $9.5 \times 10^4 \text{ M}^{-1}\text{s}^{-1}$ ,  $1.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $1.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $2.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $2.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $3.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $3.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $4.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $4.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $5.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $5.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $6.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $6.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $7.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $7.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $8.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $8.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $9.0 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ ,  $9.5 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ , or  $1.0 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$ ). Polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may exhibit low  $k_{off}$  values when bound to TNFR2, as these polypeptides are capable of interacting with distinct TNFR2 epitopes with a high affinity. Residues within these epitopes

form strong intermolecular contacts with TNFR2, which serves to slow the dissociation of the antibody-TNFR2 complex. This high receptor affinity is manifested in low  $k_{off}$  values. For instance, antibodies of the invention may exhibit  $k_{off}$  values of less than  $10^{-3} \text{ s}^{-1}$  when complexed to TNFR2 (e.g.,  $1.0 \times 10^{-3} \text{ s}^{-1}$ ,  $9.5 \times 10^{-4} \text{ s}^{-1}$ ,  $9.0 \times 10^{-4} \text{ s}^{-1}$ ,  $8.5 \times 10^{-4} \text{ s}^{-1}$ ,  $8.0 \times 10^{-4} \text{ s}^{-1}$ ,  $7.5 \times 10^{-4} \text{ s}^{-1}$ ,  $7.0 \times 10^{-4} \text{ s}^{-1}$ ,  $6.5 \times 10^{-4} \text{ s}^{-1}$ ,  $6.0 \times 10^{-4} \text{ s}^{-1}$ ,  $5.5 \times 10^{-4} \text{ s}^{-1}$ ,  $5.0 \times 10^{-4} \text{ s}^{-1}$ ,  $4.5 \times 10^{-4} \text{ s}^{-1}$ ,  $4.0 \times 10^{-4} \text{ s}^{-1}$ ,  $3.5 \times 10^{-4} \text{ s}^{-1}$ ,  $3.0 \times 10^{-4} \text{ s}^{-1}$ ,  $2.5 \times 10^{-4} \text{ s}^{-1}$ ,  $2.0 \times 10^{-4} \text{ s}^{-1}$ ,  $1.5 \times 10^{-4} \text{ s}^{-1}$ ,  $1.0 \times 10^{-4} \text{ s}^{-1}$ ,  $9.5 \times 10^{-5} \text{ s}^{-1}$ ,  $9.0 \times 10^{-5} \text{ s}^{-1}$ ,  $8.5 \times 10^{-5} \text{ s}^{-1}$ ,  $8.0 \times 10^{-5} \text{ s}^{-1}$ ,  $7.5 \times 10^{-5} \text{ s}^{-1}$ ,  $7.0 \times 10^{-5} \text{ s}^{-1}$ ,  $6.5 \times 10^{-5} \text{ s}^{-1}$ ,  $6.0 \times 10^{-5} \text{ s}^{-1}$ ,  $5.5 \times 10^{-5} \text{ s}^{-1}$ ,  $5.0 \times 10^{-5} \text{ s}^{-1}$ ,  $4.5 \times 10^{-5} \text{ s}^{-1}$ ,  $4.0 \times 10^{-5} \text{ s}^{-1}$ ,  $3.5 \times 10^{-5} \text{ s}^{-1}$ ,  $3.0 \times 10^{-5} \text{ s}^{-1}$ ,  $2.5 \times 10^{-5} \text{ s}^{-1}$ ,  $2.0 \times 10^{-5} \text{ s}^{-1}$ ,  $1.5 \times 10^{-5} \text{ s}^{-1}$ , or  $1.0 \times 10^{-5} \text{ s}^{-1}$ ).

#### 10 *Epitopes within TNFR2 bound by antagonistic TNFR2 polypeptides*

Among the difficulties in developing anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) that are capable of antagonizing TNFR2 has been the elucidation of epitopes within TNFR2 that participate in antagonistic complex formation rather than epitopes that promote signal transduction. The present invention is based in part on the discovery of epitopes within TNFR2 that, when bound, promote receptor antagonism. Particularly important epitopes that bind antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention and promote receptor antagonism are those that contain one or more residues of the KCRPG motif (SEQ ID NO: 19), located at positions 142-146 of SEQ ID NO: 7 within human TNFR2. One or more of these residues reside within larger epitopes (e.g., residues 142-149 of SEQ ID NO: 7, shown in Figure 2A, and residues 137-144 of SEQ ID NO: 7, shown in Figure 2B) that may interact with antagonistic TNFR2 antibodies of the invention. The knowledge of those residues that selectively bind antagonistic TNFR2 antibodies can be used to identify and design a wide array of antagonistic TNFR2 antibodies and antigen-binding fragments thereof using library screening techniques, e.g., those described herein or known in the art. For instance, peptides containing one or more the residues within the KCRPG sequence (e.g., the LRKCRPGFGVA motif (SEQ ID NO: 285) within human TNFR2) can be used to screen and select for antibodies and antibody-like scaffolds that bind these epitopes with high affinity and selectivity.

Importantly, antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention are capable of selectively binding an epitope of TNFR2 that contains one or more of the residues of the KCRPG motif (SEQ ID NO: 19) and distinctly do not exhibit specific binding to an epitope containing residues 56-60 of SEQ ID NO: 7 within human TNFR2 (KCSPG, SEQ ID NO: 12). Polypeptides that exhibit the ability to bind an epitope containing one or more residues of amino acids 142-146 of SEQ ID NO: 7 within human TNFR2 and an epitope containing residues 56-60 of SEQ ID NO: 7 within human TNFR2 have been shown to lack inhibitory (antagonistic) activity. As such, the ability of a TNFR2 polypeptide to discriminate among these epitopes and specifically interact with an epitope including one or more of residues 142-146 of SEQ ID NO: 7 within human TNFR2 and to not engage in specific binding with an epitope composed of residues 56-60 of SEQ ID NO: 7 within human TNFR2 characterizes antibodies of the invention that antagonize TNFR2 signaling.

In addition to one or more residues of amino acids 142-146 of SEQ ID NO: 7, antagonistic TNFR2 polypeptides, such a dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may also bind one or more residues of a larger epitope that includes at least five continuous or discontinuous residues from positions 130-149 of SEQ ID NO: 7 within human TNFR2 (KQEGCRLCAPLRKCRPGFGV, SEQ ID NO: 17), or an epitope that exhibits at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. For example, antagonistic TNFR2 antibodies of the invention may specifically bind an epitope containing residues 142-149 of SEQ ID NO: 7 within human TNFR2 (KCRPGFGV, SEQ ID NO: 20), or an epitope that exhibits at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence (so long as one or more residues of the KCRPG sequence is present in the epitope). Additionally or alternatively, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may specifically bind an epitope including residues 137-144 of SEQ ID NO: 7 within human TNFR2 (CAPLRKCR, SEQ ID NO: 11), or an epitope that exhibits at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence (so long as one or more residues of the KCRPG sequence is present in the epitope).

In addition to the KCRPG motif (SEQ ID NO: 19), it has been discovered that another important epitope present within human TNFR2 that promotes receptor antagonism contains residues 159-171 of SEQ ID NO: 7 (VVCKPCAPGTFSN, SEQ ID NO: 286). Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may therefore bind an epitope downstream of the KCRPG sequence (SEQ ID NO: 19) that contains, for instance, at least five continuous or discontinuous residues from positions 150-190 of SEQ ID NO: 7 within human TNFR2 (ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI, SEQ ID NO: 22), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. For example, in some embodiments, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof of the invention) may specifically bind an epitope that includes residues from positions 161-169 of SEQ ID NO: 7 within human TNFR2 (CKPCAPGTF, SEQ ID NO: 21), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may specifically bind an epitope that includes residues from positions 140-150 of SEQ ID NO: 7 within human TNFR2 (LRKCRPGFGVA, SEQ ID NO: 285), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. Additionally or alternatively, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may specifically bind an epitope that includes residues from positions 159-171 of SEQ ID NO: 7 within human

TNFR2 (VVCKPCAPGTFSN, SEQ ID NO: 286), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence.

In addition to the above-described epitopes, antagonistic TNFR2 polypeptides, such as dominant  
5 antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may also specifically bind an epitope within human TNFR2 that includes at least five continuous or discontinuous residues from positions 75-128 of SEQ ID NO: 7 within human TNFR2 (CDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICTCRPGWYCAL, SEQ ID NO: 13), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%,  
10 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. Anti-TNFR2 polypeptides of the invention may also specifically bind an epitope within human TNFR2 that includes at least five continuous or discontinuous residues from positions 75-91 of SEQ ID NO: 7 within human TNFR2 (CDSCEDSTYTQLWNWV, SEQ ID NO: 14), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100%  
15 sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. In some embodiments, anti-TNFR2 polypeptides of the invention may specifically bind an epitope that includes residues at positions 80-86 of SEQ ID NO: 7 within human TNFR2 (DSTYTQL, SEQ ID NO: 8), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain  
20 conservative amino acid substitutions relative to this sequence. Antagonistic TNFR2 polypeptides of the invention also may specifically bind an epitope that includes at least five continuous or discontinuous residues from positions 86-103 of SEQ ID NO: 7 within human TNFR2 (LWNWVPECLSCGSRCSDD, SEQ ID NO: 15), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino  
25 acid substitutions relative to this sequence. In particular cases, antibodies of the invention may specifically bind an epitope that includes residues from positions 91-98 of SEQ ID NO: 7 within human TNFR2 (PECLSCGS, SEQ ID NO: 9), as well as an epitope that exhibits at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. The polypeptides (e.g., single-chain  
30 polypeptides, antibodies, and antigen-binding fragments) of the invention may also specifically bind an epitope that include at least five continuous or discontinuous residues from positions 111-128 of SEQ ID NO: 7 within human TNFR2 (TREQNRICTCRPGWYCAL, SEQ ID NO: 16), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence.  
35 In some embodiments, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may specifically bind an epitope that includes residues from positions 116-123 of SEQ ID NO: 7 within human TNFR2 (RICTCRPG, SEQ ID NO: 10), as well as epitopes that exhibit at least 85% sequence identity (e.g., 85%, 90%, 95%, 97%, 99%, or 100% sequence identity) to this sequence and epitopes that contain conservative amino acid substitutions relative to this sequence. For

example, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may specifically bind an epitope containing residues 116-123 of SEQ ID NO: 7 within human TNFR2 (RICTCRPG, SEQ ID NO: 10) and residues 137-144 of SEQ ID NO: 7 within human TNFR2 (CAPLRKCR, SEQ ID NO: 11).

5 One exemplary procedure that can be used to predict the inhibitory activity of a TNFR2 polypeptide of the invention is to compare the affinity of the antibody or antibody fragment for a peptide containing the KCRPG motif (e.g., a linear peptide having the sequence LRKCRPGFGVA (SEQ ID NO: 285) or VVCKPCAPGTFSN (SEQ ID NO: 286) to the affinity of the same antibody or antibody fragment for a peptide containing the KCSPG sequence (e.g., a linear peptide having the sequence

10 QTAQMCCSKCSPGQHAKVFC, SEQ ID NO: 18). For instance, antagonistic TNFR2 antibody TNFRAB1 specifically binds the peptide fragment defined by residues 130-149 of SEQ ID NO: 7 within human TNFR2 (KQEGCRLCAPLRKCRPGFGV, SEQ ID NO: 17) with a 40-fold greater affinity than the peptide fragment defined by residues 48-67 of SEQ ID NO: 7 within human TNFR2 (QTAQMCCSKCSPGQHAKVFC, SEQ ID NO: 18). Antagonistic TNFR2 antibodies and antigen-binding

15 fragments of the invention bind an epitope containing one or more residues of the KCRPG sequence (SEQ ID NO: 19), e.g., with an affinity that is at least 10-fold greater than the affinity of the same antibody or antigen-binding fragment for a peptide that contains the KCSPG sequence of human TNFR2 (SEQ ID NO: 12). For example, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may bind an epitope containing one or more residues of the

20 KCRPG sequence (SEQ ID NO: 19) of human TNFR2 with an affinity that is 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 60-fold, 70-fold, 80-fold, 90-fold, 100-fold, 200-fold, 300-fold, 400-fold, 500-fold, 600-fold, 700-fold, 800-fold, 900-fold, 1000-fold, or more than 1000-fold greater than the affinity of the same antibody or antigen-binding fragment for a peptide that contains the KCSPG sequence (SEQ ID NO: 12) of human TNFR2. Antibodies or antibody fragments that bind epitopes containing one or more residues of

25 the KCRPG sequence (amino acids 142-146 of SEQ ID NO: 7 within human TNFR2) and epitopes containing the KCSPG motif (amino acids 56-60 of SEQ ID NO: 7 within human TNFR2) with similar affinity (e.g., less than a 10-fold difference in affinity) are not considered antagonistic TNFR2 antibodies of the invention.

### 30 *Antagonistic TNFR2 polypeptides that bind TNFR2 from non-human animals*

In addition to binding epitopes within human TNFR2 that contain the KCRPG motif, antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention also include those that specifically bind epitopes containing the equivalent motif within TNFR2 derived from non-human animals,

35 such as the KCGPG motif (SEQ ID NO: 287) within TNFR2 of non-human mammals, e.g., in TNFR2 obtained from a cow, bison, mouse, or rat, among others. The location of sequences equivalent to the human KCRPG motif in TNFR2 derived from exemplary non-human mammals is shown in Table 2, below:

Table 2. Location of sequences equivalent to KCRPG in TNFR2 from non-human mammals

Source of TNFR2	Sequence equivalent to KCRPG	Amino acid positions of equivalent sequence within TNFR2	SEQ ID NO. of full-length TNFR2 sequence	Genbank Accession No. of full-length TNFR2 sequence
Human	KCRPG	142-146	7	P20333.3
Cattle	KCGPG	142-146	280	AAI05223
Bison	KCGPG	142-146	281	XP_010848145
Mouse	KCGPG	144-148	282	AAA39752.1
Rat	KCGPG	144-148	283	Q80WY6

Epitopes within TNFR2 derived from the non-human mammals discussed above that may be bound by antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention are illustrated in the sequence alignment below. This sequence alignment shows partial sequences of TNFR2 derived from human, cattle, bison, mouse, and rat, as well as epitopes (highlighted in grey) equivalent to the human KCRPG motif.

Alignment of partial TNFR2 sequences derived from human and select non-human mammals

Human: 1 MAPVAWAALAVGLLEWAAHALPAQAVFTPYAPEPGSTCRLL--REYYDQTAQMCCSKCSPGQAKHAKVFCCTKTSIDTIVCDSC 78  
Cattle: 1 MAPTAFWAALAVGLQFWAAGRAPVPAQAVFTPYIPEPGSSCRQ--QEYXNQKIQMCCSKCPPGVRVQSLCNMILDTICASC 78  
Bison: 1 MAPTAFWAALAVGLQFWAAGRAPVPAQAVFTPYIPEPGSSCRQ--QEYXNHKIQMCCSKCPPGVRVQSLCNMILDTICASC 78  
Mouse: 1 MAPAALWVALVLELQWLWATGHTVPAQVVLTPYKPEPGYECQIS--QEYYDRKAQMCCKAKCPPGQVYKHF CNKTSIDTIVCADC 79  
Rat: 1 MAPAALWVALVLELQWLWATGHTVPAKVVLTYPKPEPGNQCQIS--QEYYDKKAQMCCKAKCPPGQVYKHF CNKTSIDTIVCADC 79

Human: 79 EDSTYITQLWNVPECLSCGSRCSDDQVEITQACTIREQNRICICRPGWYCALSKQEG--CRLCAPLFRKCHHFFGVARPGTETS 157  
Cattle: 79 ESSYITQLWNLVTACFSCNSRCSDDQVEITQACTIKQNRICICKPGWYCTILGRQEG--CRLCVVALFRKCHHFFGVAKPGTATT 157  
Bison: 79 ESSYITQLWNLVTACFSCNSRCSDDQVEITQACTIKQNRICICKPGWYCTILGRQEG--CRLCVVALFRKCHHFFGVAKPGTATT 157  
Mouse: 80 EASMYTQVWNQFRITCLSCSSCITDQVEIRACTKQNRVCAACEAGRYCALKTHSGSCRQCMRLSKCGPFFGVASSRAPNG 159  
Rat: 80 AAGMFTQVWNHLHTCLSCSSCDDQVEITHNCITKQNRVCAACNADSYCALKHLHSGNCRQCMKLSKCGPFFGVARSRTSNG 159

Human: 158 DVVCKPCAPGTFSNITSSDIDICRPHQICNVVVAIPGNASMDAVCT-----STSPTRSMAPGAVHLFPQPVSTRSQHTQPTP 231  
Cattle: 158 NVICAPCGPFTSDTTSYDITCKPHRNCSSVALPGTASTDAVCT-----SVLPTTRKVARG-----PATTRSQHMEPTL 225  
Bison: 158 NVICAPCGPFTSDTTSYDITCKPHRNCSSVALPGTASTDAVCT-----SVLPTTRKVARG-----PATTRSQHMEPTL 225  
Mouse: 160 NVLCKACAPGTFSDTTSYDITVCRPHRICSIILAPGNASTDAVCAPESPTLSAIPR-----TLVYSQPEPTRSQPLDQEP 233  
Rat: 160 NVICSACAPGTFSDTTSYDITVCRPHRICSIILAPGNASTDAVCASESPTPSAVPR-----TIYVSQPEPTRSQPMDQEP 233

Human: 232 EPSTAPSTSFLLPMGPPPA----EGSTGDFALPVGLIVGVITALGLLLIIGVVNVCVIMTIQVKKKPLCLQREAKVPHLFPADK 307  
Cattle: 226 GPSTAPSTFFLLPKVPPSPVPEQNTGNI SLPIELIVGVITALGLLLIIVVNCVIMTIQKKKPFCLQGDAAKVPHLFPANK 305  
Bison: 226 GPSTAPSTFFLLPKVPPSPVPEQNAIGNI SLPIELIVGVITALGLLLIIVVNCVIMTIQKKKPFCLQGDAAKVPHLFPANK 305  
Mouse: 234 GPSQTPS---ILTSLGSTPI--IEQSTKGGISLPIGLIIVGVTSGLLMLGLVNCIILVQRKKKPSCLQRDAKVPHPVPEDEK 308  
Rat: 234 GPSQTPH---IPVSLGSTPI--IEPSITGGISLPIGLIIVGLTTLGLLMLGLANCFILVQRKKKPSCLQRETMVPHLFPDDK 308

Human: 308 ARGTOGPEQQHLLLTAPSSSSSSLESSASALDRRAPTRNQAPQVGE--ASGAGEARASTIGSSDSSPGGHGTQVNVVTCIVN 386  
Cattle: 306 AQQAPGPEQQHLLLTAPSSSSSSLESSSTSDTKRAPTRSQLQSPGVEKASTSGEAQTGCSSESASSGGHGTQVNVVTCIVN 385  
Bison: 306 AQQAPGPEQQHLLLTAPSSSSSSLESSSTSDTKRAPTRSQLQSPGVE--ANTSGEAQTGCSSESASSGGHGTQVNVVTCIVN 384  
Mouse: 309 SQDAVGLQEQHLLLTAPSSSSSSLESSASAGDRRAPPGGHPQARVMABEQGFQEARASSRI SDSHSHGTHVNVVTCIVN 388  
Rat: 309 SQDAIGLEQQHLLLTAPSSSSSSLESSASAGDRRAPPGGHPQARVTAEAQGSQEAACAGRSRSDSSSHGSHGTHVNVVTCIVN 388

*The antagonistic TNFR2 antibody TNFRAB1*

Antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention may contain the CDR-H3 sequence of TNFRAB1, also referred to herein as TNFR2 antagonist 1, which is a murine antibody that antagonizes the TNFR $\alpha$ -TNFR2 interaction. For instance, the CDR-H3 of TNFRAB1 and variants thereof (e.g., variants that exhibit conservative amino acid substitutions relative to this CDR-H3 sequence) can be used to make an antagonistic TNFR2 antibody or antigen-binding fragment thereof of the invention, for instance, using antibody humanization methods described herein or known in the art.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may exhibit binding properties that are the same as or similar to those of TNFRAB1. These properties are as follows: In the presence of TNFR2, TNFRAB1 exhibits a high  $k_{on}$  value of  $4.98 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$ , as well as a low  $k_{off}$  of  $2.21 \times 10^{-4} \text{ s}^{-1}$  and a  $K_D$  of about 44.4 pM in complex with TNFR2. The KCRPGFGV motif (SEQ ID NO: 20), and specifically, the KCRPG sequence (SEQ ID NO: 19), has been identified as a particularly important component of the functional epitope that establishes intermolecular contacts with TNFRAB1 as determined by epitope mapping analysis (Figures 2 and 3). The interaction of these residues with anti-TNFR2 antibodies of the invention selectively promotes antagonistic activity. Significantly, a TNFR2 epitope including amino acid residues 56-60 of SEQ ID NO: 7 within human TNFR2 (KCSPG, SEQ ID NO: 12) is distinctly not a part of the conformational epitope that is specifically bound by TNFRAB1 or antagonistic TNFR2 antibodies or antibody fragments of the invention, as specific binding to both of these epitopes has been shown to lead to a loss of, or significant reduction in, antagonistic activity. As such, TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) that specifically bind both of these epitopes (KCSPG and an epitope containing at least the KCR sequence, and more specifically, the KCRPG sequence of human TNFR2) are not considered antagonistic TNFR2 antibodies of the invention.

In addition to binding an epitope contained within the sequence KCRPGFGV (SEQ ID NO: 20), TNFRAB1 also binds to a downstream epitope contained within a sequence defined by positions 161-169 of SEQ ID NO: 7 within human TNFR2 (CKPCAPGTF, SEQ ID NO: 21). TNFR2 antibodies and antibody fragments of the invention may also bind this epitope or a larger region within TNFR2 containing this epitope (e.g., a sequence that includes at least five continuous or discontinuous residues from positions 150-190 of SEQ ID NO: 7 within human TNFR2 (ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI, SEQ ID NO: 22). TNFRAB1 contains two heavy chains, as well as two light chains, as shown in Figures 1A and 1B. The heavy chains of TNFRAB1 contain the following amino acid sequence (CDRs are indicated in bold):

EVQLQESGGGLVKPGGSLKLSAAS**GF****TFSS**YVMSWVRQTPEKRLEWVAT**ISSGGS**YTYYPDSVKGRF  
TISRDNAKNTLYLQMSSLRSEDTAMYYCAR**QRVDG****YSSY**WYFDVWGAGTAVTVSS (SEQ ID NO: 2)

The sequence of the TNFRAB1 light chain is as follows (CDRs are indicated in bold):



DIVLTQSPAIMASAPGKVTITCSASSSVYYMYWFQQKPGTSPKLIWYSTSNLASGVPVRFSGSGSGTSY  
 SLTISRMEAEDAATYYCQRRNYPYTFGGGTKLEIKRA

(SEQ ID NO: 4)

5 *The antagonistic TNFR2 antibody TNFRAB2*

An antagonistic TNFR2 antibody or antibody fragment of the invention may contain, for instance, the CDR-H3 sequence of TNFRAB2, also referred to herein as TNFR2 antagonist 2, an antibody that selectively binds and inhibits TNFR2 by virtue of specifically binding various epitopes within this receptor. For instance, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention may exhibit binding properties that are the same as or similar to those of TNFRAB2. These properties are as follows: In the presence of TNFR2, TNFRAB2 exhibits a high  $k_{on}$  value of  $3.6099 \times 10^5 \text{ M}^{-1}\text{s}^{-1}$ , as well as a low  $k_{off}$  of  $2.24 \times 10^{-4} \text{ s}^{-1}$  and a  $K_D$  of about 621 pM in complex with TNFR2. An epitope containing residues 137-144 of SEQ ID NO: 7 within human TNFR2 (CAPLRKCR, SEQ ID NO: 11) has been identified as a particularly important component of the functional epitope that establishes intermolecular contacts with TNFRAB2 as determined by epitope mapping analysis (see, e.g., Example 1 and Figures 2B and 3B). Included in the invention are TNFR2 antibodies and antibody fragments that specifically bind this epitope.

In addition to binding an epitope containing residues CAPLRKCR (SEQ ID NO: 11), TNFRAB2 also binds to epitopes that include one or more residues within positions 80-86 of SEQ ID NO: 7 within human TNFR2 (DSTYTQL, SEQ ID NO: 8), positions 91-98 of SEQ ID NO: 7 within human TNFR2 (PECLSCGS, SEQ ID NO: 9), as well as positions 116-123 of SEQ ID NO: 7 within human TNFR2 (RICTCRPG, SEQ ID NO: 10). TNFR2 antibodies and antibody fragments of the invention may also bind one or more of these epitopes. Antibodies and antibody fragments of the invention can be designed and identified using the knowledge of the epitopes specifically bound by TNFRAB2. For instance, one can use any of a variety of *in vitro* peptide display techniques or combinatorial antibody library screens as described herein or known in the art in order to screen for antibodies capable of binding these epitopes with high affinity and selectivity.

The heavy chain and light chain CDRs of TNFRAB2 are shown below:

30 TNFRAB2 CDR-H1: GYTFTDY(L/I) (SEQ ID NO: 257)  
 TNFRAB2 CDR-H2: VDPEYGST (SEQ ID NO: 258)  
 TNFRAB2 CDR-H3: ARDDGSYSPFDYWG (SEQ ID NO: 259)  
 TNFRAB2 CDR-L1: QNINKY (SEQ ID NO: 260)  
 TNFRAB2 CDR-L2: TYS or YTS  
 35 TNFRAB2 CDR-L3: CLQYVNL(L/I)T (SEQ ID NO: 261)

As shown above, the CDR-H1 sequence of TNFRAB2 may contain either a leucine or isoleucine residue at the eighth position of this region. Similarly, the TNFRAB2 CDR-L2 may include a TYS or YTS tripeptide, and the TNFRAB2 CDR-L3 may contain either a leucine or isoleucine residue at the eighth

position of this region. Notably, the CDR-L2 of TNFRAB2 is flanked by the N-terminal framework residues LLIR (SEQ ID NO: 262) and the C-terminal framework residues TLE. Accordingly, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments) of the invention include those that contain one or more of the above CDRs of TNFRAB2, as well as N-terminal LLIR (SEQ ID NO: 262) and C-terminal TLE residues that flank the CDR-L2 sequence of the antagonistic TNFR2 antibody or antigen-binding fragment thereof.

#### *The antagonistic TNFR2 antibody TNFR2A3*

A representative antagonist TNFR2 antibody of the invention is TNFR2A3, a murine antibody that was discovered by immunization of a mouse with human TNFR2 and subsequent CDR mutagenesis. A precursor antibody to TNFR2A3 was identified from murine immunization experiments as a TNFR2-binding antibody that was neither antagonistic nor agonistic of TNFR2. Using recombinant gene expression techniques, TNFR2A3 was produced by replacing the CDR-H3 sequence of the precursor murine antibody with the CDR-H3 sequence ARDDGSYSPFDYFG (SEQ ID NO: 284). Upon insertion of this CDR-H3 sequence into the precursor scaffold, the resulting TNFR2A3 antibody was capable of exhibiting an antagonistic effect on the TNFR2 target. Additionally, the TNFR2A3 antibody was found to bind epitopes within human TNFR2 that are consistent with those bound by dominant antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2. As described in Example 15, TNFR2A3 binds to two distinct epitopes within human TNFR2. The first epitope spans residues 140-150 of human TNFR2 (LRKCRPGFGVA, SEQ ID NO: 285) and contains the KCRPG motif (SEQ ID NO: 19). The second epitope is a downstream sequence that contains residues 159-171 of human TNFR2 (VVCKPCAPGTFSN, SEQ ID NO: 286). For instance, dominant antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention may exhibit binding properties that are the same as or similar to those of TNFR2A3. Importantly, the binding of TNFR2A3 to these epitopes within TNFR2 is site-specific, as the TNFR2A3 antibody does not bind a human TNFR2-derived peptide containing an unrelated, distal amino acid sequence (see, e.g., Example 15). Collectively, these findings demonstrate two significant features of the CDR-H3 sequence with respect to TNFR2 antagonism: (i) that the CDR-H3 sequence of an antagonistic TNFR2 antibody largely dictates the antigen-binding properties of the system, and (ii) that the CDR-H3 motif is a modular domain that can be substituted into anti-TNFR2 antibodies that do not exhibit antagonistic activity in order to impart such antibodies with TNFR2 dominant antagonistic features.

#### *Molecular determinants of TNFR2 affinity and antagonism*

Notably, there are distinct sequence similarities between the CDR-H3 regions of the antagonistic TNFR2 antibodies TNFRAB1, TNFRAB2, and TNFR2A3. An analysis of the residues common to the CDR-H3 sequences of these antibodies provides insight into the molecular features of antibodies that bind TNFR2 and exhibit an antagonistic effect, such as a dominant antagonistic effect. Epitope mapping analysis has shown that both TNFRAB1, TNFRAB2, and TNFR2A3 bind epitopes within TNFR2 that contain residues 142-146 of SEQ ID NO: 7 and do not bind epitopes containing residues 56-60 of SEQ ID

NO: 7. The structural similarities between corresponding CDR-H3 regions provide a basis for predicting residue substitutions that may preserve or enhance TNFR2 affinity and antagonism (e.g., dominant antagonism). Inspection of the CDR-H3 sequences of these antibodies demonstrates that several residues and physicochemical characteristics are conserved throughout this region, while other positions within this CDR can be varied significantly without loss of affinity and antagonistic function. The CDR-H3 sequences of TNFRAB1, TNFRAB2, and TNFR2A3 are shown below:

**QRVDGYSSYWYFDV** (TNFRAB1 CDR-H3, SEQ ID NO: 25)

**ARDDG-S-YSPFDYWG** (TNFRAB2 CDR-H3, SEQ ID NO: 259)

**ARDDG-S-YSPFDYFG** (TNFR2A3 CDR-H3, SEQ ID NO: 284)

**-R-DG-S-Y--FD---** (Consensus sequence)

Inspection of the CDR-H3 sequences of TNFRAB1, TNFRAB2, and TNFR2A3 reveals conserved arginine, aspartic acid, glycine, serine, tyrosine, and phenylalanine residues throughout this CDR. Notably, residues of varying steric and electrostatic properties are tolerated in the remaining positions. For instance, the first position of the CDR-H3 sequence tolerates amino acid residues of contrasting size and hydrogen bond-forming tendencies, as the first position of CDR-H3 in TNFRAB1 features a polar glutamine residue containing a carboxamide side-chain with hydrogen bond donor and acceptor moieties, while an alanine residue bearing an unfunctionalized methyl side-chain is found at the corresponding position in TNFRAB2 and TNFR2A3. Additionally, the third position in the above CDR-H3 sequences features a hydrophobic valine in TNFRAB1 and an anionic aspartic acid moiety in the corresponding position of TNFRAB2. Similarly, positions ten and eleven of the CDR-H3 of TNFRAB1 contain aromatic systems, while the corresponding residues in TNFRAB2 and TNFR2A3 contain polar and cyclic aliphatic substituents.

Collectively, the shared structural features of the above CDR-H3 sequences provide insight into those residues that are important for selectively binding residues within TNFR2 that promote receptor antagonism (e.g., dominant receptor antagonism), such as residues 140-150 of human TNFR2 (LRKCRPGFGVA, SEQ ID NO: 285) and residues 159-171 of human TNFR2 (VVCKPCAPGTFSN, SEQ ID NO: 286) and demonstrate that other amino acids can be varied while retaining affinity and dominant antagonistic activity. For instance, antagonistic TNFR2 polypeptides, such a dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention may contain a CDR-H3 represented by the formula  $JZ^1JZ^2Z^4JZ^3JZ^5(J)_2Z^5Z^2Z^5$  or  $JZ^1JZ^2Z^4Z^3Z^5(J)_2Z^5Z^2Z^5(J)_2$ , wherein each J is independently a naturally occurring amino acid, each Z<sup>1</sup> is independently a naturally occurring amino acid containing a cationic side-chain at physiological pH, each Z<sup>2</sup> is independently a naturally occurring amino acid containing an anionic side-chain at physiological pH, each Z<sup>3</sup> is independently a naturally occurring amino acid containing a polar, uncharged side-chain at physiological pH, each Z<sup>4</sup> is independently a glycine or alanine, and each Z<sup>5</sup> is independently a naturally occurring amino acid containing a hydrophobic side-chain.

Similarly, antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention may contain a CDR-H3 represented by the formula JRJDGJSJY(J)<sub>2</sub>FDJ (SEQ ID NO: 278),

JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279), QZ<sup>1</sup>VZ<sup>2</sup>Z<sup>4</sup>YZ<sup>3</sup>SZ<sup>5</sup>WYZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup> (SEQ ID NO: 265), or AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266). For instance, the CDR-H3 may be derived from TNFRAB1 and have the amino acid sequence QRVDGYSSYWFYFDV (SEQ ID NO: 25). The CDR-H3 may be derived from TNFRAB2 and have the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259). In some embodiments, the CDR-H3 is derived from TNFR2A3 and has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

In addition to the above CDR-H3 sequences, other CDR sequences can be include in antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention. Additional CDR sequences that promote dominant TNFR2 antagonism can be determined, for instance, by alignment of the CDR sequences of TNFRAB1 and TNFRAB2. For example, the CDR-H1 sequences of TNFRAB1 and TNFRAB2 are shown below:

**GFTFSSY** (TNFRAB1 CDR-H1, SEQ ID NO: 23)  
**GYTFTDY (L/I)** (TNFRAB2 CDR-H1, SEQ ID NO: 257)  
**G-TF--Y-** (Consensus sequence)

Alignment of the sequences reveals a shared GXTFXXY motif, wherein "X" designates any amino acid. These CDR-H1 sequences feature a conserved glycine residue at the first position and conserved threonine, phenylalanine, and tyrosine residues at the third, fourth, and seventh positions, respectively. Inspection of these sequences demonstrates that the CDR-H1 region is tolerant of substitutions at the remaining positions. Side-chains of varying polarity are tolerated at the second position, for example, as both phenylalanine, containing an unsubstituted and hydrophobic phenyl moiety, and tyrosine, containing a protic hydroxyl substituent, are found in this position in the CDR-H1 region of TNFRAB1 and TNFRAB2, respectively. Additionally, while the fifth and sixth positions are occupied by polar serine residues in the CDR-H1 of TNFRAB1, these positions feature a threonine, containing an additional hydrophobic methyl substituent, and aspartic acid, which is anionic at physiological pH, in TNFRAB2. This diversity demonstrates that these positions can be substituted with amino acids of diverse electrostatic properties without loss of TNFR2 affinity and antagonism.

Sequence analysis of the CDR-H2 regions of TNFRAB1 and TNFRAB2 similarly reveals a set of conserved amino acids at various positions throughout these regions:

**SSG--GSY** (TNFRAB1 CDR-H2, SEQ ID NO: 24)  
**VDPEYGST** (TNFRAB2 CDR-H2, SEQ ID NO: 258)  
**-----GS-** (Consensus sequence)

Analysis of this sequence alignment demonstrates that the CDR-H2 sequences exhibit a conserved GS motif at the C-terminal end of the CDR-H2 region, with side-chains of variable molecular

size, polarity, and electrostatic charge tolerated at the remaining positions.

A similar analysis reveals molecular features common to the CDR-L sequences of TNFRAB1 and TNFRAB2. For instance, the CDR-L1 sequences of TNFRAB1 and TNFRAB2 are shown below:

5                   **SASSSVYYMY** (TNFRAB1 CDR-L1, SEQ ID NO: 26)  
                       **Q-N--INK-Y** (TNFRAB2 CDR-L1, SEQ ID NO: 260)  
                                   **Y** (Consensus residue)

10                   Inspection of these sequences reveals that a hydroxyl-containing tyrosine residue is featured at the final position of CDR-L1, while residues of varying physicochemical properties are tolerated at the remaining positions. Similarly, analysis of the CDR-L2 regions of TNFRAB1 and TNFRAB2 reveals a conserved amino acid at the final position in both regions:

15                   **STSNLAS** (TNFRAB1 CDR-L2, SEQ ID NO: 27)  
                       **TY----S or** (TNFRAB2 CDR-L2)  
                       **YT----S**  
                                   **S** (Consensus residue)

20                   Analysis of the above sequence alignment demonstrates that serine residues are featured at the third position of these CDR-L2 sequences, while substitutions are widely tolerated at the remaining residues. Similarly, the CDR-L3 sequences of TNFRAB1 and TNFRAB2 are as follows:

25                   **Q-QRRNYPY-----T** (TNFRAB1 CDR-L3, SEQ ID NO: 28)  
                       **CLQ---YVNL (L/I) T** (TNFRAB2 CDR-L3, SEQ ID NO: 261)  
                       **-----Y-----T** (Consensus sequence)

30                   Analysis of the CDR-L3 sequences of TNFRAB1 and TNFRAB2 reveals a preference for tyrosine and threonine residues at distinct positions within these regions, while amino acids of a wide range of physicochemical characteristics are tolerated at other positions, including residues with cationic side-chains (Arg), conformationally restricted side-chains (Pro), and side-chains of varying polarity (e.g., Gln, Asn, Leu, and Val). Collectively, the shared structural features of the above CDR-H and CDR-L sequences provide insight into those residues that are important for selectively binding one or more residues of the KCRPG epitope of TNFR2 (positions 142-146 of SEQ ID NO: 7, shown in SEQ ID NO: 19) in an anti-parallel dimer configuration and demonstrate that certain amino acids can be varied while retaining affinity and dominant antagonistic activity.

35                   Antagonistic TNFR2 polypeptides of the invention, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) may therefore have heavy chain and light chain CDRs that contain the above consensus sequences. For instance, TNFR2 antagonists of the invention may have a CDR-H1 having the amino acid sequence

Z<sup>4</sup>JZ<sup>3</sup>Z<sup>5</sup>(J)<sub>2</sub>Z<sup>5</sup>J; a CDR-H2 having the amino acid sequence (J)<sub>5</sub>Z<sup>4</sup>Z<sup>3</sup>J; a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Z<sup>5</sup>; a CDR-L2 having the amino acid sequence (J)<sub>2</sub>Z<sup>3</sup>; and/or a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Z<sup>5</sup>(J)<sub>4</sub>Z<sup>3</sup>; wherein each J is independently a naturally occurring amino acid; each Z<sup>1</sup> is independently a naturally occurring amino acid containing a cationic side-chain at physiological pH; each Z<sup>2</sup> is independently a naturally occurring amino acid containing an anionic side-chain at physiological pH; each Z<sup>3</sup> is independently a naturally occurring amino acid containing a polar, uncharged side-chain at physiological pH; each Z<sup>4</sup> is independently a glycine or alanine; and each Z<sup>5</sup> is independently a naturally occurring amino acid containing a hydrophobic side-chain.

In some embodiments, antagonistic TNFR2 polypeptides of the invention, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) may have a CDR-H1 having the amino acid sequence GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277); a CDR-H2 having the amino acid sequence (J)<sub>5</sub>GSJ; a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y; a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and/or a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T; wherein each J is independently a naturally occurring amino acid.

Antagonistic TNFR2 polypeptides of the invention, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) may have a CDR-H1 having the amino acid sequence Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X; a CDR-H2 having the amino acid sequence VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264); a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268); a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and/or a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271); wherein each Z<sup>1</sup> is independently an amino acid containing a cationic side-chain at physiological pH; each Z<sup>2</sup> is independently an amino acid containing an anionic side-chain at physiological pH; each Z<sup>3</sup> is independently an amino acid containing a polar, uncharged side-chain at physiological pH; each Z<sup>4</sup> is independently a glycine or alanine; each Z<sup>5</sup> is independently an amino acid containing a hydrophobic side-chain; and each X is independently leucine or isoleucine.

In some embodiments, antagonistic TNFR2 polypeptides of the invention, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) may have a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257), or an amino acid sequence having up to two amino acid substitutions relative to this sequence; a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258), or an amino acid sequence having up to two amino acid substitutions relative to this sequence; a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260), or an amino acid sequence having up to two amino acid substitutions relative to this sequence; a CDR-L2 having the amino acid sequence TYS or YTS; and/or a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261), or an amino acid sequence having up to two amino acid substitutions relative to this sequence.

For example, in some embodiments, antagonistic TNFR2 polypeptides of the invention, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) may have a CDR-H1 having the amino acid sequence GYTFTDYL (SEQ ID NO: 274), or an amino acid sequence having up to two amino acid substitutions relative to this sequence; and a CDR-L3 having the amino acid sequence CLQYVNLIT (SEQ ID NO: 273), or an amino acid

sequence having up to two amino acid substitutions relative to this sequence. The present invention is based in part on the discovery that this particular combination of CDR-H1 and CDR-L3 regions promote the selective killing of activated T-reg cells and potentiate augmented T effector cell proliferation. As described herein, these phenotypes are beneficial for the treatment of cancers and infectious diseases, as the ability to deplete activated T-reg cell populations in a patient suffering from such pathologies can lessen the attenuation of cytotoxic CD8+ T cells, thereby enabling effector cells to mount an immune response against cancerous and infectious cells (see, e.g., Example 17).

*Humanized, primatized, and chimeric antibodies*

Antibodies of the invention include human, humanized, primatized, and chimeric antibodies that contain the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3, or a CDR-H3 that exhibits at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences that contain conservative mutations relative to these CDR-H3 sequences. Antibodies of the invention also include human, humanized, primatized, and chimeric antibodies that contain the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3, or a CDR-H3 that exhibits at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences that contain conservative mutations relative to these CDR-H3 sequences. For instance, antibodies of the invention also include human, humanized, primatized, and chimeric antibodies that contain a CDR-H3 that is identical to the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 except for conservative amino acid substitutions. In some embodiments, a humanized, primatized, or chimeric antibody may contain the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3, or a CDR that exhibits at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences that contain conservative mutations relative to these CDR-H3 sequences. For example, antagonistic TNFR2 antibodies of the invention can be generated by incorporating any of the above CDR-H3 sequences into the framework regions (e.g., FW1, FW2, FW3, and FW4) of a human antibody. Exemplary framework regions that can be used for the development of a humanized anti-TNFR2 antibody containing one or more of the above CDRs include, without limitation, those described in US Patent No. 7,732,578, US Patent No. 8,093,068, and WO 2003/105782; incorporated herein by reference.

One strategy that can be used to design humanized antibodies of the invention is to align the sequences of the heavy chain variable region and light chain variable region of an antagonistic TNFR2 antibody, such as TNFRAB1, TNFRAB2, or TNFR2A3, with the heavy chain variable region and light chain variable region of a consensus human antibody. Consensus human antibody heavy chain and light chain sequences are known in the art (see e.g., the "VBASE" human germline sequence database; see also Kabat, et al., Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242, 1991; Tomlinson et al., J. Mol. Biol. 227:776-98, 1992; and Cox et al, Eur. J. Immunol. 24:827-836, 1994; incorporated herein by reference). In this way, the variable domain framework residues and CDRs can be identified by sequence alignment (see Kabat, supra). One can substitute, for example, the CDR-H3 of the consensus human antibody with the

CDR-H3 of an antagonistic TNFR2 antibody, such as a CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3, in order to produce a humanized TNFR2 antagonist antibody. Exemplary variable domains of a consensus human antibody include the heavy chain variable domain:

5 EVQLVESGGGLVQPGGSLRLSCAAS**GFTFSDYAMS**WVRQAPGKGLEWVAVISENGSDTY**YADSVKGR**  
FTISRDDSKNTLYLQMNSLRAEDTAVYYCARD**DRGGAVSYFDVW**GQGTLVTVSS (SEQ ID NO: 32)

and the light chain variable domain:

10 DIQMTQSPSSLSASVGDRTITC**RASQDVSSYLAWY**QQKPGKAPKLLI**Y AASSLES**GVPSRFGSGSGT  
DFTLTISLQPEDFATYYC**QQYNSLPY**TFGGGTKVEIKRT (SEQ ID NO: 33)

identified in US Patent No. 6,054,297; incorporated herein by reference (CDRs are shown in bold were determined according to the method of Chothia, et al., J. Mol. Biol, 196:901-917, 1987). These amino acid  
15 substitutions can be made, for example, by recombinant expression of polynucleotides encoding the heavy and light chains of a humanized antibody in a host cell using methods known in the art or described herein.

Similarly, this strategy can also be used to produce primatized anti-TNFR2 antibodies, as one can substitute, for example, the CDR-H3 of a primate antibody consensus sequence with, for example, the  
20 CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3. Consensus primate antibody sequences known in the art (see e.g., U.S. Patent Nos. 5,658,570; 5,681,722; and 5,693,780; incorporated herein by reference).

In some embodiments, it may be desirable to import particular framework residues in addition to CDR sequences from a TNFR2 antibody, such as TNFRAB1, TNFRAB2, or TNFR2A3 into the heavy and/or light chain variable domains of a human antibody. For instance, US Patent No. 6,054,297 identifies  
25 several instances when it may be advantageous to retain certain framework residues from a particular antibody heavy chain or light chain variable region in the resulting humanized antibody. In some embodiments, framework residues may engage in non-covalent interactions with the antigen and thus contribute to the affinity of the antibody for the target antigen. In other cases, individual framework residues may modulate the conformation of a CDR, and thus indirectly influence the interaction of the  
30 antibody with the antigen. Alternatively, certain framework residues may form the interface between VH and VL domains, and may therefore contribute to the global antibody structure. In other cases, framework residues may constitute functional glycosylation sites (e.g., Asn-X-Ser/Thr) which may dictate antibody structure and antigen affinity upon attachment to carbohydrate moieties. In cases such as those  
35 described above, it may be beneficial to retain certain framework residues of a TNFR2 antagonist antibody (e.g., TNFRAB1, TNFRAB2, or TNFR2A3) in the antagonistic antibodies and antigen-binding fragments thereof of the invention, such as humanized antibodies, as various framework residues may promote high epitope affinity and improved biochemical activity of the antibody or antigen-binding fragment thereof.

Antibodies of the invention also include antibody fragments, Fab domains, F(ab') molecules,



F(ab')<sub>2</sub> molecules, single-chain variable fragments (scFvs), tandem scFv fragments, diabodies, triabodies, dual variable domain immunoglobulins, multi-specific antibodies, bispecific antibodies, and heterospecific antibodies that contain the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 (e.g., QRVDGYSSYWYFDV (SEQ ID NO: 25), ARDDGSYSPFDYWG (SEQ ID NO: 259), or ARDDGSYSPFDYFG (SEQ ID NO: 284))  
5 or a CDR-H3 that exhibits at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences. Antibodies and antigen-binding fragments thereof of the invention include those that also contain CDR-H3 sequences having between one and three amino acid substitutions (e.g., conservative or nonconservative substitutions) relative to the CDR-H3 sequences of TNFRAB1, TNFRAB2, or TNFR2A3. These molecules can be expressed recombinantly, e.g., by  
10 incorporating polynucleotides encoding these proteins into expression vectors for transfection in a eukaryotic or prokaryotic cell using techniques described herein or known in the art, or synthesized chemically, e.g., by solid phase peptide synthesis methods described herein or known in the art.

Polypeptides of the invention additionally include antibody-like scaffolds that contain, for example, the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3, or a CDR-H3 sequence that exhibits at  
15 least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences that contain between one and three amino acid substitutions (e.g., conservative or nonconservative substitutions) relative to the CDR-H3 sequences of TNFRAB1, TNFRAB2, or TNFR2A3. Examples of antibody-like scaffolds include proteins that contain a tenth fibronectin type III domain (<sup>10</sup>F<sub>n</sub>3), which contains BC, DE, and FG structural loops analogous to  
20 canonical antibodies. It has been shown that the tertiary structure of the <sup>10</sup>F<sub>n</sub>3 domain resembles that of the variable region of the IgG heavy chain, and one of skill in the art can graft, e.g., the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3, or sequences having at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences containing conserved amino acid substitutions relative to these CDR-H3 sequences onto the fibronectin  
25 scaffold by replacing residues of the BC, DE, and FG loops of <sup>10</sup>F<sub>n</sub>3 with residues of the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3. This can be achieved by recombinant expression of a modified <sup>10</sup>F<sub>n</sub>3 domain in a prokaryotic or eukaryotic cell (e.g., using the vectors and techniques described herein). Examples of using the <sup>10</sup>F<sub>n</sub>3 domain as an antibody-like scaffold for the grafting of CDRs from antibodies onto the BC, DE, and FG structural loops are reported in WO 2000/034784, WO 2009/142773, WO  
30 2012/088006, and U.S. Patent No. 8,278,419; incorporated herein by reference.

### **Antagonistic TNFR2 single-chain polypeptides**

TNFR2 antagonists of the invention may be in the form of a single-chain polypeptide, such as a single-chain polypeptide that contains a CDR-H3 region described herein (e.g., the CDR-H3 region of  
35 TNFRAB1, TNFRAB2, or TNFR2A3), optionally in combination with a CDR derived from a phenotype-neutral TNFR2 antibody (i.e., an antibody that is neither antagonistic nor agonistic of TNFR2 activation). Single-chain polypeptides may be in the form of an antibody fragment, e.g., an antibody fragment described herein or known in the art, such as a scFv fragment. Single chain polypeptides may alternatively contain one or more CDRs described herein covalently bound to one another using

conventional bond-forming techniques known in the art, for instance, by an amide bond, a thioether bond, a carbon-carbon bond, or by a linker, such as a peptide linker or a multi-valent electrophile (e.g., a bis(bromomethyl) arene derivative, such as a bis(bromomethyl)benzene or bis(bromomethyl)pyridine) described herein or known in the art.

5 For instance, antagonistic TNFR2 single-chain polypeptides of the invention may have a CDR-H3 region that contains one of the above-described consensus sequences that promote selective binding to TNFR2 epitopes, such as the KCRPG motif (SEQ ID NO: 19), and induce TNFR2 antagonism. For instance, antagonistic TNFR2 single-chain polypeptides of the invention may have a CDR-H3 having the amino acid sequence  $JZ^1JZ^2Z^4JZ^3JZ^5(J)_2Z^5Z^2Z^5$  or  $JZ^1JZ^2Z^4Z^3Z^5(J)_2Z^5Z^2Z^5(J)_2$ , wherein each J is  
10 independently a naturally occurring amino acid; each  $Z^1$  is independently a naturally occurring amino acid containing a cationic side-chain at physiological pH; each  $Z^2$  is independently a naturally occurring amino acid containing an anionic side-chain at physiological pH; each  $Z^3$  is independently a naturally occurring amino acid containing a polar, uncharged side-chain at physiological pH; each  $Z^4$  is independently a glycine or alanine; and each  $Z^5$  is independently a naturally occurring amino acid containing a  
15 hydrophobic side-chain.

In some embodiments, antagonistic TNFR2 single-chain polypeptides of the invention may have a CDR-H3 having the amino acid sequence JRJDGJSJY(J)<sub>2</sub>FDJ (SEQ ID NO: 278) or JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279), wherein each J is independently a naturally occurring amino acid.

Antagonistic TNFR2 single-chain polypeptides of the invention may have a CDR-H3 having the  
20 amino acid sequence  $QZ^1VZ^2Z^4YZ^3SZ^5WYZ^5Z^2Z^5$  (SEQ ID NO: 265) or  $AZ^1DZ^2Z^4Z^3Z^5SPZ^5Z^2Z^5WG$  (SEQ ID NO: 266), wherein each  $Z^1$  is independently an amino acid containing a cationic side-chain at physiological pH; each  $Z^2$  is independently an amino acid containing an anionic side-chain at physiological pH; each  $Z^3$  is independently an amino acid containing a polar, uncharged side-chain at physiological pH; each  $Z^4$  is independently a glycine or alanine; each  $Z^5$  is independently an amino acid  
25 containing a hydrophobic side-chain; and each X is independently leucine or isoleucine.

In some embodiments, antagonistic TNFR2 single-chain polypeptides of the invention may have a CDR-H3 having the amino acid sequence QRVDGYSSYWFYFDV (SEQ ID NO: 25), ARDDGSYSPFDYWG (SEQ ID NO: 259), or an amino acid sequence having up to two amino acid  
30 substitutions relative to these sequences (e.g., one or two amino acid substitutions, such as conservative amino acid substitutions)

Single-chain polypeptides can be produced by a variety of recombinant and synthetic techniques, such as by recombinant gene expression or solid-phase peptide synthesis procedures described herein or known in the art. For instance, one of skill in the art can design polynucleotides encoding, e.g., two or more CDRs operably linked to one another in frame so as to produce a continuous, single-chain peptide  
35 containing these CDRs. Optionally, the CDRs may be separated by a spacer, such as by a framework region (e.g., a framework sequence described herein or a framework region of a germline consensus sequence of a human antibody) or a flexible linker, such as a poly-glycine or glycine/serine linker described herein or known in the art. When produced by chemical synthesis methods, native chemical ligation can optionally be used as a strategy for the synthesis of long peptides (e.g., greater than 50

amino acids). Native chemical ligation protocols are known in the art and have been described, e.g., by Dawson et al. (Science, 266:776-779, 1994); incorporated herein by reference. A detailed description of techniques for the production of single-chain polypeptides, full-length antibodies, and antibody fragments is provided in the sections that follow.

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### **Nucleic acids and expression systems**

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention can be prepared by any of a variety of established techniques. For instance, an antagonistic TNFR2 antibody or antigen-binding fragment thereof of the invention can be prepared by recombinant expression of immunoglobulin light and heavy chain genes in a host cell. To express an antibody recombinantly, a host cell can be transfected with one or more recombinant expression vectors carrying DNA fragments encoding the immunoglobulin light and heavy chains of the antibody such that the light and heavy chains are expressed in the host cell and, optionally, secreted into the medium in which the host cells are cultured, from which medium the antibodies can be recovered. Standard recombinant DNA methodologies are used to obtain antibody heavy and light chain genes, incorporate these genes into recombinant expression vectors and introduce the vectors into host cells, such as those described in Molecular Cloning; A Laboratory Manual, Second Edition (Sambrook, Fritsch and Maniatis (eds), Cold Spring Harbor, N. Y., 1989), Current Protocols in Molecular Biology (Ausubel et al., eds., Greene Publishing Associates, 1989), and in U.S. Patent No. 4,816,397; incorporated herein by reference.

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#### *Vectors for expression of antagonistic TNFR2 polypeptides*

Viral genomes provide a rich source of vectors that can be used for the efficient delivery of exogenous genes into the genome of a cell (e.g., a eukaryotic or prokaryotic cell). Viral genomes are particularly useful vectors for gene delivery because the polynucleotides contained within such genomes are typically incorporated into the genome of a target cell by generalized or specialized transduction. These processes occur as part of the natural viral replication cycle, and do not require added proteins or reagents in order to induce gene integration. Examples of viral vectors include a retrovirus, adenovirus (e.g., Ad5, Ad26, Ad34, Ad35, and Ad48), parvovirus (e.g., adeno-associated viruses), coronavirus, negative strand RNA viruses such as orthomyxovirus (e.g., influenza virus), rhabdovirus (e.g., rabies and vesicular stomatitis virus), paramyxovirus (e.g. measles and Sendai), positive strand RNA viruses, such as picornavirus and alphavirus, and double stranded DNA viruses including adenovirus, herpesvirus (e.g., Herpes Simplex virus types 1 and 2, Epstein-Barr virus, cytomegalovirus), and poxvirus (e.g., vaccinia, modified vaccinia Ankara (MVA), fowlpox and canarypox). Other viruses useful for delivering polynucleotides encoding antibody light and heavy chains or antibody fragments of the invention include Norwalk virus, togavirus, flavivirus, reoviruses, papovavirus, hepadnavirus, and hepatitis virus, for example. Examples of retroviruses include: avian leukosis-sarcoma, mammalian C-type, B-type viruses, D-type viruses, HTLV-BLV group, lentivirus, spumavirus (Coffin, J. M., Retroviridae: The viruses and their replication, *In Fundamental Virology*, Third Edition, B. N. Fields, et al., Eds., Lippincott-Raven Publishers,

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Philadelphia, 1996). Other examples include murine leukemia viruses, murine sarcoma viruses, mouse mammary tumor virus, bovine leukemia virus, feline leukemia virus, feline sarcoma virus, avian leukemia virus, human T cell leukemia virus, baboon endogenous virus, Gibbon ape leukemia virus, Mason Pfizer monkey virus, simian immunodeficiency virus, simian sarcoma virus, Rous sarcoma virus and  
5 lentiviruses. Other examples of vectors are described, for example, in McVey et al., (U.S. Patent. No. 5,801,030); incorporated herein by reference.

#### *Genome editing techniques*

In addition to viral vectors, a variety of additional methods have been developed for the  
10 incorporation of genes, e.g., those encoding antibody light and heavy chains, single-chain polypeptides, single-chain variable fragments (scFvs), tandem scFvs, Fab domains, F(ab')<sub>2</sub> domains, diabodies, and triabodies, among others, into the genomes of target cells for polypeptide expression. One such method that can be used for incorporating polynucleotides encoding anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) into prokaryotic or eukaryotic cells  
15 includes transposons. Transposons are polynucleotides that encode transposase enzymes and contain a polynucleotide sequence or gene of interest flanked by excision sites at the 5' and 3' positions. Once a transposon has been delivered into a cell, expression of the transposase gene commences and results in active enzymes that cleave the gene of interest from the transposon. This activity is mediated by the site-specific recognition of transposon excision sites by the transposase. In some embodiments, these  
20 excision sites may be terminal repeats or inverted terminal repeats. Once excised from the transposon, the gene of interest can be integrated into the genome of a prokaryotic or eukaryotic cell by transposase-catalyzed cleavage of similar excision sites that exist within nuclear genome of the cell. This allows the gene encoding an anti-TNFR2 antibody or fragment or domain thereof to be inserted into the cleaved  
25 nuclear DNA at the excision sites, and subsequent ligation of the phosphodiester bonds that join the gene of interest to the DNA of the prokaryotic or eukaryotic cell genome completes the incorporation process. In some embodiments, the transposon may be a retrotransposon, such that the gene encoding the antibody is first transcribed to an RNA product and then reverse-transcribed to DNA before incorporation in the prokaryotic or eukaryotic cell genome. Exemplary transposon systems include the piggybac transposon (described in detail in WO 2010/085699) and the sleeping beauty transposon (described in  
30 detail in US20050112764); incorporated herein by reference.

Another useful method for the integration of nucleic acid molecules encoding anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) into the genome of a prokaryotic or eukaryotic cell is the clustered regularly interspaced short palindromic repeats (CRISPR)/Cas system, which is a system that originally evolved as an adaptive defense mechanism in  
35 bacteria and archaea against infection by viruses. The CRISPR/Cas system consists of palindromic repeat sequences within plasmid DNA and an associated Cas9 nuclease. This ensemble of DNA and protein directs site specific DNA cleavage of a target sequence by first incorporating foreign DNA into CRISPR loci. Polynucleotides containing these foreign sequences and the repeat-spacer elements of the CRISPR locus are in turn transcribed in a host cell to create a guide RNA, which can subsequently

anneal to a target sequence and localize the Cas9 nuclease to this site. In this manner, highly site-specific cas9-mediated DNA cleavage can be engendered in a foreign polynucleotide because the interaction that brings cas9 within close proximity of the target DNA molecule is governed by RNA:DNA hybridization. As a result, one can theoretically design a CRISPR/Cas system to cleave any target DNA molecule of interest. This technique has been exploited in order to edit eukaryotic genomes (Hwang et al., Nat. Biotech., 31:227-229, 2013) and can be used as an efficient means of site-specifically editing eukaryotic or prokaryotic genomes in order to cleave DNA prior to the incorporation of a polynucleotide encoding an anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention. The use of CRISPR/Cas to modulate gene expression has been described in US Patent No. 8,697,359, which is incorporated herein by reference.

Alternative methods for site-specifically cleaving genomic DNA prior to the incorporation of a polynucleotide encoding a TNFR2 antibody or antibody fragment of the invention include the use of zinc finger nucleases and transcription activator-like effector nucleases (TALENs). Unlike the CRISPR/Cas system, these enzymes do not contain a guiding polynucleotide to localize to a specific target sequence. Target specificity is instead controlled by DNA binding domains within these enzymes. Zinc finger nucleases and TALENs for use in genome editing applications are described in Urnov et al. (Nat. Rev. Genet., 11:636-646, 2010); and in Joung et al., (Nat. Rev. Mol. Cell. Bio. 14:49-55, 2013); incorporated herein by reference. Additional genome editing techniques that can be used to incorporate polynucleotides encoding antibodies of the invention into the genome of a prokaryotic or eukaryotic cell include the use of ARCUS™ meganucleases that can be rationally designed so as to site-specifically cleave genomic DNA. The use of these enzymes for the incorporation of polynucleotides encoding antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention into the genome of a prokaryotic or eukaryotic cell is particularly advantageous in view of the structure-activity relationships that have been established for such enzymes. Single-chain meganucleases can thus be modified at certain amino acid positions in order to create nucleases that selectively cleave DNA at desired locations. These single-chain nucleases have been described extensively, e.g., in U.S. Patent Nos. 8,021,867 and 8,445,251; incorporated herein by reference.

### 30 *Polynucleotide sequence elements*

To express antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention, polynucleotides encoding partial or full-length light and heavy chains, e.g., polynucleotides that encode a CDR-H3 region as described herein, can be inserted into expression vectors such that the genes are operatively linked to transcriptional and translational control sequences. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. Polynucleotides encoding the light chain gene and the heavy chain of a TNFR2 antibody can be inserted into separate vectors, or, optionally, both polynucleotides can be incorporated into the same expression vector using established techniques described herein or known in the art.

In addition to polynucleotides encoding the heavy and light chains of an antibody (or a polynucleotide encoding a single-chain polypeptide or an antibody fragment, such as a scFv molecule), the recombinant expression vectors of the invention may carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The design of the expression vector, including the selection of regulatory sequences, may depend on such factors as the choice of the host cell to be transformed or the level of expression of protein desired. For instance, suitable regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (e.g., the adenovirus major late promoter (AdMLP)) and polyoma. For further description of viral regulatory elements, and sequences thereof, see e.g., U.S. Patent No. 5, 168,062, U.S. Patent No. 4,510,245, and U.S. Patent No. 4,968,615.

In addition to the antibody chain genes and regulatory sequences, the recombinant expression vectors of the invention can carry additional sequences, such as sequences that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker genes. A selectable marker gene facilitates selection of host cells into which the vector has been introduced (see e.g., U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017). For example, typically the selectable marker gene confers resistance to cytotoxic drugs, such as G418, puromycin, blasticidin, hygromycin or methotrexate, to a host cell into which the vector has been introduced. Suitable selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in DHFR<sup>r</sup> host cells with methotrexate selection/amplification) and the neo gene (for G418 selection). In order to express the light and heavy chains of a TNFR2 antibody or a TNFR2 antibody fragment, the expression vector(s) containing polynucleotides encoding the heavy and light chains can be transfected into a host cell by standard techniques.

#### *Polynucleotides encoding modified antagonistic TNFR2 polypeptides*

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention may contain the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3, but feature differences in the sequence of one or more of the remaining CDRs relative to the corresponding sequence in TNFRAB1, TNFRAB2, or TNFR2A3. Similarly, polypeptides of the invention may contain the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 but may feature differences in one or more framework regions. For instance, one or more framework regions of TNFRAB1, TNFRAB2, or TNFR2A3 may be substituted with the framework region of a human antibody. Exemplary framework regions include, for example, human framework regions described in US 7,829,086, and primate framework regions as described in EP 1945668; incorporated herein by reference. To generate nucleic acids encoding such TNFR2 antibodies, DNA fragments encoding, e.g., at least one, or both, of the light chain variable regions and the heavy chain variable regions can be produced by chemical synthesis (e.g., by solid phase polynucleotide synthesis techniques), *in vitro* gene amplification (e.g., by polymerase chain reaction techniques), or by replication of the polynucleotide in a host organism. For instance,

nucleic acids encoding anti-TNFR2 antibodies of the invention may be obtained by amplification and modification of germline DNA or cDNA encoding light and heavy chain variable sequences so as to incorporate the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 into the framework residues of a consensus antibody. In some embodiments, a humanized antagonistic TNFR2 antibody may include the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3, or a variant thereof that has at least 85% sequence identity (e.g., 90%, 95%, 97%, 99%, or 100% sequence identity) to any of these CDR-H3 sequences or sequences that contain between one and three amino acid substitutions (e.g., conservative or nonconservative substitutions) relative to the CDR-H3 sequences of TNFRAB1, TNFRAB2, or TNFR2A3. This can be achieved, for example, by performing site-directed mutagenesis of germline DNA or cDNA and amplifying the resulting polynucleotides using the polymerase chain reaction (PCR) according to established procedures. Germline DNA sequences for human heavy and light chain variable region genes are known in the art (see, e.g., the "VBASE" human germline sequence database; see also Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242, 1991; Tomlinson et al., J. Mol. Biol. 227:776-798, 1992; and Cox et al., Eur. J. Immunol. 24:827-836, 1994; incorporated herein by reference). Chimeric nucleic acid constructs encoding human heavy and light chain variable regions containing the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 can be produced, e.g., using established cloning techniques known in the art. Additionally, a polynucleotide encoding a heavy chain variable region containing the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 can be synthesized and used as a template for mutagenesis to generate a variant as described herein using routine mutagenesis techniques. Alternatively, a DNA fragment encoding the variant can be directly synthesized (e.g., by established solid phase nucleic acid chemical synthesis procedures).

Once DNA fragments encoding VH segments containing the CDR-H3 of TNFRAB1, TNFRAB2, or TNFR2A3 are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, e.g., to convert the variable region genes to full-length antibody chain genes, to Fab fragment genes or to a scFv gene. In these manipulations, a VL- or VH-encoding DNA fragment is operatively linked to another DNA fragment encoding another protein, such as an antibody constant region or a flexible linker.

The isolated DNA encoding the VH region of an anti-TNFR2 antibody of the invention can be converted to a full-length heavy chain gene (as well as a Fab heavy chain gene), e.g., by operatively linking the VH-encoding DNA to another DNA molecule encoding heavy chain constant region domains (CH1, CH2, CH3, and, optionally, CH4). The sequences of human heavy chain constant region genes are known in the art (see e.g., Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242, 1991) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgG1, IgG2, IgG3, IgG4, IgA, IgE, IgM or IgD constant region, and in certain embodiments is an IgG1 constant region. For a Fab fragment heavy chain gene, the VH-encoding DNA can be operatively linked to another DNA molecule encoding only the heavy chain CH1 domain.

Isolated DNA encoding the VL region of an anti-TNFR2 antibody can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operatively linking the VL-encoding DNA to another DNA molecule encoding the light chain constant region, CL. The sequences of human light chain constant region genes are known in the art (see e.g., Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition (U.S. Department of Health and Human Services, NIH Publication No. 91 -3242, 1991)) and DNA fragments encompassing these regions can be obtained, e.g., by amplification in a prokaryotic or eukaryotic cell of a polynucleotide encoding these regions, by PCR amplification, or by chemical polynucleotide synthesis. The light chain constant region can be a kappa ( $\kappa$ ) or lambda ( $\lambda$ ) constant region, but in certain embodiments is a kappa constant region. To create a scFv gene, the VH and VL-encoding DNA fragments are operatively linked to another fragment encoding a flexible linker, e.g., a polynucleotide encoding a flexible, hydrophilic amino acid sequence, such as the amino acid sequence (Gly<sub>4</sub>Ser)<sub>3</sub>, such that the V<sub>H</sub> and V<sub>L</sub> sequences can be expressed as a contiguous single-chain protein, with the V<sub>L</sub> and V<sub>H</sub> regions joined by the linker (see e.g., Bird et al., Science 242:423-426, 1988; Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883, 1988; McCafferty et al., Nature 348:552-554, 1990).

Recombinant DNA technology can also be used to remove some or all of the DNA encoding either or both of the light and heavy chains that is not necessary for binding to TNFR2. The molecules expressed from such truncated DNA molecules are also encompassed by the antibodies of the invention. In addition, bifunctional antibodies can be produced in which one heavy contains a CDR-H3 sequence derived from TNFRAB1, TNFRAB2, or TNFR2A3, and the other heavy chain and/or the light chains are specific for an antigen other than TNFR2. Such antibodies can be generated, e.g., by crosslinking a heavy chain containing the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3 and a light chain of an anti-TNFR2 antibody, such as an anti-TNFR2 antibody that is neither agonistic nor antagonistic, to a heavy chain and light chain of a second antibody by standard chemical crosslinking methods (e.g., by disulfide bond formation). Bifunctional antibodies can also be made by expressing a nucleic acid molecule engineered to encode a bifunctional antibody in a prokaryotic or eukaryotic cell.

Dual specific antibodies, i.e., antibodies that bind TNFR2 and a different antigen using the same binding site, can be produced by mutating amino acid residues in the light chain and/or heavy chain CDRs. In some embodiments, dual specific antibodies that bind two antigens, such as TNFR2 and a second cell-surface receptor, can be produced by mutating amino acid residues in the periphery of the antigen binding site (Bostrom et al., Science 323: 1610-1614, 2009). Dual functional antibodies can be made by expressing a polynucleotide engineered to encode a dual specific antibody.

Modified antagonistic TNFR2 antibodies and antibody fragments of the invention can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984 The Pierce Chemical Co., Rockford, 111; incorporated herein by reference). Variant antibodies can also be generated using a cell-free synthetic platform (see, e.g., Chu et al., Biochemia No. 2, 2001 (Roche Molecular Biologicals); incorporated herein by reference).



*Host cells for expression of antagonistic TNFR2 polypeptides*

It is possible to express the polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) of the invention in either prokaryotic or eukaryotic host cells. In certain embodiments, expression of polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) is performed in eukaryotic cells, e.g., mammalian host cells, for optimal secretion of a properly folded and immunologically active antibody. Exemplary mammalian host cells for expressing the recombinant antibodies or antigen-binding fragments thereof of the invention include Chinese Hamster Ovary (CHO cells) (including DHFR CHO cells, described in Urlaub and Chasin (1980, Proc. Natl. Acad. Sci. USA 77:4216-4220), used with a DHFR selectable marker, e.g., as described in Kaufman and Sharp (1982, Mol. Biol. 159:601-621), NSO myeloma cells, COS cells, 293 cells, and SP2/0 cells. Additional cell types that may be useful for the expression of antibodies and fragments thereof include bacterial cells, such as BL-21(DE3) *E. coli* cells, which can be transformed with vectors containing foreign DNA according to established protocols. Additional eukaryotic cells that may be useful for expression of antibodies include yeast cells, such as auxotrophic strains of *S. cerevisiae*, which can be transformed and selectively grown in incomplete media according to established procedures known in the art. When recombinant expression vectors encoding antibody genes are introduced into mammalian host cells, the antibodies are produced by culturing the host cells for a period of time sufficient to allow for expression of the antibody in the host cells or secretion of the antibody into the culture medium in which the host cells are grown.

Polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) can be recovered from the culture medium using standard protein purification methods. Host cells can also be used to produce portions of intact antibodies, such as Fab fragments or scFv molecules. The invention also includes methods in which the above procedure is varied according to established protocols known in the art. For example, it can be desirable to transfect a host cell with DNA encoding either the light chain or the heavy chain (but not both) of an anti-TNFR2 antibody of the invention in order to produce an antigen-binding fragment of the antibody.

Once an anti-TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or antigen-binding fragment) thereof of the invention has been produced by recombinant expression, it can be purified by any method known in the art, such as a method useful for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for TNFR2 after Protein A or Protein G selection, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Further, the anti-TNFR2 polypeptides of the invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification or to produce therapeutic conjugates (see "Antagonistic TNFR2 polypeptide conjugates," below).

Once isolated, an anti-TNFR2 single-chain polypeptide, antibody, or antigen-binding fragments thereof can, if desired, be further purified, e.g., by high performance liquid chromatography (see, e.g., Fisher, Laboratory Techniques in Biochemistry and Molecular Biology (Work and Burdon, eds., Elsevier,

1980); incorporated herein by reference), or by gel filtration chromatography, such as on a Superdex™ 75 column (Pharmacia Biotech AB, Uppsala, Sweden).

### **Platforms for generating and affinity-maturing antagonistic anti-TNFR2 polypeptides**

#### *5 Mapping epitopes of TNFR2 that promote receptor antagonism*

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be produced by screening libraries of polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) for functional molecules that are capable of binding epitopes within TNFR2 that selectively promote receptor antagonism rather than receptor activation. Such epitopes can be modeled by screening antibodies or antigen-binding fragments thereof against a series of linear or cyclic peptides containing residues that correspond to a desired epitope within TNFR2.

As an example, peptides containing individual fragments isolated from TNFR2 that promote receptor antagonism can be synthesized by peptide synthesis techniques described herein or known in the art. These peptides can be immobilized on a solid surface and screened for molecules that bind antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof), such as TNFRAB1, TNFRAB2, or TNFR2A3, e.g., using an ELISA-based screening platform using established procedures. Using this assay, peptides that specifically bind TNFRAB1, TNFRAB2, or TNFR2A3 with high affinity therefore contain residues within epitopes of TNFR2 that preferentially bind these antibodies. Peptides identified in this manner (e.g., peptides having the sequence of any one of SEQ ID NOs: 11, 19, 20, 34-117, 285, and 286, or a peptide containing between about 10 and about 30 continuous or discontinuous amino acids between positions 80 and 130 of SEQ ID NO: 7) can be used to screen libraries of antibodies and antigen-binding fragments thereof in order to identify anti-TNFR2 antibodies of the invention. Moreover, since these peptides act as surrogates for epitopes within TNFR2 that promote receptor antagonism, antibodies generated using this screening technique may bind the corresponding epitopes in TNFR2 and are expected to be antagonistic of receptor activity.

#### *30 Screening of libraries for antagonistic TNFR2 polypeptides*

Methods for high throughput screening of polypeptide (e.g., single-chain polypeptide, antibody, or antibody fragment) libraries for molecules capable of binding epitopes within TNFR2 (e.g., peptides having the sequence of SEQ ID NO: 285 or 286) include, without limitation, display techniques including phage display, bacterial display, yeast display, mammalian display, ribosome display, mRNA display, and cDNA display. The use of phage display to isolate ligands that bind biologically relevant molecules has been reviewed, e.g., in Felici et al. (Biotechnol. Annual Rev. 1:149-183, 1995), Katz (Annual Rev. Biophys. Biomol. Struct. 26:27-45, 1997), and Hoogenboom et al. (Immunotechnology 4:1-20, 1998). Several randomized combinatorial peptide libraries have been constructed to select for polypeptides that bind different targets, e.g., cell surface receptors or DNA (reviewed by Kay (Perspect. Drug Discovery Des. 2, 251-268, 1995), Kay et al., (Mol. Divers. 1:139-140, 1996)). Proteins and multimeric proteins have

been successfully phage-displayed as functional molecules (see EP 0349578A, EP 4527839A, EP 0589877A; Chiswell and McCafferty (Trends Biotechnol. 10, 80-84 1992)). In addition, functional antibody fragments (e.g. Fab, single-chain Fv [scFv]) have been expressed (McCafferty et al. (Nature 348: 552-554, 1990), Barbas et al. (Proc. Natl. Acad. Sci. USA 88:7978-7982, 1991), Clackson et al. (Nature 5 352:624-628, 1991)). These references are hereby incorporated by reference in their entirety.

(i) *Phage display techniques*

As an example, phage display techniques can be used in order to screen libraries of polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) for functional 10 molecules capable of binding cyclic or polycyclic peptides containing epitopes within TNFR2 that promote receptor antagonism (e.g., peptides having the sequence of SEQ ID NO: 285 or 286). For instance, libraries of polynucleotides encoding single-chain antibody fragments, such as scFv fragments, that contain randomized hypervariable regions can be obtained using established procedures (e.g., solid phase polynucleotide synthesis or error-prone PCR techniques, see McCullum et al. (Meth. Mol. Biol., 15 634:103-109, 2010); incorporated herein by reference). These randomized polynucleotides can subsequently be incorporated into a viral genome such that the randomized antibody chains encoded by these genes are expressed on the surface of filamentous phage, e.g., by a covalent bond between the antibody chain and a coat protein (e.g., pIII coat protein on the surface of M13 phage). This provides a physical connection between the genotype and phenotype of the antibody chain. In this way, libraries of 20 phage that display diverse antibody chains containing random mutations in hypervariable regions can be screened for the ability of the exterior antibody chains to bind TNFR2 epitopes (e.g., peptides having the sequence of SEQ ID NO: 285 or 286) that are immobilized to a surface using established procedures. For instance, such peptides can be physically bound to the surface of a microtiter plate by forming a covalent bond between the peptide and an epitope tag (e.g., biotin) and incubating the peptide in wells of a 25 microtiter plate that have been previously coated with a complementary tag (e.g., avidin) that binds the tag attached to the peptide with high affinity. Suitable epitope tags include, without limitation, maltose-binding protein, glutathione-S-transferase, a poly-histidine tag, a FLAG-tag, a myc-tag, human influenza hemagglutinin (HA) tag, biotin, streptavidin. Peptides containing the epitopes presented by these molecules are capable of being immobilized on surfaces containing such complementary molecules as 30 maltose, glutathione, a nickel-containing complex, an anti-FLAG antibody, an anti-myc antibody, an anti-HA antibody, streptavidin, or biotin, respectively. In this way, phage can be incubated with a surface containing an immobilized TNFR2-derived peptide for a time suitable to allow binding of the antibody to the constrained peptide and in the presence of an appropriate buffer system (e.g., one that contains physiological salt concentration, ionic strength, and is maintained at physiological pH by a buffering agent). The surface can then be washed (e.g., with phosphate buffer containing 0.1% Tween-20) so as to 35 remove phage that do not present antibody chains that interact with the TNFR2-derived peptides with an affinity greater than a particular threshold value.

The affinity of the polypeptides that remain after this initial panning (i.e., screening) step can be modulated by adjusting the conditions of the washing step (e.g., by including mildly acidic or basic

components, or by including other TNFR2-derived peptides at a low concentration in order to compete with immobilized peptides for antigen-binding sites). In this way, the population of phage that remains bound to the surfaces of the microtiter plate following the washing step is enriched for phage that bind TNFR2-derived peptide epitopes that promote receptor antagonism. The remaining phage can then be amplified by eluting the phage from the surface containing these peptides (e.g., by altering the ambient pH, ionic strength, or temperature) so as to diminish protein-protein interaction strength. The isolated phage can then be amplified, e.g., by infecting bacterial cells, and the resulting phage can optionally be subjected to panning by additional iterations of screening so as to further enrich the population of phage for those harboring higher-affinity anti-TNFR2 polypeptides. Following these panning stages, phage that display high-affinity antibodies or antigen-binding fragments thereof can subsequently be isolated and the genomes of these phage can be sequenced in order to identify the polynucleotide and polypeptide sequences of the encoded antibodies. Phage display techniques such as this can be used to generate, e.g., antibody chains, such as scFv fragments, tandem scFv fragments, and other antigen-binding fragments of the invention that can be used as antagonists of TNFR2. Exemplary phage display protocols for the identification of antibody chains and antigen-binding fragments thereof that bind a particular antigen with high affinity are well-established and are described, e.g., in US Patent No. 7,846,892, WO 1997/002342, US Patent No. 8,846,867, and WO 2007/132917; incorporated herein by reference. Similar phage display techniques can be used to generate antibody-like scaffolds (e.g., <sup>10</sup>Fn3 domains) of the invention that bind epitopes within TNFR2 that promote receptor antagonism (e.g., epitopes presented by peptides with the sequence of SEQ ID NO: 285 or 286). Exemplary phage display protocols for the identification of antibody-like scaffold proteins are described, e.g., in WO 2009/086116; incorporated herein by reference).

(ii) *Cell-based display techniques*

Other *in vitro* display techniques that exploit the linkage between genotype and phenotype of a solvent-exposed polypeptide include yeast and bacterial display. Yeast display techniques are established in the art and are often advantageous in that high quantities of antibodies (often up to 30,000) can be presented on the surface of an individual yeast cell (see, e.g., Boder et al. (Nat Biotechnol. 15:553, 1997); incorporated herein by reference). The larger size of yeast cells over filamentous phage enables an additional screening strategy, as one can use flow cytometry to both analyze and sort libraries of yeast. For instance, established procedures can be used to generate libraries of bacterial cells or yeast cells that express polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) containing randomized hypervariable regions (see, e.g., see US Patent No. 7,749,501 and US 2013/0085072; the teachings of each which are incorporated herein by reference). For instance, large libraries of yeast cells that express polynucleotides encoding naïve scFv fragments can be made using established procedures (de Bruin et al., Nat Biotechnol 17:397, 1999; incorporated herein by reference). Yeast cells expressing these polynucleotides can then be incubated with two different fluorescent molecules during the panning steps: one dye that binds conserved residues within the antibody and thus reflects the amount of antibody displayed, and another dye that fluoresces at a different

wavelength and binds the antigen and thus indicates the amount of antigen bound. For instance, one of skill in the art can use a TNFR2-derived peptide containing the sequence of SEQ ID NO: 285 or 286 that has been conjugated to an epitope tag (e.g., biotin), optionally at the N- or C-terminus of the peptide or at a residue that is not expected to interfere with antibody-antigen binding. This enables a fluorescent dye labeled with a complementary tag (e.g., avidin) to localize to the antibody-antigen complex. This results in great flexibility and immediate feedback on the progress of a selection. In contrast to phage display, by normalizing to antibody display levels, antibodies with higher affinities, rather than greater expression levels can easily be selected. In fact, it is possible to distinguish and sort antibodies whose affinities differ by only two-fold (VanAntwerp and Wittrup (*Biotechnol Prog* 16:31, 2000)).

(iii) *Nucleotide display techniques*

Display techniques that utilize *in vitro* translation of randomized polynucleotide libraries also provide a powerful approach to generating anti-TNFR2 antibodies of the invention. For instance, randomized DNA libraries encoding polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) that contain mutations within designated hypervariable regions can be obtained, e.g., using established PCR-based mutagenesis techniques as described herein. The polynucleotides of these libraries may contain transcription regulating sequences, such as promoters and transcription terminating sequences, and may additionally encode sequences that increase the rate of translation of the resulting mRNA construct (e.g., IRES sequences, 5' and 3' UTRs, a poly-adenylation tract, etc). These polynucleotide libraries can be incubated in an appropriately buffered solution containing RNA polymerase and RNA nucleoside triphosphates (NTPs) in order to enable transcription of the DNA sequences to competent mRNA molecules, which can subsequently be translated by large and small ribosomal subunits, aminoacyl tRNA molecules, and translation initiation and elongation factors present in solution (e.g., using the PURExpress® *In Vitro* Protein Synthesis Kit, New England Biolabs®). Designed mRNA modifications can enable the antibody product to remain covalently bound to the mRNA template by a chemical bond to puromycin (e.g., see Keefe (*Curr. Protoc. Mol. Biol.*, Chapter 24, Unit 24.5, 2001); incorporated herein by reference). This genotype-phenotype linkage can thus be used to select for antibodies that bind a TNFR2-derived peptide (e.g., a peptide that has the sequence SEQ ID NO: 285 or 286) by incubating mRNA:antibody fusion constructs with a peptide immobilized to a surface and panning in a fashion similar to phage display techniques (see, e.g., WO 2006/072773; incorporated herein by reference).

Optionally, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be generated using a similar technique, except the antibody product may be bound non-covalently to the ribosome-mRNA complex rather than covalently via a puromycin linker. This platform, known as ribosome display, has been described, e.g., in US Patent No. 7,074,557; incorporated herein by reference. Alternatively, antibodies can be generated using cDNA display, a technique analogous to mRNA display with the exception that cDNA, rather than mRNA, is covalently bound to an antibody product via a puromycin linker. cDNA display techniques offer the advantage of being able to perform panning steps under increasingly stringent conditions, e.g., under

conditions in which the salt concentration, ionic strength, pH, and/or temperature of the environment is adjusted in order to screen for antibodies with particularly high affinity for TNFR2-derived peptides. This is due to the higher natural stability of double-stranded cDNA over single-stranded mRNA. cDNA display screening techniques are described, e.g., in Ueno et al. (Methods Mol. Biol., 805:113-135, 2012);

5 incorporated herein by reference.

In addition to generating anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention, *in vitro* display techniques (e.g., those described herein and those known in the art) also provide methods for improving the affinity of an anti-TNFR2 polypeptide of the invention. For instance, rather than screening libraries of antibodies and fragments thereof containing completely randomized hypervariable regions, one can screen narrower libraries of antibodies and antigen-binding fragments thereof that feature targeted mutations at specific sites within hypervariable regions. This can be accomplished, e.g., by assembling libraries of polynucleotides encoding antibodies or antigen-binding fragments thereof that encode random mutations only at particular sites within hypervariable regions. These polynucleotides can then be expressed in, e.g., filamentous phage, bacterial cells, yeast cells, mammalian cells, or *in vitro* using, e.g., ribosome display, mRNA display, or cDNA display techniques in order to screen for antibodies or antigen-binding fragments thereof that specifically bind TNFR2 epitopes (e.g., peptides containing the sequence of SEQ ID NO: 285 or 286) with improved binding affinity. Yeast display, for instance, is well-suited for affinity maturation, and has been used previously to improve the affinity of a single-chain antibody to a  $K_D$  of 48 fM (Boder et al. (Proc Natl Acad Sci USA 97:10701, 2000)).

Additional *in vitro* techniques that can be used for the generation and affinity maturation of antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention include the screening of combinatorial libraries of antibodies or antigen-binding fragments thereof for functional molecules capable of specifically binding TNFR2-derived peptides (e.g., a peptide having the amino acid sequence of SEQ ID NO: 285 or 286). Combinatorial antibody libraries can be obtained, e.g., by expression of polynucleotides encoding randomized hypervariable regions of an antibody or antigen-binding fragment thereof in a eukaryotic or prokaryotic cell. This can be achieved, e.g., using gene expression techniques described herein or known in the art. Heterogeneous mixtures of antibodies can be purified, e.g., by Protein A or Protein G selection, sizing column chromatography), centrifugation, differential solubility, and/or by any other standard technique for the purification of proteins. Libraries of combinatorial libraries thus obtained can be screened, e.g., by incubating a heterogeneous mixture of these antibodies with a peptide derived from TNFR2 that has been immobilized to a surface (e.g., a peptide having the amino acid sequence of SEQ ID NO: 285 or 286 immobilized to the surface of a solid-phase resin or a well of a microtiter plate) for a period of time sufficient to allow antibody-antigen binding. Non-binding antibodies or fragments thereof can be removed by washing the surface with an appropriate buffer (e.g., a solution buffered at physiological pH (approximately 7.4) and containing physiological salt concentrations and ionic strength, and optionally containing a detergent, such as TWEEN-20). Antibodies that remain bound can subsequently be detected, e.g., using an ELISA-based detection protocol (see, e.g., US Patent No. 4,661,445;

incorporated herein by reference).

Additional techniques for screening combinatorial libraries of polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) for those that specifically bind TNFR2-derived peptides (e.g., a peptide containing the amino acid sequence of SEQ ID NO: 285 or 286) include the screening of one-bead-one-compound libraries of antibody fragments. Antibody fragments can be chemically synthesized on a solid bead (e.g., using established split-and-pool solid phase peptide synthesis protocols) composed of a hydrophilic, water-swallowable material such that each bead displays a single antibody fragment. Heterogeneous bead mixtures can then be incubated with a TNFR2-derived peptide that is optionally labeled with a detectable moiety (e.g., a fluorescent dye) or that is conjugated to an epitope tag (e.g., biotin, avidin, FLAG tag, HA tag) that can later be detected by treatment with a complementary tag (e.g., avidin, biotin, anti-FLAG antibody, anti-HA antibody, respectively). Beads containing antibody fragments that specifically bind a TNFR2-derived peptide (e.g., a peptide containing the amino acid sequence of SEQ ID NO: 285 or 286) can be identified by analyzing the fluorescent properties of the beads following incubation with a fluorescently-labeled antigen or complementary tag (e.g., by confocal fluorescent microscopy or by fluorescence-activated bead sorting; see, e.g., Muller et al. (J. Biol. Chem., 16500-16505, 1996); incorporated herein by reference). Beads containing antibody fragments that specifically bind TNFR2-derived peptides can thus be separated from those that do not contain high-affinity antibody fragments. The sequence of an antibody fragment that specifically binds a TNFR2-derived peptide can be determined by techniques known in the art, including, e.g., Edman degradation, tandem mass spectrometry, matrix-assisted laser-desorption time-of-flight mass spectrometry (MALDI-TOF MS), nuclear magnetic resonance (NMR), and 2D gel electrophoresis, among others (see, e.g., WO 2004/062553; incorporated herein by reference).

#### *Negative screens of polypeptides*

In addition to the above-described methods for screening for a single-chain polypeptide, antibody, or antibody fragment that specifically binds to an epitope derived from human TNFR2 that promotes receptor antagonism, one can additionally perform negative screens in order to eliminate antibodies or antibody fragments that may also bind an epitope that contains the KCSPG sequence. For instance, mixtures of antibodies or antibody fragments isolated as a result of any of the above-described screening techniques can be screened for antibodies or antibody fragments that also specifically bind to a peptide derived from human TNFR2 that contains the KCSPG motif, such as a peptide containing residues 48-67 of SEQ ID NO: 7 (QTAQMCCSKCSPGQHAKVFC, SEQ ID NO: 18). This can be accomplished using any of the above-described methods or variations thereof, e.g., such that the antibodies or antibody fragments being screened are those that were previously identified as being capable of specifically binding a peptide containing one or more residues of the KCRPG sequence (e.g., at least the KCR sequence). Exemplary techniques useful for a negative screen include those described above or known in the art, such as phage display, yeast display, bacterial display, ribosome display, mRNA display, cDNA display, or surface-based combinatorial library screens (e.g., in an ELISA format). This screening technique represents a useful strategy for identifying an antagonistic TNFR2 antibody or antibody fragment, as antibodies or antibody

fragments capable of binding TNFR2 epitopes containing the KCSPG sequence and one or more residues of the KCRPG sequence have been shown to lack, or to have significantly reduced, antagonistic activity.

#### 5 *Immunization of a non-human mammal*

Another strategy that can be used to produce antagonistic TNFR2 antibodies and antigen-binding fragments thereof of the invention includes immunizing a non-human mammal. Examples of non-human mammals that can be immunized in order to produce antagonistic TNFR2 antibodies and fragments thereof of the invention include rabbits, mice, rats, goats, guinea pigs, hamsters, horses, and sheep, as well as non-human primates. For instance, established procedures for immunizing primates are known in the art (see, e.g., WO 1986/6004782; incorporated herein by reference). Immunization represents a robust method of producing monoclonal antibodies by exploiting the antigen specificity of B lymphocytes. For example, monoclonal antibodies can be prepared by the Kohler-Millstein procedure (described, e.g., in EP 0110716; incorporated herein by reference), wherein spleen cells from a non-human animal (e.g., a primate) immunized with a peptide that presents a TNFR2-derived antigen that promotes receptor antagonism (e.g., a peptide containing the amino acid sequence of SEQ ID NO: 285 or 286). A clonally-expanded B lymphocyte produced by immunization can be isolated from the serum of the animal and subsequently fused with a myeloma cell in order to form a hybridoma. Hybridomas are particularly useful agents for antibody production, as these immortalized cells can provide a lasting supply of an antigen-specific antibody. Antibodies from such hybridomas can subsequently be isolated using techniques known in the art, e.g., by purifying the antibodies from the cell culture medium by affinity chromatography, using reagents such as Protein A or Protein G.

#### **Antagonistic TNFR2 polypeptide conjugates**

Prior to administration of antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention to a mammalian subject (e.g., a human), it may be desirable to conjugate the antibody or fragment thereof to a second molecule, e.g., to modulate the activity of the antibody *in vivo*. Antagonistic TNFR2 antibodies and fragments thereof can be conjugated to other molecules at either the N-terminus or C-terminus of a light or heavy chain of the antibody using any one of a variety of established conjugation strategies that are well-known in the art. Examples of pairs of reactive functional groups that can be used to covalently tether an antagonistic TNFR2 antibody or fragment thereof to another molecule include, without limitation, thiol pairs, carboxylic acids and amino groups, ketones and amino groups, aldehydes and amino groups, thiols and alpha,beta-unsaturated moieties (such as maleimides or dehydroalanine), thiols and alpha-halo amides, carboxylic acids and hydrazides, aldehydes and hydrazides, and ketones and hydrazides.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) can be covalently appended directly to another molecule by chemical conjugation as described. Alternatively, fusion proteins containing antagonistic TNFR2 antibodies and fragments thereof can be expressed recombinantly from a cell (e.g., a eukaryotic cell or prokaryotic cell). This can be accomplished,



for example, by incorporating a polynucleotide encoding the fusion protein into the nuclear genome of a cell (e.g., using techniques described herein or known in the art). Optionally, antibodies and fragments thereof of the invention can be joined to a second molecule by forming a covalent bond between the antibody and a linker. This linker can then be subsequently conjugated to another molecule, or the linker can be conjugated to another molecule prior to ligation to the anti-TNFR2 antibody or fragment thereof. Examples of linkers that can be used for the formation of a conjugate include polypeptide linkers, such as those that contain naturally occurring or non-naturally occurring amino acids. In some embodiments, it may be desirable to include D-amino acids in the linker, as these residues are not present in naturally-occurring proteins and are thus more resistant to degradation by endogenous proteases. Fusion proteins containing polypeptide linkers can be made using chemical synthesis techniques, such as those described herein, or through recombinant expression of a polynucleotide encoding the fusion protein in a cell (e.g., a prokaryotic or eukaryotic cell). Linkers can be prepared using a variety of strategies that are well known in the art, and depending on the reactive components of the linker, can be cleaved by enzymatic hydrolysis, photolysis, hydrolysis under acidic conditions, hydrolysis under basic conditions, oxidation, disulfide reduction, nucleophilic cleavage, or organometallic cleavage (Leriche et al., *Bioorg. Med. Chem.*, 20:571-582, 2012).

#### *Drug-polypeptide conjugates*

An antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, and antigen-binding fragment thereof) of the invention can additionally be conjugated to, admixed with, or administered separately from a therapeutic agent, such as a cytotoxic molecule. Conjugates of the invention may be applicable to the treatment or prevention of a disease associated with aberrant cell proliferation, such as a cancer described herein. Exemplary cytotoxic agents that can be conjugated to, admixed with, or administered separately from an antagonistic TNFR2 polypeptide include, without limitation, antineoplastic agents such as: acivicin; aclarubicin; acodazole hydrochloride; acronine; adozelesin; adriamycin; aldesleukin; altretamine; ambomycin; a. metantrone acetate; aminoglutethimide; amsacrine; anastrozole; anthramycin; asparaginase; asperlin; azacitidine; azetepa; azotomycin; batimastat; benzodepa; bicalutamide; bisantrene hydrochloride; bisnafide dimesylate; bizelesin; bleomycin sulfate; brequinar sodium; bropirimine; busulfan; cactinomycin; calusterone; camptothecin; caracemide; carbetimer; carboplatin; carmustine; carubicin hydrochloride; carzelesin; cedefingol; chlorambucil; cirolemycin; cisplatin; cladribine; combretastatin a-4; crisnatol mesylate; cyclophosphamide; cytarabine; dacarbazine; dactinomycin; daunorubicin hydrochloride; daunomycin; decitabine; dexormaplatin; dezaguanine; dezaguanine mesylate; diaziqone; docetaxel; dolasatins; doxorubicin; doxorubicin hydrochloride; droloxifene; droloxifene citrate; dromostanolone propionate; duazomycin; edatrexate; eflornithine hydrochloride; ellipticine; elsamitrucin; enloplatin; enpromate; epipropidine; epirubicin hydrochloride; erbulozole; esorubicin hydrochloride; estramustine; estramustine phosphate sodium; etanidazole; ethiodized oil i 131; etoposide; etoposide phosphate; etoprine; fadrozole hydrochloride; fazarabine; fenretinide; floxuridine; fludarabine phosphate; fluorouracil; 5-fdump; flurocitabine; fosquidone; fostriecin sodium; gemcitabine; gemcitabine hydrochloride; gold au 198; homocamptothecin; hydroxyurea; idarubicin hydrochloride; ifosfamide; ilmofosine; interferon alfa-2a; interferon alfa-2b; interferon alfa-n1; interferon alfa-n3; interferon beta-i a; interferon gamma-

i b; iproplatin; irinotecan hydrochloride; lanreotide acetate; letrozole; leuprolide acetate; liarozole hydrochloride; lometrexol sodium; lomustine; losoxantrone hydrochloride; masoprocol; maytansine; mechlorethamine hydrochloride; megestrol acetate; melengestrol acetate; melphalan; menogaril; mercaptopurine; methotrexate; methotrexate sodium; metoprime; meturedopa; mitindomide; mitocarcin; 5 mitocromin; mitogillin; mitomalcin; mitomycin; mitosper; mitotane; mitoxantrone hydrochloride; mycophenolic acid; nocodazole; nogalamycin; ormaplatin; oxisuran; paclitaxel; pegaspargase; peliomycin; pentamustine; peploycinsulfate; perfosfamide; pipobroman; piposulfan; piroxantrone hydrochloride; plicamycin; plomestane; porfimer sodium; porfiromycin; prednimustine; procarbazine hydrochloride; puromycin; puromycin hydrochloride; pyrazofurin; rhizoxin; rhizoxin d; riboprime; rogletimide; safingol; safingol hydrochloride; 10 semustine; simtrazene; sparfosate sodium; sparsomycin; spirogermanium hydrochloride; spiromustine; spiroplatin; streptonigrin; streptozocin; strontium chloride sr 89; sulofenur; talisomycin; taxane; taxoid; tecogalan sodium; tegafur; teloxantrone hydrochloride; temoporfin; teniposide; teroxirone; testolactone; thiamiprine; thioguanine; thiotepa; thymitaq; tiazoferin; tirapazamine; tomudex; top53; topotecan hydrochloride; toremifene citrate; trestolone acetate; triciribine phosphate; trimetrexate; trimetrexate 15 glucuronate; triptorelin; tubulozole hydrochloride; uracil mustard; uredepa; vapreotide; verteporfin; vinblastine; vinblastine sulfate; vincristine; vincristine sulfate; vindesine; vindesine sulfate; vinepidine sulfate; vinglycinate sulfate; vinleurosine sulfate; vinorelbine tartrate; vinrosidine sulfate; vinzolidine sulfate; vorozole; zeniplatin; zinostatin; zorubicin hydrochloride; 2-chlorodeoxyadenosine; 2' deoxyformycin; 9-aminocamptothecin; raltitrexed; N-propargyl-5,8-dideazafolic acid; 2chloro-2'-arabino-fluoro-2'-deoxyadenosine; 2-chloro-2'- 20 deoxyadenosine; anisomycin; trichostatin A; hPRL-G129R; CEP-751; linomide; sulfur mustard; nitrogen mustard (mechlor ethamine); cyclophosphamide; melphalan; chlorambucil; ifosfamide; busulfan; N-methyl-Nnitrosourea (MNU); N, N'-Bis (2-chloroethyl)-N-nitrosourea (BCNU); N- (2-chloroethyl)-N' cyclohexyl-N-nitrosourea (CCNU); N- (2-chloroethyl)-N'- (trans-4-methylcyclohexyl)-N-nitrosourea (MeCCNU); N- (2-chloroethyl)-N'- (diethyl) ethylphosphonate-N-nitrosourea (fotemustine); streptozotocin; diacarbazine (DTIC); 25 mitozolomide; temozolomide; thiotepa; mitomycin C; AZQ; adozelesin; cisplatin; carboplatin; ormaplatin; oxaliplatin; C1-973; DWA 2114R; JM216; JM335; Bis (platinum); tomudex; azacitidine; cytarabine; gemcitabine; 6-mercaptopurine; 6-thioguanine; hypoxanthine; teniposide 9-amino camptothecin; topotecan; CPT-11; Doxorubicin; Daunomycin; Epirubicin; darubicin; mitoxantrone; losoxantrone; Dactinomycin (Actinomycin D); amsacrine; pyrazoloacridine; all-trans retinol; 14-hydroxy-retro-retinol; all-trans retinoic acid; 30 N- (4- hydroxyphenyl) retinamide; 13-cis retinoic acid; 3-methyl TTNEB; 9-cis retinoic acid; fludarabine (2-F-ara-AMP); or 2-chlorodeoxyadenosine (2-Cda).

Other therapeutic compounds that can be conjugated to, admixed with, or administered separately from an antagonistic TNFR2 single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention in order to treat, prevent, or study the progression of a disease associated with aberrant cell 35 proliferation include, but are not limited to, cytotoxic agents such as 20-pi-1,25 dihydroxyvitamin D3; 5-ethynyluracil; abiraterone; acylfulvene; adecyphenol; adozelesin; aldesleukin; ALL-TK antagonists; altretamine; ambamustine; amidox; amifostine; aminolevulinic acid; amrubicin; amsacrine; anagrelide; anastrozole; andrographolide; angiogenesis inhibitors; antagonist D; antagonist G; antarelix; anti-dorsalizing morphogenetic protein-1; antiandrogen, prostatic carcinoma; antiestrogen; antineoplaston; antisense

oligonucleotides; aphidicolin glycinate; apoptosis gene modulators; apoptosis regulators; apurinic acid; ara-  
 CDP-DL-PTBA; argininedeaminase; asulacrine; atamestane; atrimustine; axinastatin 1; axinastatin 2;  
 axinastatin 3; azasetron; azatoxin; azatyrosine; baccatin III derivatives; balanol; batimastat; BCR/ABL  
 antagonists; benzochlorins; benzoylstauosporine; beta lactam derivatives; beta-aethine; betaclamycin B;  
 5 betulinic acid; bFGF inhibitor; bicalutamide; bisantrene; bisaziridinylspermine; bisnafide; bistratene A;  
 bizelesin; breflate; bleomycin A2; bleomycin B2; bropridine; budotitane; buthionine sulfoximine; calcipotriol;  
 calphostin C; camptothecin derivatives (e.g., 10-hydroxy-camptothecin); canarypox IL-2; capecitabine;  
 carboxamide-amino-triazole; carboxyamidotriazole; CaRest M3; CARN 700; cartilage derived inhibitor;  
 carzelesin; casein kinase inhibitors (ICOS); castanospermine; cecropin B; cetorelix; chlorins;  
 10 chloroquinoxaline sulfonamide; cicaprost; cis-porphyrin; cladribine; clomifene analogues; clotrimazole;  
 collismycin A ; collismycin B; combretastatin A4; combretastatin analogue; conagenin; crambescidin 816 ;  
 crisnatol; cryptophycin 8; cryptophycin A derivatives; curacin A; cyclopentantraquinones; cycloplatain;  
 cypemycin; cytarabine ocfosfate; cytolytic factor; cytosstatin; dacliximab; decitabine; dehydrodidemnin B;  
 2'deoxycoformycin (DCF); deslorelin; dexifosfamide; dexrazoxane; dexverapamil; diaziquone; didemnin B;  
 15 didox; diethylnorspermine; dihydro-5-azacytidine; dihydrotaxol, 9- ; dioxamycin; diphenyl spiromustine;  
 discodermolide; docosanol; dolasetron; doxifluridine; droloxifene; dronabinol; duocarmycin SA; ebselen;  
 ecomustine; edelfosine; edrecolomab; eflornithine; elemene; emitefur; epirubicin; ephithilones (A, R = H; B, R  
 = Me); ephithilones; epristeride; estramustine analogue; estrogen agonists; estrogen antagonists; etanidazole;  
 etoposide; etoposide 4'-phosphate (etopofos); exemestane; fadrozole; fazarabine; fenretinide; filgrastim;  
 20 finasteride; flavopiridol; flezelastine; fluasterone; fludarabine; fluorodaunorubicin hydrochloride; forfenimex;  
 formestane; fostriecin; fotemustine; gadolinium texaphyrin; gallium nitrate; galocitabine; ganirelix; gelatinase  
 inhibitors; gemcitabine; glutathione inhibitors; hepsulfam; heregulin; hexamethylene bisacetamide;  
 homoharringtonine (HHT); hypericin; ibandronic acid; idarubicin; idoxifene; idramantone; ilmofosine; ilomastat;  
 imidazoacridones; imiquimod; immunostimulant peptides; insulin-like growth factor-1 receptor inhibitor;  
 25 interferon agonists; interferons; interleukins; iobenguane; iododoxorubicin; ipomeanol; irinotecan; iroplact;  
 irsogladine; isobengazole; isohomohalicondrin B; itasetron; jasplakinolide; kahalalide F; lamellarin-N  
 triacetate; lanreotide; leinamycin; lenograstim; lentinan sulfate; leptolstatin; letrozole; leukemia inhibiting  
 factor; leukocyte alpha interferon; leuprolide + estrogen + progesterone; leuprorelin; levamisole; liarozole;  
 linear polyamine analogue; lipophilic disaccharide peptide; lipophilic platinum compounds; lissoclinamide 7;  
 30 lobaplatin; lombricine; lometrexol; lonidamine; losoxantrone; lovastatin; loxoribine; lurtotecan; lutetium  
 texaphyrin; lysofylline; lytic peptides; maytansine; manostatatin A; marimastat; masoprocol; maspin; matrilysin  
 inhibitors; matrix metalloproteinase inhibitors; menogaril; mnerbarone; meterelin; methioninase;  
 metoclopramide; MIF inhibitor; ifepristone; miltefosine; mirimostim; mismatched double stranded RNA;  
 mithracin; mitoguazone; mitolactol; mitomycin analogues; mitonafide; mitotoxin fibroblast growth factor-  
 35 saporin; mitoxantrone; mofarotene; molgramostim; monoclonal antibody, human chorionic gonadotrophin;  
 monophosphoryl lipid A + myobacterium cell wall sk; mopidamol; multiple drug resistance gene inhibitor;  
 multiple tumor suppressor 1-based therapy; mustard anticancer agent; mycaperoxide B; mycobacterial cell  
 wall extract; myriaporone; N-acetyldinaline; N-substituted benzamides; nafarelin; nagrestip; naloxone +  
 pentazocine; napavin; naphterpin; nartograstim; nedaplatin; nemorubicin; neridronic acid; neutral

endopeptidase; nilutamide; nisamycin; nitric oxide modulators; nitroxide antioxidant; nitrullyn; 06-  
 benzylguanine; octreotide; okicenone; oligonucleotides; onapristone; ondansetron; ondansetron; oracin; oral  
 cytokine inducer; ormaplatin; osaterone; oxaliplatin; oxaunomycin; paclitaxel analogues; paclitaxel derivatives;  
 palauamine; palmitoylrhizoxin; pamidronic acid; panaxytriol; panomifene; parabactin; pazelliptine;  
 5 pegaspargase; peldesine; pentosan polysulfate sodium; pentostatin; pentozole; perflubron; perfosfamide;  
 perillyl alcohol; phenazinomycin; phenylacetate; phosphatase inhibitors; picibanil; pilocarpine hydrochloride;  
 pirarubicin; piritrexim; placetin A; placetin B; plasminogen activator inhibitor; platinum complex; platinum  
 compounds; platinum-triamine complex; podophyllotoxin; porfimer sodium; porfiromycin; propyl bis-acridone;  
 prostaglandin J2; proteasome inhibitors; protein A-based immune modulator; protein kinase C inhibitor;  
 10 protein kinase C inhibitors, microalgal; protein tyrosine phosphatase inhibitors; purine nucleoside  
 phosphorylase inhibitors; purpurins; pyrazoloacridine; pyridoxylated hemoglobin polyoxyethylene conjugate;  
 raf antagonists; raltitrexed; ramosetron; ras farnesyl protein transferase inhibitors; ras inhibitors; ras-GAP  
 inhibitor; retelliptine demethylated; rhenium Re 186 etidronate; rhizoxin; ribozymes; RII retinamide;  
 rogletimide; rohitukine; romurtide; roquinimex; rubiginone B 1; ruboxyl; safingol; saintopin; SarCNU;  
 15 sarcophytol A; sargramostim; Sdi 1 mimetics; semustine; senescence derived inhibitor 1; sense  
 oligonucleotides; signal transduction inhibitors; signal transduction modulators; single-chain antigen binding  
 protein; sizofiran; sobuzoxane; sodium borocaptate; sodium phenylacetate; solverol; somatomedin binding  
 protein; sonermin; sparfosic acid; spicamycin D; spiromustine; splenopentin; spongistatin 1; squalamine; stem  
 cell inhibitor; stem-cell division inhibitors; stipiamide; stromelysin inhibitors; sulfinosine; superactive vasoactive  
 20 intestinal peptide antagonist; suradista; suramin; swainsonine; synthetic glycosaminoglycans; tallimustine;  
 tamoxifen methiodide; tauromustine; tazarotene; tecogalan sodium; tegafur; tellurapyrylium; telomerase  
 inhibitors; temoporfin; temozolomide; teniposide; tetrachlorodecaoxide; tetrazomine; thaliblastine; thalidomide;  
 thiocoraline; thrombopoietin; thrombopoietin mimetic; thymalfasin; thymopoietin receptor agonist; thymotrinan;  
 thyroid stimulating hormone; tin ethyl etiopurpurin; tirapazamine; titanocene dichloride; topotecan; topsentin;  
 25 toremifene; totipotent stem cell factor; translation inhibitors; tretinoin; triacetyluridine; triciribine; trimetrexate;  
 triptorelin; tropisetron; turosteride; tyrosine kinase inhibitors; tyrphostins; UBC inhibitors; ubenimex; urogenital  
 sinus-derived growth inhibitory factor; urokinase receptor antagonists; vapreotide; variolin B; vector system,  
 erythrocyte gene therapy; velaresol; veramine; verdins; verteporfin; vinorelbine; vinxaltine; vitaxin; vorozole;  
 zanoterone; zeniplatin; zilascorb; and zinostatin stimalamer.

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#### *Labeled anti-TNFR2 polypeptides*

In some embodiments, antagonistic TNFR2 single-chain polypeptides, antibodies, or antigen-binding  
 fragments thereof may be conjugated to another molecule (e.g., an epitope tag) for the purpose of purification  
 or detection. Examples of such molecules that are useful in protein purification include those that present  
 35 structural epitopes capable of being recognized by a second molecule. This is a common strategy that is  
 employed in protein purification by affinity chromatography, in which a molecule is immobilized on a solid  
 support and exposed to a heterogeneous mixture containing a target protein conjugated to a molecule  
 capable of binding the immobilized compound. Examples of epitope tag molecules that can be conjugated to  
 antagonistic TNFR2 antibodies or fragments thereof for the purposes of molecular recognition include, without

limitation, maltose-binding protein, glutathione-S-transferase, a poly-histidine tag, a FLAG-tag, a myc-tag, human influenza hemagglutinin (HA) tag, biotin, streptavidin. Conjugates containing the epitopes presented by these molecules are capable of being recognized by such complementary molecules as maltose, glutathione, a nickel-containing complex, an anti-FLAG antibody, an anti-myc antibody, an anti-HA antibody, streptavidin, or biotin, respectively. For example, one can purify an antagonistic TNFR2 antibody or fragment thereof of the invention that has been conjugated to an epitope tag from a complex mixture of other proteins and biomolecules (e.g., DNA, RNA, carbohydrates, phospholipids, etc) by treating the mixture with a solid phase resin containing an complementary molecule that can selectively recognize and bind the epitope tag of the antagonistic anti-TNFR2 antibody or fragment thereof. Examples of solid phase resins include agarose beads, which are compatible with purifications in aqueous solution.

An antagonistic TNFR2 single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention can also be covalently appended to a fluorescent molecule, e.g., to detect the antibody or antigen-binding fragment thereof by fluorimetry and/or by direct visualization using fluorescence microscopy. Exemplary fluorescent molecules that can be conjugated to antibodies of the invention include green fluorescent protein, cyan fluorescent protein, yellow fluorescent protein, red fluorescent protein, phycoerythrin, allophycocyanin, hoescht, 4',6-diamidino-2-phenylindole (DAPI), propidium iodide, fluorescein, coumarin, rhodamine, tetramethylrhoadmine, and cyanine. Additional examples of fluorescent molecules suitable for conjugation to antibodies of the invention are well-known in the art and have been described in detail in, e.g., U.S. Patent Nos. 7,417,131 and 7,413,874, each of which is incorporated by reference herein.

Antagonistic TNFR2 polypeptides containing a fluorescent molecule are particularly useful for monitoring the cell-surface localization properties of antibodies and fragments thereof of the invention. For instance, one can expose cultured mammalian cells (e.g., T-reg cells) to antagonistic TNFR2 antibodies or fragments thereof of the invention that have been covalently conjugated to a fluorescent molecule and subsequently analyze these cells using conventional fluorescent microscopy techniques known in the art. Confocal fluorescent microscopy is a particularly powerful method for determining cell-surface localization of antagonistic anti-TNFR2 antibodies or fragments thereof, as individual planes of a cell can be analyzed in order to distinguish antibodies or fragments thereof that have been internalized into a cell's interior, e.g., by receptor-mediated endocytosis, from those that are bound to the external face of the cell membrane. Additionally, cells can be treated with antagonistic TNFR2 antibodies conjugated to a fluorescent molecule that emits visible light of a particular wavelength (e.g., fluorescein, which fluoresces at about 535 nm) and an additional fluorescent molecule that is known to localize to a particular site on the T-reg cell surface and that fluoresces at a different wavelength (e.g., a molecule that localizes to CD25 and that fluoresces at about 599 nm). The resulting emission patterns can be visualized by confocal fluorescence microscopy and the images from these two wavelengths can be merged in order to reveal information regarding the location of the antagonistic TNFR2 antibody or antigen-binding fragment thereof on the T-reg cell surface with respect to other receptors.

Bioluminescent proteins can also be incorporated into a fusion protein for the purposes of detection and visualization of an antagonistic anti-TNFR2 polypeptide, such as a single-chain

polypeptide, antibody, or fragment thereof. Bioluminescent proteins, such as Luciferase and aequorin, emit light as part of a chemical reaction with a substrate (e.g., luciferin and coelenterazine). Exemplary bioluminescent proteins suitable for use as a diagnostic sequence and methods for their use are described in, e.g., U.S. Patent Nos. 5,292,658, 5,670,356, 6,171,809, and 7,183,092, each of which is  
5 herein incorporated by reference. Antagonistic TNFR2 antibodies or fragments thereof labeled with bioluminescent proteins are a useful tool for the detection of antibodies of the invention following an *in vitro* assay. For instance, the presence of an antagonistic TNFR2 antibody that has been conjugated to a bioluminescent protein can be detected among a complex mixture of additional proteins by separating the components of the mixture using gel electrophoresis methods known in the art (e.g., native gel analysis)  
10 and subsequently transferring the separated proteins to a membrane in order to perform a Western blot. Detection of the antagonistic TNFR2 antibody among the mixture of other proteins can be achieved by treating the membrane with an appropriate Luciferase substrate and subsequently visualizing the mixture of proteins on film using established protocols.

The polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof)  
15 of the invention can also be conjugated to a molecule comprising a radioactive nucleus, such that an antibody or fragment thereof of the invention can be detected by analyzing the radioactive emission pattern of the nucleus. Alternatively, an antagonistic TNFR2 antibody or fragment thereof can be modified directly by incorporating a radioactive nucleus within the antibody during the preparation of the protein. Radioactive isotopes of methionine ( $^{35}\text{S}$ ), nitrogen ( $^{15}\text{N}$ ), or carbon ( $^{13}\text{C}$ ) can be incorporated into antibodies or fragments  
20 thereof of the invention by, e.g., culturing bacteria in media that has been supplemented with nutrients containing these isotopes. Optionally, tyrosine derivatives containing a radioactive halogen can be incorporated into an antagonistic TNFR2 antibody or fragment thereof by, e.g., culturing bacterial cells in media supplemented with radiolabeled tyrosine. It has been shown that tyrosine functionalized with a radioactive halogen at the C2 position of the phenol system are rapidly incorporated into elongating  
25 polypeptide chains using the endogenous translation enzymes *in vivo* (U.S. Patent No. 4,925,651; incorporated herein by reference). The halogens include fluorine, chlorine, bromine, iodine, and astatine. Additionally, antagonistic TNFR2 antibodies or fragments thereof can be modified following isolation and purification from cell culture by functionalizing antibodies or fragments thereof of the invention with a radioactive isotope. The halogens represent a class of isotopes that can be readily incorporated into a purified  
30 protein by aromatic substitution at tyrosine or tryptophan, e.g., via reaction of one or more of these residues with an electrophilic halogen species. Examples of radioactive halogen isotopes include  $^{18}\text{F}$ ,  $^{75}\text{Br}$ ,  $^{77}\text{Br}$ ,  $^{122}\text{I}$ ,  $^{123}\text{I}$ ,  $^{124}\text{I}$ ,  $^{125}\text{I}$ ,  $^{129}\text{I}$ ,  $^{131}\text{I}$ , or  $^{211}\text{At}$ .

Another alternative strategy for the incorporation of a radioactive isotope is the covalent attachment of a chelating group to the antagonistic anti-TNFR2 polypeptide, such as a single-chain polypeptide, antibody, or  
35 fragment thereof. Chelating groups can be covalently appended to an antagonistic TNFR2 antibody or fragment thereof by attachment to a reactive functional group, such as a thiol, amino group, alcohol, or carboxylic acid. The chelating groups can then be modified to contain any of a variety of metallic radioisotopes, including, without limitation, such radioactive nuclides as  $^{125}\text{I}$ ,  $^{67}\text{Ga}$ ,  $^{111}\text{In}$ ,  $^{99}\text{Tc}$ ,  $^{169}\text{Yb}$ ,  $^{186}\text{Re}$ ,  $^{123}\text{I}$ ,  $^{124}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{99\text{m}}\text{Tc}$ ,  $^{111}\text{In}$ ,  $^{64}\text{Cu}$ ,  $^{67}\text{Cu}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{177}\text{Lu}$ ,  $^{90}\text{Y}$ ,  $^{77}\text{As}$ ,  $^{72}\text{As}$ ,  $^{86}\text{Y}$ ,  $^{89}\text{Zr}$ ,  $^{211}\text{At}$ ,  $^{212}\text{Bi}$ ,  $^{213}\text{Bi}$ , or  $^{225}\text{Ac}$ .

In some embodiments, it may be desirable to covalently conjugate the polypeptides (e.g., single-chain polypeptides, antibodies, or fragments thereof) of the invention with a chelating group capable of binding a metal ion from heavy elements or rare earth ions, such as  $Gd^{3+}$ ,  $Fe^{3+}$ ,  $Mn^{3+}$ , or  $Cr^{2+}$ . Conjugates containing chelating groups that are coordinated to such paramagnetic metals are useful as in MRI imaging applications.

5 Paramagnetic metals include, but are not limited to, chromium (III), manganese (II), iron (II), iron (III), cobalt (II), nickel (II), copper (II), praseodymium (III), neodymium (III), samarium (III), gadolinium (III), terbium (III), dysprosium (III), holmium (III), erbium (III), and ytterbium (III). In this way, antagonistic TNFR2 antibodies can be detected by MRI spectroscopy. For instance, one can administer antagonistic TNFR2 antibodies or fragments thereof conjugated to chelating groups bound to paramagnetic ions to a mammalian subject (e.g., a  
10 human patient) in order to monitor the distribution of the antibody following administration. This can be achieved by administration of the antibody to a patient by any of the administration routes described herein, such as intravenously, and subsequently analyzing the location of the administered antibody by recording an MRI of the patient according to established protocols.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding  
15 fragments thereof) can additionally be conjugated to other molecules for the purpose of improving the solubility and stability of the protein in aqueous solution. Examples of such molecules include PEG, PSA, bovine serum albumin (BSA), and human serum albumin (HSA), among others. For instance, one can conjugate an antagonistic TNFR2 antibody or fragment thereof to carbohydrate moieties in order to evade detection of the antibody or fragment thereof by the immune system of the patient receiving treatment. This  
20 process of hyperglycosylation reduces the immunogenicity of therapeutic proteins by sterically inhibiting the interaction of the protein with B cell receptors in circulation. Alternatively, antagonistic TNFR2 antibodies or fragments thereof can be conjugated to molecules that prevent clearance from human serum and improve the pharmacokinetic profile of antibodies of the invention. Exemplary molecules that can be conjugated to or  
25 inserted within anti-TNFR2 antibodies or fragments thereof of the invention so as to attenuate clearance and improve the pharmacokinetic profile of these antibodies and fragments include salvage receptor binding epitopes. These epitopes are found within the Fc region of an IgG immunoglobulin and have been shown to bind Fc receptors and prolong antibody half-life in human serum. The insertion of salvage receptor binding epitopes into anti-TNFR2 antibodies or fragments thereof can be achieved, e.g., as described in US Patent No. 5,739,277; incorporated herein by reference.

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### **Modified antagonistic TNFR2 polypeptides**

In addition to conjugation to other therapeutic agents and labels for identification or visualization, anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments  
35 thereof) of the invention can also be modified so as to improve their pharmacokinetic profile, biophysical stability, or inhibitory capacity. For instance, any cysteine residue not involved in maintaining the proper conformation of the anti-TNFR2 antibody or fragment thereof may be substituted with an isosteric or isolectronic amino acid (e.g., serine) in order to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cystine bond(s) may be added to the antibody or fragment thereof to improve its stability (particularly where the antibody is an antibody fragment, such as an Fv fragment).

This can be accomplished, e.g., by altering a polynucleotide encoding the antibody heavy and light chains or a polynucleotide encoding an antibody fragment so as to encode one or more additional pairs of cysteine residues that can form disulfide bonds under oxidative conditions in order to reinforce antibody tertiary structure (see, e.g., US Patent No. 7,422,899; incorporated herein by reference).

5           Another useful modification that may be made to anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention includes altering the glycosylation profile of these antibodies and fragments thereof. This can be achieved, e.g., by substituting, inserting, or deleting amino acids in an antagonistic TNFR2 antibody so as to insert or remove a glycosylation site. Glycosylation of antibodies typically occurs in N-linked or O-linked fashion.

10          N-linked glycosylation is a process whereby the attachment of a carbohydrate moiety to an antibody occurs at the side-chain of an asparagine residue. Consensus amino acid sequences for N-linked glycosylation include the tripeptide sequences asparagine-X-serine (NXS) and asparagine-X-threonine (NXT), where X is any amino acid except proline. The insertion of either of these tripeptide sequences in a polypeptide (e.g., an anti-TNFR2 antibody) creates a potential glycosylation site. O-linked glycosylation

15          refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine are also competent substrates for glycoside formation. Addition of glycosylation sites to an anti-TNFR2 antibody can thus be accomplished by altering the amino acid sequence of the antibody (e.g., using recombinant expression techniques as described herein) such that it contains one or more of the above-

20          described tripeptide sequences to promote N-linked glycosylation, or one or more serine or threonine residues to the sequence of the original antibody engender O-linked glycosylation (see, e.g., US Patent No. 7,422,899; incorporated herein by reference).

          In alternative cases, it may be desirable to modify the antibody or fragment thereof of the invention with respect to effector function, e.g., so as to enhance antigen-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be

25          achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. For instance, cysteine residues may be introduced in the Fc region of an anti-TNFR2 antibody or fragment thereof (e.g., by recombinant expression techniques as described herein), so as to facilitate additional inter-chain disulfide bond formation in this region. The homodimeric antibody thus generated may have

30          increased conformational constraint, which may foster improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described, for example, in Wolff et al. (Canc. Res., 53:2560-2565, 1993); incorporated herein by reference. Alternatively, an antibody can be engineered which has dual Fc regions and may

35          thereby have enhanced complement lysis and ADCC capabilities (see Stevenson et al. (Anti-Canc. Drug Des., 3:219-230, 1989); incorporated herein by reference).

          The serum half-life of anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be improved in some embodiments by incorporating one more amino acid modifications, such as by altering the CH1 or CL region of the Fab



domain to introduce a salvage receptor motif, e.g., that found in the two loops of a CH2 domain of an Fc region of an IgG. Such alterations are described, for instance, in U.S. Patent No. 5,869,046 and U.S. Patent No. 6,121,022; incorporated herein by reference. Additional framework modifications can also be made to reduce immunogenicity of the antibody or fragment thereof or to reduce or remove T cell epitopes that reside therein, as described for instance in US2003/0153043; incorporated herein by reference.

### Methods of treatment

Antagonistic TNFR2 polypeptides, such a dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) that contain a CDR-H1 and CDR-H2 derived from a phenotype-neutral TNFR2 antibody and a CDR-H3 represented by the formula  $JZ^1JZ^2Z^4JZ^3JZ^5(J)_2Z^5Z^2Z^5$  or  $JZ^1JZ^2Z^4Z^3Z^5(J)_2Z^5Z^2Z^5(J)_2$  (wherein each J is independently a naturally occurring amino acid, each  $Z^1$  is independently a naturally occurring amino acid containing a cationic side-chain at physiological pH, each  $Z^2$  is independently a naturally occurring amino acid containing an anionic side-chain at physiological pH, each  $Z^3$  is independently a naturally occurring amino acid containing a polar, uncharged side-chain at physiological pH, each  $Z^4$  is independently a glycine or alanine, and each  $Z^5$  is independently a naturally occurring amino acid containing a hydrophobic side-chain) can be used to treat a patient suffering from a cell proliferation disorder (such as a cancer described herein), an infectious disease (such as a viral, bacterial, fungal, or parasitic infection described herein), or another disease mediated by TNFR2 signaling.

For instance, antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, or antigen-binding fragments thereof) that contain a CDR-H1 and CDR-H2 derived from a phenotype-neutral TNFR2 antibody and a CDR-H3 represented by the formula JRJDGJSJY(J)<sub>2</sub>FDJ (SEQ ID NO: 278), JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279), QZ<sup>1</sup>VZ<sup>2</sup>Z<sup>4</sup>YZ<sup>3</sup>SZ<sup>5</sup>WYZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup> (SEQ ID NO: 265), or AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266) can be used to treat a patient suffering from a cell proliferation disorder (such as a cancer described herein), an infectious disease (such as a viral, bacterial, fungal, or parasitic infection described herein), or another disease mediated by TNFR2 signaling.

In some embodiments, the CDR-H3 is derived from TNFRAB1 and have the amino acid sequence QRVDGYSSYWYFDV (SEQ ID NO: 25). The CDR-H3 may be derived from TNFRAB2 and have the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259). In some embodiments, the CDR-H3 is derived from TNFR2A3 and has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

### Methods of treating cell proliferation disorders

Antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention are useful therapeutics for the treatment of a wide array of cancers and cell proliferation disorders. Antagonistic TNFR2 polypeptides, such as dominant antagonistic TNFR2 polypeptides (e.g., single-chain

polypeptides, antibodies, and antigen-binding fragments thereof) can be administered to a mammalian subject, such as a human, suffering from a cell proliferation disorder, such as cancer, e.g., to enhance the effectiveness of the adaptive immune response against the target cancer cells.

In particular, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be administered to a mammalian subject, such as a human, to reduce or inhibit T-reg cell growth and activation, which allows tumor-infiltrating T-lymphocytes to localize to cells presenting tumor-associated antigens and to promote cytotoxicity. In addition, polypeptides of the invention may synergize with existing adoptive T cell therapy platforms, as one of the limitations on the effectiveness of this strategy has been the difficulty of prolonging cytotoxicity of tumor-reactive T cells following infusion into a mammalian subject (e.g., a human). Polypeptides of the invention may also promote the activity of allogeneic T-lymphocytes, which may express foreign MHC proteins and may be increasingly susceptible to inactivation by the host immune system. For example, antibodies and antigen-binding fragments thereof of the invention can mitigate the T-reg-mediated depletion of tumor-reactive T cells by suppressing the growth and proliferation of T-reg cells that typically accompanies T cell infusion. For instance, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may be capable of reducing the growth of T-reg cells by about 50% to about 200% relative to untreated cells (e.g., 50%, 75%, 100%, 125%, 150%, 175%, or 200%). The reduction in cellular growth does not require the presence of TNF $\alpha$ . In some embodiments, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may be capable of restricting the growth of T-reg cells in the presence of TNF $\alpha$  to between 90% and 150% relative to untreated cells (e.g., 90%, 100%, 110%, 120%, 130%, 140%, or 150%). Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention are also capable of restricting the proliferation of T-reg cells to less than 70% (e.g., 60%, 50%, 40%, 30%, 20%, 10%, 5%, or 1%) of that of an untreated population of T-reg cells. Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention are also capable of decreasing the survival of T-reg cells by about 10% (e.g., by about 20%, 30%, 40%, or 50%, or more) relative to an untreated population of T-reg cells.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be administered to a mammalian subject (e.g., a human) suffering from cancer in order to improve the condition of the patient by promoting the immune response against cancer cells and tumorigenic material. Antibodies of the invention can be administered to a subject, e.g., via any of the routes of administration described herein. Antibodies of the invention can also be formulated with excipients, biologically acceptable carriers, and may be optionally conjugated to, admixed with, or co-administered separately (e.g., sequentially) with additional therapeutic agents, such as anti-cancer agents. Cancers that can be treated by administration of antibodies or antigen-binding fragments thereof of the invention include such cancers as leukemia, lymphoma, liver cancer, bone cancer, lung cancer, brain cancer, bladder cancer, gastrointestinal cancer, breast cancer, cardiac cancer, cervical cancer, uterine cancer, head and neck cancer, gallbladder cancer, laryngeal cancer, lip and oral cavity cancer, ocular cancer, melanoma, pancreatic cancer, prostate cancer, colorectal cancer, testicular

cancer, and throat cancer. Particular cancers that can be treated by administration of antibodies or antigen-binding fragments thereof of the invention include, without limitation, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), adrenocortical carcinoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytoma, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, extrahepatic cancer, ewing sarcoma family, osteosarcoma and malignant fibrous histiocytoma, central nervous system embryonal tumors, central nervous system germ cell tumors, craniopharyngioma, ependymoma, bronchial tumors, burkitt lymphoma, carcinoid tumor, primary lymphoma, chordoma, chronic myeloproliferative neoplasms, colon cancer, extrahepatic bile duct cancer, ductal carcinoma in situ (DCIS), endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, extracranial germ cell tumor, extragonadal germ cell tumor, fallopian tube cancer, fibrous histiocytoma of bone, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular germ cell tumor, gestational trophoblastic disease, glioma, childhood brain stem glioma, hairy cell leukemia, hepatocellular cancer, langerhans cell histiocytosis, hodgkin lymphoma, hypopharyngeal cancer, islet cell tumors, pancreatic neuroendocrine tumors, wilms tumor and other childhood kidney tumors, langerhans cell histiocytosis, small cell lung cancer, cutaneous T cell lymphoma, intraocular melanoma, merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasm, myelodysplastic syndromes, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-hodgkin lymphoma (NHL), non-small cell lung cancer (NSCLC), epithelial ovarian cancer, germ cell ovarian cancer, low malignant potential ovarian cancer, pancreatic neuroendocrine tumors, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, pleuropulmonary blastoma, primary peritoneal cancer, rectal cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, kaposi sarcoma, rhabdomyosarcoma, sézary syndrome, small intestine cancer, soft tissue sarcoma, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, urethral cancer, endometrial uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, and Waldenström macroglobulinemia.

For example, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be administered to a patient (e.g., a mammalian patient, such as a human patient) in order to treat T cell lymphoma (e.g., Hodgkin's or cutaneous non-Hodgkin's lymphoma cells), ovarian cancer, colon cancer, multiple myeloma, or renal cell carcinoma.

An anti-TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, or antigen-binding fragment thereof) of the invention can also be co-administered with a therapeutic antibody that exhibits reactivity towards a cancer cell. In this way, antagonistic TNFR2 polypeptides (e.g., antibodies or fragments thereof) of the invention may synergize not only with the adaptive immune response, e.g., by prolonging T-lymphocyte tumor reactivity, but also with other inhibitors of tumor cell growth. Examples of additional therapeutic antibodies that can be used to treat cancer and other cell proliferation disorders include those that exhibit reactivity with a tumor antigen or a cell-surface protein that is overexpressed on

the surface of a cancer cell. Exemplary antibodies that can be admixed, co-administered, or sequentially administered with antagonistic TNFR2 antibodies of the invention include, without limitation, Trastuzamb (HERCEPTIN®), Bevacizumab (AVASTIN®), Cetuximab (ERBITUX®), Panitumumab (VECTIBIX®), Ipilimumab (YERVOY®), Rituximab (RITUXAN® and MABTHERA®), Alemtuzumab (CAMPATH®),  
5 Ofatumumab (ARZERRA®), Gemtuzumab ozogamicin (MYLOTARG®), Brentuximab vedotin (ADCETRIS®), <sup>90</sup>Y-Ibritumomab Tiuxetan (ZEVALIN®), and <sup>131</sup>I-Tositumomab (BEXXAR®), which are described in detail in Scott et al. (Cancer Immun., 12:14-21, 2012); incorporated herein by reference.

A physician having ordinary skill in the art can readily determine an effective amount of an antagonistic TNFR2 polypeptide, such as single-chain polypeptide, antibody, or antibody fragment for  
10 administration to a mammalian subject (e.g., a human) in need thereof. For example, a physician could start prescribing doses of a polypeptide of the invention at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. Alternatively, a physician may begin a treatment regimen by administering an antagonistic  
15 TNFR2 polypeptide, such as a single-chain polypeptide, antibody, or antibody fragment at a high dose and subsequently administer progressively lower doses until a therapeutic effect is achieved (e.g., a reduction in the volume of one or more tumors, a decrease in the population of T-reg cells, or remission of a cell proliferation disorder). In general, a suitable daily dose of a single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention will be an amount of the compound which is the lowest  
20 dose effective to produce a therapeutic effect. An antibody or antigen-binding fragment thereof of the invention may be administered by injection, e.g., by intravenous, intramuscular, intraperitoneal, or subcutaneous injection, optionally proximal to the site of the target tissue (e.g., a tumor). A daily dose of a therapeutic composition of an antibody or antigen-binding fragment thereof of the invention may be administered as a single dose or as two, three, four, five, six or more doses administered separately at  
25 appropriate intervals throughout the day, week, month, or year, optionally, in unit dosage forms. While it is possible for an antibody or fragment thereof of the invention to be administered alone, it may also be administered as a pharmaceutical formulation in combination with excipients, carriers, and optionally, additional therapeutic agents.

Polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be monitored for their ability to attenuate the progression of a cell proliferation  
30 disease, such as cancer, by any of a variety of methods known in the art. For instance, a physician may monitor the response of a mammalian subject (e.g., a human) to treatment with a polypeptide, such as a single-chain polypeptide, antibody, or antibody fragment of the invention by analyzing the volume of one or more tumors in the patient. For example, polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention may be capable of reducing tumor volume by between  
35 1% and 100% (e.g., 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100%). Alternatively, a physician may monitor the responsiveness of a subject (e.g., a human) to treatment with antagonistic TNFR2 polypeptides, such as single-chain polypeptides, antibodies, or antigen-binding fragments thereof of the invention by analyzing the T-reg cell population in the lymph of a particular subject. For instance, a physician may withdraw a sample of blood from a mammalian subject (e.g., a

human) and determine the quantity or density of T-reg cells (e.g., CD4+ CD25+ FOXP3+ T-reg cells or CD17+ T-reg cells) using established procedures, such as fluorescence activated cell sorting.

*Methods of treating infectious diseases*

5 Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can also be used for treating infectious diseases, such as those caused by any one or more of a virus, a bacterium, a fungus, or a parasite (e.g., a eukaryotic parasite). For instance, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) can be administered to a mammalian subject (e.g., a human)  
10 suffering from an infectious disease in order to treat the disease, as well as to alleviate one or more symptoms of the disease.

For example, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be used for treating, or alleviating one or more symptoms of, viral infections in a mammalian subject, such as a human, that are caused by, e.g., a  
15 member of the *Flaviviridae* family (e.g., a member of the *Flavivirus*, *Pestivirus*, and *Hepacivirus* genera), which includes the hepatitis C virus, Yellow fever virus; Tick-borne viruses, such as the Gadgets Gully virus, Kadam virus, Kyasanur Forest disease virus, Langat virus, Omsk hemorrhagic fever virus, Powassan virus, Royal Farm virus, Karshi virus, tick-borne encephalitis virus, Neudoerfl virus, Sofjin virus, Louping ill virus and the Negishi virus; seabird tick-borne viruses, such as the Meaban virus,  
20 Saumarez Reef virus, and the Tyuleniy virus; mosquito-borne viruses, such as the Aroa virus, dengue virus, Kedougou virus, Cacipacore virus, Koutango virus, Japanese encephalitis virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey meningoencephalo-myelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus,  
25 Uganda S virus, Wesselsbron virus, yellow fever virus; and viruses with no known arthropod vector, such as the Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, Tamana bat virus, and the Cell fusing agent virus; a member of the *Arenaviridae* family, which includes the Ippy virus, Lassa virus (e.g., the Josiah, LP, or GA391 strain), lymphocytic choriomeningitis virus (LCMV), Mobala virus, Mopeia virus, Amapari virus, Flexal virus, Guanarito virus, Junin virus, Latino virus, Machupo virus, Oliveros virus, Paraná virus, Pichinde virus, Pirital virus, Sabiá virus, Tacaribe virus, Tamiami virus, Whitewater Arroyo virus, Chapare virus, and Lujó virus; a member of the *Bunyaviridae* family (e.g., a member of the *Hantavirus*, *Nairovirus*, *Orthobunyavirus*, and *Phlebovirus* genera), which includes the Hantaan virus, Sin  
35 Nombre virus, Dugbe virus, Bunyamwera virus, Rift Valley fever virus, La Crosse virus, California encephalitis virus, and Crimean-Congo hemorrhagic fever (CCHF) virus; a member of the *Filoviridae* family, which includes the Ebola virus (e.g., the Zaire, Sudan, Ivory Coast, Reston, and Uganda strains) and the Marburg virus (e.g., the Angola, Ci67, Musoke, Popp, Ravn and Lake Victoria strains); a member of the *Togaviridae* family (e.g., a member of the *Alphavirus* genus), which includes the Venezuelan

equine encephalitis virus (VEE), Eastern equine encephalitis virus (EEE), Western equine encephalitis virus (WEE), Sindbis virus, rubella virus, Semliki Forest virus, Ross River virus, Barmah Forest virus, O'nyong'nyong virus, and the chikungunya virus; a member of the *Poxviridae* family (e.g., a member of the *Orthopoxvirus* genus), which includes the smallpox virus, monkeypox virus, and vaccinia virus; a member of the *Herpesviridae* family, which includes the herpes simplex virus (HSV; types 1, 2, and 6), human herpes virus (e.g., types 7 and 8), cytomegalovirus (CMV), Epstein-Barr virus (EBV), Varicella-Zoster virus, and Kaposi's sarcoma associated-herpesvirus (KSHV); a member of the *Orthomyxoviridae* family, which includes the influenza virus (A, B, and C), such as the H5N1 avian influenza virus or H1N1 swine flu; a member of the *Coronaviridae* family, which includes the severe acute respiratory syndrome (SARS) virus; a member of the *Rhabdoviridae* family, which includes the rabies virus and vesicular stomatitis virus (VSV); a member of the *Paramyxoviridae* family, which includes the human respiratory syncytial virus (RSV), Newcastle disease virus, hendravirus, nipahvirus, measles virus, rinderpest virus, canine distemper virus, Sendai virus, human parainfluenza virus (e.g., 1, 2, 3, and 4), rhinovirus, and mumps virus; a member of the *Picornaviridae* family, which includes the poliovirus, human enterovirus (A, B, C, and D), hepatitis A virus, and the coxsackievirus; a member of the *Hepadnaviridae* family, which includes the hepatitis B virus; a member of the *Papillomaviridae* family, which includes the human papilloma virus; a member of the *Parvoviridae* family, which includes the adeno-associated virus; a member of the *Astroviridae* family, which includes the astrovirus; a member of the *Polyomaviridae* family, which includes the JC virus, BK virus, and SV40 virus; a member of the *Calciviridae* family, which includes the Norwalk virus; a member of the *Reoviridae* family, which includes the rotavirus; and a member of the *Retroviridae* family, which includes the human immunodeficiency virus (HIV; e.g., types 1 and 2), and human T-lymphotropic virus Types I and II (HTLV-1 and HTLV-2, respectively); Friend Leukemia Virus; and transmissible spongiform encephalopathy, such as chronic wasting disease. Particularly, methods of the invention include administering an antagonistic TNFR2 antibody (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7), such as a TNFR2 antibody that contains the CDR-H3 sequence or a variant thereof of TNFRAB1, TNFRAB2, or TNFR2A3) to a human in order to treat an HIV infection (such as a human suffering from AIDS).

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can also be used for treating, or alleviating one or more symptoms of, bacterial infections in a mammalian subject (e.g., a human). Examples of bacterial infections that may be treated by administration of an antagonistic TNFR2 polypeptide, such as a single-chain polypeptide, antibody, or antibody fragment of the invention include, without limitation, those caused by bacteria within the genera *Streptococcus*, *Bacillus*, *Listeria*, *Corynebacterium*, *Nocardia*, *Neisseria*, *Actinobacter*, *Moraxella*, *Enterobacteriaceae* (e.g., *E. coli*, such as O157:H7), *Pseudomonas* (such as *Pseudomonas aeruginosa*), *Escherichia*, *Klebsiella*, *Serratia*, *Enterobacter*, *Proteus*, *Salmonella*, *Shigella*, *Yersinia*, *Haemophilus*, *Bordetella* (such as *Bordetella pertussis*), *Legionella*, *Pasturella*, *Francisella*, *Brucella*, *Bartonella*, *Clostridium*, *Vibrio*, *Campylobacter*, *Staphylococcus*, *Mycobacterium*

(such as *Mycobacterium tuberculosis* and *Mycobacterium avium paratuberculosis*, and *Helicobacter* (such as *Helicobacter pylori* and *Helicobacter hepaticus*). Particularly, methods of the invention include administering an antagonistic TNFR2 polypeptide, such as a single-chain polypeptide, antibody, or antigen-binding fragment thereof that contains a CDR-H3 region as described herein (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7), such as a TNFR2 antibody that contains the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3) to a human or a non-human mammal in order to treat a *Mycobacterium tuberculosis* infection. Particular methods of the invention include administering an antagonistic TNFR2 polypeptide (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7), such as a TNFR2 antibody that contains the CDR-H3 sequence or a variant thereof of TNFRAB1, TNFRAB2, or TNFR2A3) to bovine mammals or bison in order to treat a *Mycobacterium tuberculosis* infection. Additionally, methods of the invention include administering an antagonistic TNFR2 polypeptide (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7), such as a TNFR2 antibody that contains the CDR-H3 sequence or a variant thereof of TNFRAB1, TNFRAB2, or TNFR2A3) to a human or a non-human mammal in order to treat a *Mycobacterium avium paratuberculosis* infection. Particular methods of the invention include administering an antagonistic TNFR2 polypeptide (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7), such as a TNFR2 antibody that contains the CDR-H3 sequence or a variant thereof of TNFRAB1, TNFRAB2, or TNFR2A3) to bovine mammals or bison in order to treat a *Mycobacterium avium paratuberculosis* infection.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can also be administered to a mammalian subject (e.g., a human) for treating, or alleviating one or more symptoms of, parasitic infections caused by a protozoan parasite (e.g., an intestinal protozoa, a tissue protozoa, or a blood protozoa) or a helminthic parasite (e.g., a nematode, a helminth, an adenophorea, a secementea, a trematode, a fluke (blood flukes, liver flukes, intestinal flukes, and lung flukes), or a cestode). Exemplary protozoan parasites that can be treated according to the methods of the invention include, without limitation, *Entamoeba histolytica*, *Giardia lamblia*, *Cryptosporidium muris*, *Trypanosomatida gambiense*, *Trypanosomatida rhodesiense*, *Trypanosomatida cruzi*, *Leishmania mexicana*, *Leishmania braziliensis*, *Leishmania tropica*, *Leishmania donovani*, *Leishmania major*, *Toxoplasma gondii*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium falciparum*, *Plasmodium yoelli*, *Trichomonas vaginalis*, and *Histomonas meleagridis*. Exemplary helminthic parasites include *richuris trichiura*, *Ascaris lumbricoides*, *Enterobius*

*vermicularis*, *Ancylostoma duodenale*, *Necator americanus*, *Strongyloides stercoralis*, *Wuchereria bancrofti*, and *Dracunculus medinensis*, *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Fasciola hepatica*, *Fasciola gigantica*, *Heterophyes*, *Paragonimus westermani*, *Taenia solium*, *Taenia saginata*, *Hymenolepis nana*, and *Echinococcus granulosus*. Additional parasitic infections that

5 can be treated according to the methods of the invention include *Onchocercas volvulus*.

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) can also be administered to a mammalian subject (e.g., a human) in order to treat, or to alleviate one or more symptoms of, fungal infections. Examples of fungal infections that may be treated according to the methods of the invention include, without limitation, those caused by, e.g.,

10 *Aspergillus*, *Candida*, *Malassezia*, *Trichosporon*, *Fusarium*, *Acremonium*, *Rhizopus*, *Mucor*, *Pneumocystis*, and *Absidia*. Exemplary fungal infections that can be treated according to the methods of the invention also include *Pneumocystis carinii*, *Paracoccidioides brasiliensis* and *Histoplasma capsulatum*.

### 15 **Pharmaceutical compositions**

Pharmaceutical compositions containing an antagonistic TNFR2 polypeptide, such as a single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention can be prepared using methods known in the art. Pharmaceutical compositions of the invention may contain an antagonistic TNFR2 antibody, such as a dominant antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide,

20 antibody, or antigen-binding fragment thereof) that contains a CDR-H1 and CDR-H2 derived from a phenotype-neutral TNFR2 antibody and a CDR-H3 represented by the formula  $JZ^1JZ^2Z^4JZ^3JZ^5(J)_2Z^5Z^2Z^5$  or  $JZ^1JZ^2Z^4Z^3Z^5(J)_2Z^5Z^2Z^5(J)_2$  (wherein each J is independently a naturally occurring amino acid, each  $Z^1$  is independently a naturally occurring amino acid containing a cationic side-chain at physiological pH, each  $Z^2$  is independently a naturally occurring amino acid containing an anionic side-chain at

25 physiological pH, each  $Z^3$  is independently a naturally occurring amino acid containing a polar, uncharged side-chain at physiological pH, each  $Z^4$  is independently a glycine or alanine, and each  $Z^5$  is independently a naturally occurring amino acid containing a hydrophobic side-chain).

For instance, pharmaceutical compositions of the invention may contain an antagonistic TNFR2 polypeptide, such as a dominant antagonistic TNFR2 polypeptide (e.g., single-chain polypeptides,

30 antibodies, or antigen-binding fragments thereof) that contains a CDR-H1 and CDR-H2 derived from a phenotype-neutral TNFR2 antibody and a CDR-H3 represented by the formula JRJDGJSJY(J)<sub>2</sub>FDJ (SEQ ID NO: 278), JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279), QZ<sup>1</sup>VZ<sup>2</sup>Z<sup>4</sup>YZ<sup>3</sup>SZ<sup>5</sup>WYZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup> (SEQ ID NO: 265), or AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266).

In some embodiments, the CDR-H3 is derived from TNFRAB1 and have the amino acid sequence QRVDGYSSYWYFDV (SEQ ID NO: 25). The CDR-H3 may be derived from TNFRAB2 and have the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259). In some embodiments, the CDR-H3 is derived from TNFR2A3 and has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

Pharmaceutical compositions of the invention can be prepared using, e.g., physiologically



acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980); incorporated herein by reference), and in a desired form, e.g., in the form of lyophilized formulations or aqueous solutions. The compositions can also be prepared so as to contain the active agent (e.g., an antagonistic anti-TNFR2 antibody or fragment thereof) at a desired concentration. For example, a pharmaceutical composition of the invention may contain at least 10% (e.g., 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, 99%, 99.5%, 99.9%, or 100%) active agent by weight (w/w).

Additionally, an active agent (e.g., an antagonistic TNFR2 polypeptide of the invention, such as a dominant antagonistic TNFR2 polypeptide of the invention) that can be incorporated into a pharmaceutical formulation can itself have a desired level of purity. For example, a polypeptide, such as a single-chain polypeptide, antibody, or antigen-binding fragment thereof of the invention may be characterized by a certain degree of purity after isolating the antibody from cell culture media or after chemical synthesis, e.g., of a single-chain antibody fragment (e.g., scFv) by established solid phase peptide synthesis methods or native chemical ligation as described herein. An antagonistic TNFR2 polypeptide of the invention may be at least 10% pure prior to incorporating the antibody into a pharmaceutical composition (e.g., 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, 99%, 99.5%, 99.9%, 99.99%, or 100% pure).

Pharmaceutical compositions of anti-TNFR2 polypeptides of the invention can be prepared for storage as lyophilized formulations or aqueous solutions by mixing the antibody having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers typically employed in the art, e.g., buffering agents, stabilizing agents, preservatives, isotoniifiers, non-ionic detergents, antioxidants, and other miscellaneous additives. See, e.g., *Remington's Pharmaceutical Sciences*, 16th edition (Osol, ed. 1980; incorporated herein by reference). Such additives must be nontoxic to the recipients at the dosages and concentrations employed.

#### *Buffering agents*

Buffering agents help to maintain the pH in the range which approximates physiological conditions. They can be present at concentration ranging from about 2 mM to about 50 mM. Suitable buffering agents for use with antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention include both organic and inorganic acids and salts thereof such as citrate buffers {e.g., monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, etc.}, succinate buffers {e.g., succinic acid- monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid-disodium succinate mixture, etc.}, tartrate buffers (e.g., tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, etc.), fumarate buffers {e.g., fumaric acid-monosodium fumarate mixture, fumaric acid- disodium fumarate mixture, monosodium fumarate-disodium fumarate mixture, etc.}, gluconate buffers {e.g., gluconic acid-sodium glyconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium glyuconate mixture, etc.}, oxalate buffer {e.g., oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium

oxalate mixture, etc.), lactate buffers {e.g., lactic acid-sodium lactate mixture, lactic acid-sodium hydroxide mixture, lactic acid-potassium lactate mixture, etc.) and acetate buffers {e.g., acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, etc.}. Additionally, phosphate buffers, histidine buffers and trimethylamine salts such as Tris can be used.

#### 5 *Preservatives*

Preservatives can be added to a composition of the invention to retard microbial growth, and can be added in amounts ranging from 0.2%-1% (w/v). Suitable preservatives for use with antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention include phenol, benzyl alcohol, meta-cresol, methyl paraben, propyl paraben,  
10 octadecyldimethylbenzyl ammonium chloride, benzalconium halides (e.g., chloride, bromide, and iodide), hexamethonium chloride, and alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol. Isotonifiers sometimes known as "stabilizers" can be added to ensure isotonicity of liquid compositions of the invention and include polyhydric sugar alcohols, for example trihydric or higher sugar alcohols, such as glycerin, arabitol, xylitol, sorbitol and mannitol. Stabilizers refer  
15 to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, etc., organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol,  
20 sorbitol, xylitol, ribitol, myoinisitol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thioctic acid, sodium thioglycolate, thioglycerol,  $\alpha$ -monothioglycerol and sodium thio sulfate; low molecular weight polypeptides (e.g., peptides of 10 residues or fewer); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophilic polymers, such as polyvinylpyrrolidone  
25 monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trisaccharides such as raffinose; and polysaccharides such as dextran. Stabilizers can be present in the range from 0.1 to 10,000 weights per part of weight active protein.

#### *Detergents*

30 Non-ionic surfactants or detergents (also known as "wetting agents") can be added to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein. Suitable non-ionic surfactants include polysorbates (20, 80, etc.), polyoxamers (184, 188 etc.), Pluronic polyols, polyoxyethylene sorbitan monoethers (TWEEN®-20,  
35 TWEEN®-80, etc.). Non-ionic surfactants can be present in a range of about 0.05 mg/mL to about 1.0 mg/mL, for example about 0.07 mg/mL to about 0.2 mg/mL. Additional miscellaneous excipients include bulking agents (e.g., starch), chelating agents (e.g., EDTA), antioxidants (e.g., ascorbic acid, methionine, vitamin E), and cosolvents.

*Other pharmaceutical carriers*

Alternative pharmaceutically acceptable carriers that can be incorporated into a composition of the invention may include dextrose, sucrose, sorbitol, mannitol, starch, rubber arable, potassium phosphate, arginate, gelatin, potassium silicate, microcrystalline cellulose, polyvinylpyrrolidone, cellulose, water, syrups, methyl cellulose, methylhydroxy benzoate, propylhydroxy benzoate, talc, magnesium stearate, and mineral oils, but not limited to. A composition containing an antagonistic TNFR2 antibody of the invention may further include a lubricant, a humectant, a sweetener, a flavoring agent, an emulsifier, a suspending agent, and a preservative. Details of suitable pharmaceutically acceptable carriers and formulations can be found in *Remington's Pharmaceutical Sciences* (19th ed., 1995), which is incorporated herein by reference.

*Compositions and methods for combination therapy*

Pharmaceutical compositions of the invention may optionally include more than one active agent. For instance, compositions of the invention may contain an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, or antigen-binding fragment thereof) conjugated to, admixed with, or administered separately from another pharmaceutically active molecule, e.g., a cytotoxic agent, an antibiotic, or a T-lymphocyte (e.g., a gene-edited T-lymphocyte for use in CAR-T therapy). For instance, an antagonistic TNFR2 polypeptide or therapeutic conjugate thereof (e.g., a drug-antibody conjugate described herein), may be admixed with one or more additional active agents that can be used to treat cancer or another cell proliferation disorder (e.g., neoplasm). Alternatively, pharmaceutical compositions of the invention may be formulated for co-administration or sequential administration with one or more additional active agents that can be used to treat cancer or other cell proliferation disorders. Examples of additional active agents that can be used to treat cancer and other cell proliferation disorders and that can be conjugated to, admixed with, or administered separately from an antagonistic TNFR2 polypeptide of the invention include cytotoxic agents (e.g., those described herein), as well as antibodies that exhibit reactivity with a tumor antigen or a cell-surface protein that is overexpressed on the surface of a cancer cell. Exemplary antibodies that can be conjugated to, admixed with, or administered separately from antagonistic TNFR2 antibodies of the invention include, without limitation, Trastuzumab (HERCEPTIN®), Bevacizumab (AVASTIN®), Cetuximab (ERBITUX®), Panitumumab (VECTIBIX®), Ipilimumab (YERVOY®), Rituximab (RITUXAN® and MABTHERA®), Alemtuzumab (CAMPATH®), Ofatumumab (ARZERRA®), Gemtuzumab ozogamicin (MYLOTARG®), Brentuximab vedotin (ADCETRIS®), <sup>90</sup>Y-Ibritumomab Tiuxetan (ZEVALIN®), and <sup>131</sup>I-Tositumomab (BEXXAR®), which are described in detail in Scott et al. (*Cancer Immun.*, 12:14-21, 2012); incorporated herein by reference.

Additional agents that can be conjugated to, admixed with, or administered separately from antagonistic TNFR2 polypeptides of the invention include T-lymphocytes that exhibit reactivity with a specific antigen associated with a particular pathology. For instance, antagonistic TNFR2 polypeptides of the invention can be formulated for administration with a T cell that expresses a chimeric antigen receptor (CAR-T) in order to treat a cell proliferation disorder, such as a cancer described herein. Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) can synergize with CAR-T

therapy by preventing T-reg cells from deactivating T-lymphocytes that have been genetically modified so as to express tumor-reactive antigen receptors. In this way, CAR-T cells can be administered to a patient prior to, concurrently with, or after administration of an antagonistic TNFR2 polypeptide in order to treat a mammalian subject (e.g., a human) suffering from a cell proliferation disorder, such as cancer.

5 CAR-T therapy is a particularly robust platform for targeting cancer cells in view of the ability to genetically engineer T-lymphocytes to express an antigen receptor specific to a tumor-associated antigen. For instance, identification of antigens overexpressed on the surfaces of tumors and other cancer cells can inform the design and discovery of chimeric T cell receptors, which are often composed of cytoplasmic and transmembrane domains derived from a naturally-occurring T cell receptor operatively linked to an  
10 extracellular scFv fragment that specifically binds to a particular antigenic peptide. T cells can be genetically modified in order to express an antigen receptor that specifically binds to a particular tumor antigen by any of a variety of genome editing techniques described herein or known in the art. Exemplary techniques for modifying a T cell genome so as to incorporate a gene encoding a chimeric antigen receptor include the CRISPER/Cas, zinc finger nuclease, TALEN, ARCUS™ platforms described herein. Methods for the genetic  
15 engineering of CAR-T lymphocytes have been described, e.g., in WO 2014/127261, WO 2014/039523, WO 2014/099671, and WO 20120790000; the disclosures of each of which are incorporated by reference herein.

CAR-T cells useful in the compositions and methods of the invention include those that have been genetically modified such that the cell does not express the endogenous T cell receptor. For instance, a CAR-T cell may be modified by genome-editing techniques, such as those described herein, so as to suppress  
20 expression of the endogenous T cell receptor in order to prevent graft-versus-host reactions in a patient receiving a CAR-T infusion. Additionally or alternatively, CAR-T cells can be genetically modified so as to reduce the expression of one or more endogenous MHC proteins. This is a particularly useful technique for the infusion of allogeneic T-lymphocytes, as recognition of foreign MHC proteins represents one mechanism that promotes allograft rejection. One of skill in the art can also modify a T-lymphocyte so as to suppress the  
25 expression of immune suppressor proteins, such as programmed cell death protein 1 (PD-1) and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4). These proteins are cell surface receptors that, when activated, attenuate T cell activation. Infusion of CAR-T cells that have been genetically modified so as to diminish the expression of one or more immunosuppressor proteins represents one strategy that can be used to prolong the T-lymphocyte-mediated cytotoxicity *in vivo*.

30 In addition to deleting specific genes, one can also modify CAR-T cells in order to express a T cell receptor with a desired antigen specificity. For instance, one can genetically modify a T-lymphocyte in order to express a T cell receptor that specifically binds to a tumor-associated antigen in order to target infused T cells to cancer cells. An exemplary T cell receptor that may be expressed by a CAR-T cell is one that binds PD-L1, a cell surface protein that is often overexpressed on various tumor cells. As PD-L1 activates PD-1 on the  
35 surface of T-lymphocytes, targeting this tumor antigen with CAR-T therapy can synergize with antagonistic TNFR2 antibodies or antibody fragments of the invention in order to increase the duration of an immune response mediated by a T-lymphocyte *in vivo*. CAR-T cells can also be modified so as to express a T cell receptor that specifically binds an antigen associated with one or more infectious disease, such as an antigen derived from a viral protein, a bacterial cell, a fungus, or other parasitic organism.

Other pharmaceutical compositions of the invention include those that contain an antagonistic TNFR2 antibody or antibody fragment, interferon alpha, and/or one or more antibiotics that can be administered to a patient (e.g., a human patient) suffering from an infectious disease. For instance, an antagonistic TNFR2 antibody or antibody fragment can be conjugated to, admixed with, or administered separately from an antibiotic useful for treating one or more infectious diseases, such as amikacin, gentamicin, kanamycin, neomycin, netilmicin, tobramycin, paromomycin, streptomycin, spectinomycin, geldanamycin, herbimycin, rifaximin, loracarbef, ertapenem, doripenem, imipenem, meropenem, cefadroxil, cefazolin, cefazlexin, cefaclor, cefoxitin, cefprozil, cefuroxime, cefdinir, cefditoren, cefoperazone, clindamycin, lincomycin, daptomycin, erythromycin, linezolid, torezolid, amoxicillin, ampicillin, bacitracin, ciprofloxacin, doxycycline, and tetracycline, among others.

#### *Immunotherapy agents*

An antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) described herein may be admixed, conjugated, administered with, or administered separately from, an immunotherapy agent, for instance, for the treatment of a cancer or infectious disease, such as a cancer or infectious disease described herein. Exemplary immunotherapy agents useful in conjunction with the compositions and methods of the invention include, without limitation, an anti-CTLA-4 agent, an anti-PD-1 agent, an anti-PD-L1 agent, an anti-PD-L2 agent, an anti-TNF- $\alpha$  cross-linking agent, an anti-TRAIL cross-linking agent, an anti-CD27 agent, an anti-CD30 agent, an anti-CD40 agent, an anti-4-1BB agent, an anti-GITR agent, an anti-OX40 agent, an anti-TRAILR1 agent, an anti-TRAILR2 agent, and an anti-TWEAKR agent, as well as, for example, agents directed toward the immunological targets described in Table 1 of Mahoney et al., Cancer Immunotherapy, 14:561-584 (2015), the disclosure of which is incorporated herein by reference in its entirety. For instance, immunological target 4-1BB ligand may be targeted with an anti-4-1BB ligand antibody; immunological target OX40L may be targeted with an anti-OX40L antibody; immunological target GITR may be targeted with an anti-GITR antibody; immunological target CD27 may be targeted with an anti-CD27 antibody; immunological target TL1A may be targeted with an anti-TL1A antibody; immunological target CD40L may be targeted with an anti-CD40L antibody; immunological target LIGHT may be targeted with an anti-LIGHT antibody; immunological target BTLA may be targeted with an anti-BTLA antibody; immunological target LAG3 may be targeted with an anti-LAG3 antibody; immunological target TIM3 may be targeted with an anti-TIM3 antibody; immunological target Singlecs may be targeted with an anti-Singlecs antibody; immunological target ICOS ligand may be targeted with an anti-ICOS ligand antibody; immunological target B7-H3 may be targeted with an anti-B7-H3 antibody; immunological target B7-H4 may be targeted with an anti-B7-H4 antibody; immunological target VISTA may be targeted with an anti-VISTA antibody; immunological target TMIGD2 may be targeted with an anti-TMIGD2 antibody; immunological target BTNL2 may be targeted with an anti-BTNL2 antibody; immunological target CD48 may be targeted with an anti-CD48 antibody; immunological target KIR may be targeted with an anti-KIR antibody; immunological target LIR may be targeted with an anti-LIR antibody; immunological target ILT may be targeted with an anti-ILT antibody; immunological target NKG2D may be targeted with an anti-

NKG2D antibody; immunological target NKG2A may be targeted with an anti-NKG2A antibody; immunological target MICA may be targeted with an anti-MICA antibody; immunological target MICB may be targeted with an anti-MICB antibody; immunological target CD244 may be targeted with an anti-CD244 antibody; immunological target CSF1R may be targeted with an anti-CSF1R antibody; immunological target IDO may be targeted with an anti-IDO antibody; immunological target TGF $\beta$  may be targeted with an anti-TGF $\beta$  antibody; immunological target CD39 may be targeted with an anti-CD39 antibody; immunological target CD73 may be targeted with an anti-CD73 antibody; immunological target CXCR4 may be targeted with an anti-CXCR4 antibody; immunological target CXCL12 may be targeted with an anti-CXCL12 antibody; immunological target SIRPA may be targeted with an anti-SIRPA antibody; immunological target CD47 may be targeted with an anti-CD47 antibody; immunological target VEGF may be targeted with an anti-VEGF antibody; and immunological target neuropilin may be targeted with an anti-neuropilin antibody (see, e.g., Table 1 of Mahoney et al.).

Additional examples of immunotherapy agents that can be used in conjunction with the compositions and methods described herein include Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, gabapentin, antibodies to lymphoid cell surface receptors and/or lymphokines, antibodies to surface cancer proteins, and/or small molecular therapies like Vorinostat.

Using the methods of the invention, an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) described herein may be co-administered with (e.g., admixed with) or administered separately from an immunotherapy agent. For example, an antagonistic TNFR2 polypeptide of the invention (such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to a patient, such as a human patient suffering from a cancer or infectious disease, simultaneously or at different times. In some embodiments, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) is administered to the patient prior to administration of an immunotherapy agent to the patient. Alternatively, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to the patient after an immunotherapy agent. For example, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to the patient after a failed immunotherapy treatment. A physician of skill in the art can monitor the efficacy of immunotherapy treatment to determine whether the therapy has successfully ameliorated the pathology being treated (such as a cancer or infectious disease, e.g., a cancer or infectious disease described herein) using methods described herein and known in the art.

For instance, a physician of skill in the art may monitor the quantity of cancer cells in a sample isolated from a patient (e.g., a blood sample or biopsy sample), such as a human patient, for instance, using flow cytometry or FACS analysis. Additionally or alternatively, a physician of skill in the art can monitor the progression of a cancerous disease in a patient, for instance, by monitoring the size of one or more tumors in the patient, for example, by CT scan, MRI, or X-ray analysis. A physician of skill in the art

may monitor the progression of a cancer, such as a cancer described herein, by evaluating the quantity and/or concentration of tumor biomarkers in the patient, such as the quantity and/or concentration of cell surface-bound tumor associated antigens or secreted tumor antigens present in the blood of the patient as an indicator of tumor presence. A finding that the quantity of cancer cells, the size of a tumor, and/or the quantity or concentration of one or more tumor antigens present in the patient or in a sample isolated from the patient has not decreased, for instance, by a statistically significant amount following administration of the immunotherapy agent within a specified time period (e.g., from 1 day to 6 months, such as 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, or 6 months) can indicate that the immunotherapy treatment has failed to ameliorate the cancer. Based on this indication, a physician of skill in the art may administer an antagonistic TNFR2 polypeptide of the invention, such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein. Similarly, a physician of skill in the art may monitor the quantity of bacterial, fungal, or parasitic cells, or the quantity of viral particles in a sample isolated from a patient suffering from an infectious disease, such as an infectious disease described herein. Additionally or alternatively, a physician of skill in the art may monitor the progression of an infectious disease by evaluating the symptoms of a patient suffering from such a pathology. For instance, a physician may monitor the patient by determining whether the frequency and/or severity of one or more symptoms of the infectious disease have stabilized (e.g., remained the same) or decreased following treatment with an immunotherapy agent. A finding that the quantity of bacterial, fungal, or parasitic cells or viral particles in a sample isolated from the patient and/or a finding that the frequency or severity of one or more symptoms of the infectious disease have not decreased, for instance, by a statistically significant amount following administration of the immunotherapy agent within a specified time period (e.g., from 1 day to 6 months, such as 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, or 6 months) can indicate that the immunotherapy treatment has failed to ameliorate the infectious disease. Based on this indication, a physician of skill in the art may administer an antagonistic TNFR2 polypeptide of the invention, such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein.

#### *Chemotherapy agents and radiation therapy*

Additionally or alternatively, an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) described herein may be admixed, conjugated, administered with, or administered separately from, a chemotherapy agent, for example, for the treatment of cancer, such as a cancer described herein. Exemplary chemotherapy agents useful in conjunction with the compositions and methods of the invention include, without limitation, Abiraterone Acetate, ABITREXATE® (Methotrexate), ABRAXANE® (Paclitaxel Albumin), ADRIAMYCIN®, bleomycin, vinblastine, and dacarbazine (ABVD), ADRIAMYCIN®, bleomycin, vincristine sulfate, and etoposide phosphate (ABVE), ADRIAMYCIN®, bleomycin, vincristine sulfate, etoposide phosphate, prednisone, and cyclophosphamide (ABVE-PC), doxorubicin and cyclophosphamide (AC), doxorubicin, cyclophosphamide, and paclitaxel or docetaxel (AC-T), ADCETRIS® (Brentuximab Vedotin), cytarabine,

daunorubicin, and etoposide (ADE), ado-trastuzumab emtansine, ADRIAMYCIN® (doxorubicin hydrochloride), afatinib dimaleate, AFINITOR® (Everolimus), AKYNZEO® (netupitant and palonosetron hydrochloride), ALDARA® (imiquimod), aldesleukin, ALECENSA® (alectinib), alectinib, alemtuzumab, ALKERAN® for Injection (Melphalan Hydrochloride), ALKERAN® tablets (melphalan), ALIMTA® (pemetrexed disodium), ALOXI® (palonosetron hydrochloride), AMBOCHLORIN® (chlorambucil), AMBOCLOLIN® (Chlorambucil), aminolevulinic acid, anastrozole, aprepitant, AREDIA® (pamidronate disodium), ARIMIDEX® (anastrozole), AROMASIN® (exemestane), ARRANON® (nelarabine), arsenic trioxide, ARZERRA® (ofatumumab), asparaginase *Erwinia chrysanthemi*, AVASTIN® (bevacizumab), axitinib, azacitidine, BEACOPP Becenum (carmustine), BELEODAQ® (Belinostat), belinostat, bendamustine hydrochloride, bleomycin, etoposide, and cisplatin (BEP), bevacizumab, bexarotene, BEXXAR® (tositumomab and iodine <sup>131</sup>I tositumomab), bicalutamide, BiCNU (carmustine), bleomycin, blinatumomab, BLINCYTO® (blinatumomab), bortezomib, BOSULIF® (bosutinib), bosutinib, brentuximab vedotin, busulfan, BUSULFEX® (busulfan), cabazitaxel, cabozantinib-S-malate, CAF, CAMPATH® (alemtuzumab), CAMPTOSAR® (irinotecan hydrochloride), capecitabine, CAPOX, CARAC® (fluorouracil), carboplatin, CARBOPLATIN-TAXOL®, carfilzomib, CARMUBRIS® (carmustine), carmustine, carmustine implant, CASODEX® (bicalutamide), CEENU (lomustine), cisplatin, etoposide, and methotrexate (CEM), ceritinib, CERUBIDINE® (daunorubicin hydrochloride), CERVARIX® (recombinant HPV bivalent vaccine), cetuximab, chlorambucil, chlorambucil-prednisone, CHOP, cisplatin, CLAFEN® (cyclophosphamide), clofarabine, CLOFAREX® (clofarabine), CLOLAR® (Clofarabine), CMF, cobimetinib, cometriq (cabozantinib-S-malate), COPDAC, COPP, COPP-ABV, COSMEGEN® (dactinomycin), COTELLIC® (cobimetinib), crizotinib, CVP, cyclophosphamide, CYFOS® (ifosfamide), CYRAMZA® (ramucirumab), cytarabine, cytarabine liposome, CYTOSAR-U® (cytarabine), CYTOXAN® (cyclophosphamide), dabrafenib, dacarbazine, DACOGEN® (decitabine), dactinomycin, daratumumab, DARZALEX® (daratumumab), dasatinib, daunorubicin hydrochloride, decitabine, degarelix, denileukin diftitox, denosumab, DEPOCYT® (cytarabine liposome), dexamethasone, dexrazoxane hydrochloride, dinutuximab, docetaxel, DOXIL® (doxorubicin hydrochloride), doxorubicin hydrochloride, DOX-SL® (doxorubicin hydrochloride), DTIC-DOME® (dacarbazine), EFUDEX (fluorouracil), ELITEK® (rasburicase), ELLENCE® (epirubicin hydrochloride), elotuzumab, ELOXATIN® (oxaliplatin), eltrombopag olamine, EMEND® (aprepitant), EMPLICITI® (elotuzumab), enzalutamide, epirubicin hydrochloride, EPOCH, ERBITUX® (cetuximab), eribulin mesylate, ERIVEDGE® (vismodegib), erlotinib hydrochloride, ERWINAZE® (asparaginase *Erwinia chrysanthemi*), ETOPOPHOS® (etoposide phosphate), etoposide, etoposide phosphate, EVACET® (doxorubicin hydrochloride liposome), everolimus, EVISTA® (raloxifene hydrochloride), EVOMELA® (melphalan hydrochloride), exemestane, 5-FU (5-fluorouracil), FARESTON® (toremifene), FARYDAK® (panobinostat), FASLODEX® (fulvestrant), FEC, FEMARA® (letrozole), filgrastim, FLUDARA® (fludarabine phosphate), fludarabine phosphate, FLUOROPLEX® (fluorouracil), fluorouracil injection, flutamide, FOLEX® (methotrexate), FOLEX® PFS (methotrexate), FOLFIRI, FOLFIRI-bevacizumab, FOLFIRI-cetuximab, FOLFIRINOX, FOLFOX, FOLOTYN® (pralatrexate), FU-LV, fulvestrant, GARDASIL® (recombinant HPV quadrivalent vaccine), GARDASIL 9® (recombinant HPV nonavalent vaccine), GAZYVA® (obinutuzumab), gefitinib, gemcitabine hydrochloride, gemcitabine-



cisplatin, gemcitabine-oxaliplatin, gemtuzumab ozogamicin, GEMZAR® (gemcitabine hydrochloride),  
 GILOTRIF® (afatinib dimaleate), GLEEVEC® (imatinib mesylate), GLIADEL® (carmustine implant),  
 GLIADEL® wafer (carmustine implant), glucarpidase, goserelin acetate, HALAVEN® (eribulin mesylate),  
 HERCEPTIN® (trastuzumab), HPV bivalent vaccine, HYCAMTIN® (topotecan hydrochloride), Hyper-  
 5 CVAD, IBRANCE (palbociclib), IBRITUMOMAB® tiuxetan, ibrutinib, ICE, ICLUSIG® (ponatinib  
 hydrochloride), IDAMYCIN® (idarubicin hydrochloride), idarubicin hydrochloride, idelalisib, IFEX®  
 (ifosfamide), ifosfamide, ifosfamidum, IL-2 (aldesleukin), imatinib mesylate, IMBRUVICA® (ibrutinib),  
 ilmiquimod, IMLYGIC® (talimogene laherparepvec), INLYTA (axitinib), recombinant interferon alpha-2b,  
 intron A, tositumomab, such as <sup>131</sup>I tositumomab, ipilimumab, IRESSA® (gefitinib), irinotecan  
 10 hydrochloride, ISTODAX® (romidepsin), ixabepilone, ixazomib citrate, IXEMPRA® (ixabepilone),  
 JAKAFI® (ruxolitinib phosphate), JEVTANA® (cabazitaxel), KADCYLA® (ado-trastuzumab emtansine),  
 KEOXIFENE® (raloxifene hydrochloride), KEPIVANCE® (palifermin), KEYTRUDA® (pembrolizumab),  
 KYPROLIS® (carfilzomib), lanreotide acetate, lapatinib ditosylate, lenalidomide, lenvatinib mesylate,  
 LENVIMA® (lenvatinib mesylate), letrozole, leucovorin calcium, leukeran (chlorambucil), leuprolide  
 15 acetate, levulan (aminolevulinic acid), LINFOLIZIN® (chlorambucil), LIPODOX® (doxorubicin  
 hydrochloride liposome), lomustine, LONSURF® (trifluridine and tipiracil hydrochloride), LUPRON®  
 (leuprolide acetate), LYNPARZA® (olaparib), MARQIBO® (vincristine sulfate liposome), MATULANE®  
 (procarbazine hydrochloride), mechlorethamine hydrochloride, megestrol acetate, MEKINIST®  
 (trametinib), melphalan, melphalan hydrochloride, mercaptopurine, MESNEX® (mesna),  
 20 METHAZOLASTONE® (temozolomide), methotrexate, methotrexate LPF, MEXATE® (methotrexate),  
 MEXATE-AQ® (methotrexate), mitomycin C, mitoxantrone hydrochloride, MITOZYTREX® (mitomycin C),  
 MOPP, MOZOBIL® (plerixafor), MUSTARGEN® (mechlorethamine hydrochloride), MUTAMYCIN®  
 (mitomycin C), MYLERAN® (busulfan), MYLOSAR® (azacitidine), MYLOTARG® (gemtuzumab  
 ozogamicin), nanoparticle paclitaxel, NAVELBINE® (vinorelbine tartrate), NECITUMUMAB, nelarabine,  
 25 NEOSAR® (cyclophosphamide), netupitant and palonosetron hydrochloride, NEUPOGEN® (filgrastim),  
 NEXAVAR® (sorafenib tosylate), NILOTINIB, NINLARO® (ixazomib citrate), nivolumab, NOLVADEX®  
 (tamoxifen citrate), NPLATE® (romiplostim), obinutuzumab, ODOMZO® (sonidegib), OEPA,  
 ofatumumab, OFF, olaparib, omacetaxine mepesuccinate, ONCASPAR® (pegaspargase), ondansetron  
 hydrochloride, ONIVYDE® (irinotecan hydrochloride liposome), ONTAK® (denileukin diftitox), OPDIVO®  
 30 (nivolumab), OPPA, osimertinib, oxaliplatin, paclitaxel, paclitaxel albumin-stabilized nanoparticle  
 formulation, PAD, palbociclib, palifermin, palonosetron hydrochloride, palonosetron hydrochloride and  
 netupitant, pamidronate disodium, panitumumab, panobinostat, PARAPLAT® (carboplatin),  
 PARPLATIN® (carboplatin), pazopanib hydrochloride, PCV, pegaspargase, peginterferon alpha-2b, PEG-  
 INTRON® (peginterferon alpha-2b), pembrolizumab, pemetrexed disodium, PERJETA® (pertuzumab),  
 35 pertuzumab, PLATINOL® (cisplatin), PLATINOL-AQ® (cisplatin), plerixafor, pomalidomide, POMALYST®  
 (pomalidomide), ponatinib hydrochloride, PORTRAZZA® (necitumumab), pralatrexate, prednisone,  
 procarbazine hydrochloride, PROLEUKIN® (aldesleukin), PROLIA® (denosumab), PROMACTA  
 (eltrombopag olamine), PROVENGE® (sipuleucel-T), PURINETHOL® (mercaptopurine), PURIXAN®  
 (mercaptopurine), <sup>223</sup>Ra dichloride, raloxifene hydrochloride, ramucirumab, rasburicase, R-CHOP, R-

CVP, recombinant human papillomavirus (HPV), recombinant interferon alpha-2b, regorafenib, R-EPOCH, REVLIMID® (lenalidomide), RHEUMATREX® (methotrexate), RITUXAN® (rituximab), rolapitant hydrochloride, romidepsin, romiplostim, rubidomycin (daunorubicin hydrochloride), ruxolitinib phosphate, SCLEROSOL® intrapleural aerosol (talc), siltuximab, sipuleucel-T, somatuline depot (lanreotide acetate),

5 sonidegib, sorafenib tosylate, SPRYCEL® (dasatinib), STANFORD V, sterile talc powder (talc), STERITALC® (talc), STIVARGA® (regorafenib), sunitinib malate, SUTENT® (sunitinib malate), SYLATRON® (peginterferon alpha-2b), SYLVANT® (siltuximab), SYNOVIR® (thalidomide), SYNTRIBO® (omacetaxine mepesuccinate), thioguanine, TAC, TAFINLAR® (dabrafenib), TAGRISSO® (osimertinib), talimogene laherparepvec, tamoxifen citrate, tarabine PFS (cytarabine), TARCEVA (erlotinib

10 hydrochloride), TARGRETIN® (bexarotene), TASIGNA® (nilotinib), TAXOL® (paclitaxel), TAXOTERE® (docetaxel), TEMODAR® (temozolomide), temsirolimus, thalidomide, THALOMID® (thalidomide), thioguanine, thiotepa, TOLAK® (topical fluorouracil), topotecan hydrochloride, toremifene, TORISEL® (temsirolimus), TOTECT® (dexrazoxane hydrochloride), TPF, trabectedin, trametinib, TREANDA® (bendamustine hydrochloride), trifluridine and tipiracil hydrochloride, TRISENOX® (arsenic trioxide),

15 TYKERB® (lapatinib ditosylate), UNITUXIN® (dinutuximab), uridine triacetate, VAC, vandetanib, VAMP, VARUBI® (rolapitant hydrochloride), vectibix (panitumumab), VelP, VELBAN® (vinblastine sulfate), VELCADE® (bortezomib), VELSAR (vinblastine sulfate), VEMURAFENIB, VIADUR (leuprolide acetate), VIDAZA (azacitidine), vinblastine sulfate, VINCASAR® PFS (vincristine sulfate), vincristine sulfate, vinorelbine tartrate, VIP, vismodegib, VISTOGARD® (uridine triacetate), VORAXAZE® (glucarpidase),

20 vorinostat, VOTRIENT® (pazopanib hydrochloride), WELLCOVORIN® (leucovorin calcium), XALKORI® (crizotinib), XELODA® (capecitabine), XELIRI, XELOX, XGEVA® (denosumab), XOFIGO® (<sup>223</sup>Ra dichloride), XTANDI® (enzalutamide), YERVOY® (ipilimumab), YONDELIS® (trabectedin), ZALTRAP® (ziv-aflibercept), ZARXIO® (filgrastim), ZELBORAF® (vemurafenib), ZEVALIN® (ibrutinomab tiuxetan), ZINECARD® (dexrazoxane hydrochloride), ziv-aflibercept, ZOFRAN® (ondansetron hydrochloride),

25 ZOLADEX® (goserelin acetate), zoledronic acid, ZOLINZA® (vorinostat), ZOMETA® (zoledronic acid), ZYDELIG® (idelalisib), ZYKADIA® (ceritinib), and ZYTIGA (abiraterone acetate).

Using the methods of the invention, an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) described herein may be co-administered with (e.g., admixed with) or administered separately from a chemotherapy agent for the

30 treatment of cancer. For example, an antagonistic TNFR2 polypeptide of the invention (such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to a patient, such as a human patient suffering from a cancer, simultaneously or at different times. In some embodiments, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) is administered to the patient

35 prior to administration of a chemotherapy agent to the patient. Alternatively, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to the patient after a chemotherapy agent. For example, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to the patient after a failed chemotherapy

treatment. A physician of skill in the art can monitor the efficacy of chemotherapy treatment to determine whether the therapy has successfully ameliorated the pathology being treated (such as a cancer described herein) using methods described herein and known in the art.

5 For instance, a physician of skill in the art may monitor the quantity of cancer cells in a sample isolated from a patient (e.g., a blood sample or biopsy sample), such as a human patient, for instance, using flow cytometry or FACS analysis. Additionally or alternatively, a physician of skill in the art can monitor the progression of a cancerous disease in a patient, for instance, by monitoring the size of one or more tumors in the patient, for example, by CT scan, MRI, or X-ray analysis. A physician of skill in the art may monitor the progression of a cancer, such as a cancer described herein, by evaluating the quantity and/or concentration of tumor biomarkers in the patient, such as the quantity and/or concentration of cell surface-bound tumor associated antigens or secreted tumor antigens present in the blood of the patient as an indicator of tumor presence. A finding that the quantity of cancer cells, the size of a tumor, and/or the quantity or concentration of one or more tumor antigens present in the patient or a sample isolated from the patient has not decreased, for instance, by a statistically significant amount following  
10 administration of the chemotherapy agent within a specified time period (e.g., from 1 day to 6 months, such as 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, or 6 months) can indicate that the chemotherapy treatment has failed to ameliorate the cancer. Based on this indication, a physician of skill in the art may administer an antagonistic TNFR2 polypeptide of the invention, such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein.  
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Additionally or alternatively, an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) described herein may be administered simultaneously with, or administered separately from, radiation therapy. For instance, a physician of skill in the art may administer radiation therapy to a patient, such as a human patient suffering from a cancer described herein, by treating the patient with external and/or internal electromagnetic radiation. The energy delivered by such radiation, which is typically in the form of X-rays, gamma rays, and similar forms of low-wavelength energy, can cause oxidative damage to the DNA of cancer cells, thereby leading to cell death, for instance, by apoptosis. External radiation therapy can be administered, for instance, using machinery such as a radiation beam to expose the patient to a controlled pulse of electromagnetic  
30 radiation. Additionally or alternatively, the patient may be administered internal radiation, for instance, by administering to the patient a therapeutic agent that contains a radioactive substituent, such as agents that contain  $^{223}\text{Ra}$  or  $^{131}\text{I}$ , which emit high-energy alpha and beta particles, respectively. Exemplary therapeutic agents that may be conjugated to a radiolabel include, for example, small molecule chemotherapeutics, antibodies, and antigen-binding fragments thereof, among others. For instance, an antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct) of the invention may be conjugated to a radioactive substituent or a moiety that ligate such a substituent, for example, using bond-forming techniques known in the art or described herein. Such conjugates can be administered to the subject in order to deliver a therapeutic dosage of radiation therapy and a TNFR2 antagonist of the invention in a simultaneous administration (see, for  
35

example, "Antagonistic TNFR2 polypeptide conjugates," above).

In some embodiments, the antagonistic TNFR2 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) is administered to the patient after failed radiation treatment. A physician of skill in the art can monitor the efficacy of radiation  
5 treatment to determine whether the therapy has successfully ameliorated the pathology being treated (such as a cancer described herein) using, e.g., methods described herein. For instance, a physician of skill in the art may monitor the quantity of cancer cells in a sample isolated from a patient (e.g., a blood sample or biopsy sample), such as a human patient, for instance, using flow cytometry or FACS analysis. Additionally or alternatively, a physician of skill in the art can monitor the progression of a cancerous  
10 disease in a patient, for instance, by monitoring the size of one or more tumors in the patient, for example, by CT scan, MRI, or X-ray analysis. A physician of skill in the art may monitor the progression of a cancer, such as a cancer described herein, by evaluating the quantity and/or concentration of tumor biomarkers in the patient, such as the quantity and/or concentration of cell surface-bound tumor associated antigens or secreted tumor antigens present in the blood of the patient as an indicator of  
15 tumor presence. A finding that the quantity of cancer cells, the size of a tumor, and/or the quantity or concentration of one or more tumor antigens present in the patient or a sample isolated from the patient has not decreased, for instance, by a statistically significant amount following administration of the radiation therapy within a specified time period (e.g., from 1 day to 6 months, such as 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5  
20 months, or 6 months) can indicate that the radiation treatment has failed to ameliorate the cancer. Based on this indication, a physician of skill in the art may administer an antagonistic TNFR2 polypeptide of the invention, such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein.

In some embodiments, a physician of skill in the art may administer to a patient suffering from  
25 cancer a chemotherapeutic agent, radiation therapy, and a TNFR2 antagonist of the invention (such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein). The TNFR2 antagonist of the invention, chemotherapeutic agent, and radiation therapy may be administered to the patient simultaneously (for instance, in a single pharmaceutical composition or as multiple compositions administered to the patient at the same time) or at different times. In some embodiments,  
30 the TNFR2 antagonist (such as an antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct of the invention) is administered to the patient first, and the chemotherapeutic agent and radiation therapy follow. Alternatively, the TNFR2 antagonist (such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct of the invention) may be administered to the patient following chemotherapy and radiation treatment. For example, the antagonistic TNFR2  
35 polypeptide (e.g., a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein) may be administered to the patient after failed chemotherapy and/or radiation treatment.

A physician of skill in the art can monitor the efficacy of chemotherapy and radiation treatment to determine whether the therapy has successfully ameliorated the pathology being treated (such as a

cancer described herein) using methods described herein, such as the methods described above. For instance, a physician of skill in the art may monitor the quantity of cancer cells in a sample isolated from a patient (e.g., a blood sample or biopsy sample), such as a human patient, for instance, using flow cytometry or FACS analysis. Additionally or alternatively, a physician of skill in the art can monitor the progression of a cancerous disease in a patient, for instance, by monitoring the size of one or more tumors in the patient, for example, by CT scan, MRI, or X-ray analysis. A physician of skill in the art may monitor the progression of a cancer, such as a cancer described herein, by evaluating the quantity and/or concentration of tumor biomarkers in the patient, such as the quantity and/or concentration of cell surface-bound tumor associated antigens or secreted tumor antigens present in the blood of the patient as an indicator of tumor presence and even measure serum soluble TNFR2. One skilled in the art would expect a decrease in the number of activated T-regs, and increase in the numbers of T effectors and a decrease in the total number of cancer cells. Because of the specificity of these TNFR2 antibodies for cancer, the clinical monitoring would be expected to be most dramatic in the tumor microenvironment. A finding that the quantity of cancer cells, the size of a tumor, and/or the quantity or concentration of one or more tumor antigens present in the patient or a sample isolated from the patient has not decreased, for instance, by a statistically significant amount following administration of the chemotherapy agent and radiation within a specified time period (e.g., from 1 day to 6 months, such as 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, or 6 months) can indicate that the chemotherapy and radiation treatment has failed to ameliorate the cancer. Based on this indication, a physician of skill in the art may administer an antagonistic TNFR2 polypeptide of the invention, such as a single-chain polypeptide, antibody, antigen-binding fragment thereof, or construct described herein.

#### *Blood-brain barrier penetration*

In certain embodiments, antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure that the therapeutic compositions of the invention cross the BBB (if desired), they can be formulated, for example, in liposomes. Methods of manufacturing liposomes have been described, e.g., U.S. Patent Nos. 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties that are selectively transported into specific cells or organs, thereby enhancing targeted drug delivery (see, e.g., V. V. Ranade (*J. Clin. Pharmacol.* 29:685, 1989)). Exemplary targeting moieties include, e.g., folate or biotin (see, e.g., U.S. Patent. No. 5,416,016); mannosides (Umezawa et al. (*Biochem. Biophys. Res. Commun.* 153:1038, 1988)); antibodies (P. G. Bloeman et al. (*FEBS Lett.* 357:140, 1995); M. Owais et al. (*Antimicrob. Agents Chemother.* 39:180, 1995)); surfactant protein A receptor (Briscoe et al. (*Am. J. Physiol.* 1233:134, 1995)); the disclosures of each of which are incorporated herein by reference.

**Routes of administration and dosing**

Antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention can be administered to a mammalian subject (e.g., a human) by a variety of routes such as orally, transdermally, subcutaneously, intranasally, intravenously, 5 intramuscularly, intraocularly, intratumorally, parenterally, topically, intrathecally and intracerebroventricularly. The most suitable route for administration in any given case will depend on the particular polypeptide administered, the patient, pharmaceutical formulation methods, administration methods (e.g., administration time and administration route), the patient's age, body weight, sex, severity of the diseases being treated, the patient's diet, and the patient's excretion rate.

10 The effective dose of an anti-TNFR2 polypeptide of the invention can range from about 0.0001 to about 100 mg/kg of body weight per single (e.g., bolus) administration, multiple administrations or continuous administration, or to achieve a serum concentration of 0.0001-5000 µg/mL serum concentration per single (e.g., bolus) administration, multiple administrations or continuous administration, or any effective range or value therein depending on the condition being treated, the route of 15 administration and the age, weight, and condition of the subject. In certain embodiments, e.g., for the treatment of cancer, each dose can range from about 0.0001 mg to about 500 mg/kg of body weight. For instance, a pharmaceutical composition of the invention may be administered in a daily dose in the range of 0.001-100 mg/kg (body weight). The dose may be administered one or more times (e.g., 2-10 times) per day, week, month, or year to a mammalian subject (e.g., a human) in need thereof.

20 Therapeutic compositions can be administered with medical devices known in the art. For example, in an embodiment, a therapeutic composition of the invention can be administered with a needleless hypodermic injection device, such as the devices disclosed in U.S. Pat. Nos. 5,399,163; 5,383,851; 5,312,335; 5,064,413; 4,941,880; 4,790,824; or 4,596,556. Examples of well-known implants and modules useful in the invention include: U.S. Pat. No. 4,487,603, which discloses an implantable 25 micro-infusion pump for dispensing medication at a controlled rate; U.S. Pat. No. 4,486,194, which discloses a therapeutic device for administering medicaments through the skin; U.S. Pat. No. 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; U.S. Pat. No. 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; U.S. Pat. No. 4,439,196, which discloses an osmotic drug delivery system having multi-chamber 30 compartments; and U.S. Pat. No. 4,475,196, which discloses an osmotic drug delivery system. These patents are incorporated herein by reference. Many other such implants, delivery systems, and modules are known to those skilled in the art.

**Kits containing antagonistic anti-TNFR2 polypeptides**

35 This invention also includes kits that contain antagonistic anti-TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof). The kits provided herein may contain any of the antagonistic TNFR2 polypeptides described above, as well as any of the polynucleotides encoding these antibodies, vectors containing these polynucleotides, or cells engineered to express and secrete antibodies of the invention (e.g., prokaryotic or eukaryotic cells). A kit of this

invention may include reagents that can be used to produce the compositions of the invention (e.g., antagonistic anti-TNFR2 polypeptides, such as single-chain polypeptides, antibodies, conjugates containing antagonistic anti-TNFR2 polypeptides, polynucleotides encoding antagonistic anti-TNFR2 polypeptides, vectors containing these polynucleotides). Optionally, kits of the invention may include reagents that can induce the expression of antagonistic TNFR2 polypeptides within cells (e.g., mammalian cells), such as doxycycline or tetracycline. In other cases, a kit of the invention may contain a compound capable of binding and detecting a fusion protein that contains an antagonistic TNFR2 antibody and an epitope tag. For instance, in such cases a kit of the invention may contain maltose, glutathione, a nickel-containing complex, an anti-FLAG antibody, an anti-myc antibody, an anti-HA antibody, biotin, or streptavidin.

Kits of the invention may also include reagents that are capable of detecting an antagonistic TNFR2 polypeptide (e.g., single-chain polypeptide, antibody, or fragment thereof) directly. Examples of such reagents include secondary antibodies that selectively recognize and bind particular structural features within the Fc region of an anti-TNFR2 antibody of the invention. Kits of the invention may contain secondary antibodies that recognize the Fc region of an antagonistic TNFR2 antibody and that are conjugated to a fluorescent molecule. These antibody-fluorophore conjugates provide a tool for analyzing the localization of antagonistic anti-TNFR2 antibodies, e.g., in a particular tissue or cultured mammalian cell using established immunofluorescence techniques. In some embodiments, kits of the invention may include additional fluorescent compounds that exhibit known sub-cellular localization patterns. These reagents can be used in combination with another antibody-fluorophore conjugate, e.g., one that specifically recognizes a different receptor on the cell surface in order to analyze the localization of an anti-TNFR2 antibody relative to other cell-surface proteins.

Kits of the invention may also contain a reagent that can be used for the analysis of a patient's response to treatment by administration of antagonistic TNFR2 polypeptides (e.g., single-chain polypeptides, antibodies, and antigen-binding fragments thereof) of the invention. For instance, kits of the invention may include an antagonistic TNFR2 antibody and one or more reagents that can be used to determine the quantity of T-reg cells in a blood sample withdrawn from a subject (e.g., a human) that is undergoing treatment with an antibody of the invention. Such a kit may contain, e.g., antibodies that selectively bind cell-surface antigens presented by T-reg cells, such as CD4 and CD25. Optionally, these antibodies may be labeled with a fluorescent dye, such as fluorescein or tetramethylrhodamine, in order to facilitate analysis of T-reg cells by fluorescence-activated cell sorting (FACS) methods known in the art. Kits of the invention may optionally contain one or more reagents that can be used to quantify tumor-reactive T-lymphocytes in order to determine the effectiveness of an antagonistic TNFR2 antibody of the invention in restoring tumor-infiltrating lymphocyte proliferation. For instance, kits of the invention may contain an antibody that selectively binds cell-surface markers on the surface of a cytotoxic T cell, such as CD8 or CD3. Optionally, these antibodies may be labeled with fluorescent molecules so as to enable quantitation by FACS analysis.

A kit of the invention may also contain one or more reagents useful for determining the affinity and selectivity of an antagonistic TNFR2 polypeptide of the invention for one or more peptides derived

from TNFR2 (e.g., a peptide containing the sequence of any one of SEQ ID NOs: 11, 19, 20, 34-117, 285, or 286). For instance, a kit may contain an antagonistic TNFR2 polypeptide and one or more reagents that can be used in an ELISA assay to determine the  $K_D$  of an antibody of the invention for one or more peptides that present a TNFR2 epitope in a conformation similar to that of the epitope in the native protein. A kit may contain, e.g., a microtiter plate containing wells that have been previously conjugated to avidin, and may contain a library of TNFR2-derived peptides, each of which conjugated to a biotin moiety. Such a kit may optionally contain a secondary antibody that specifically binds to the Fc region of an antagonistic TNFR2 antibody of the invention, and the secondary antibody may be conjugated to an enzyme (e.g., horseradish peroxidase) that catalyzes a chemical reaction that results in the emission of luminescent light.

Kits of the invention may also contain antagonistic TNFR2 polypeptides of the invention and reagents that can be conjugated to such an antibody, including those previously described (e.g., a cytotoxic agent, a fluorescent molecule, a bioluminescent molecule, a molecule containing a radioactive isotope, a molecule containing a chelating group bound to a paramagnetic ion, etc). These kits may additionally contain instructions for how the conjugation of an antagonistic TNFR2 antibody of the invention to a second molecule, such as those described above, can be achieved.

A kit of the invention may also contain a vector containing a polynucleotide that encodes an antagonistic anti-TNFR2 polypeptide, such as any of the vectors described herein. Alternatively, a kit may include mammalian cells (e.g., CHO cells) that have been genetically altered to express and secrete antagonistic TNFR2 antibodies or fragments thereof from the nuclear genome of the cell. Such a kit may also contain instructions describing how expression of the antagonistic TNFR2 antibody or fragment thereof from a polynucleotide can be induced, and may additionally include reagents (such as, e.g., doxycycline or tetracycline) that can be used to promote the transcription of these polynucleotides. Such kits may be useful for the manufacture of antagonistic TNFR2 antibodies or antigen-binding fragments thereof of the invention.

Other kits of the invention may include tools for engineering a prokaryotic or eukaryotic cell (e.g., a CHO cell or a BL21(DE3) *E. coli* cell) so as to express and secrete an antagonistic TNFR2 polypeptide of the invention from the nuclear genome of the cell. For example, a kit may contain CHO cells stored in an appropriate media and optionally frozen according to methods known in the art. The kit may also provide a vector containing a polynucleotide that encodes a nuclease (e.g., such as the CRISPER/Cas, zinc finger nuclease, TALEN, ARCUS™ nucleases described herein) as well as reagents for expressing the nuclease in the cell. The kit can additionally provide tools for modifying the polynucleotide that encodes the nuclease so as to enable one to alter the DNA sequence of the nuclease in order to direct the cleavage of a specific target DNA sequence of interest. Examples of such tools include primers for the amplification and site-directed mutagenesis of the polynucleotide encoding the nuclease of interest. The kit may also include restriction enzymes that can be used to selectively excise the nuclease-encoding polynucleotide from the vector and subsequently re-introduce the modified polynucleotide back into the vector once the user has modified the gene. Such a kit may also include a DNA ligase that can be used to catalyze the formation of covalent phosphodiester linkages between the modified nuclease-encoding



polynucleotide and the target vector. A kit of the invention may also provide a polynucleotide encoding an antagonistic anti-TNFR2 antibody or fragment thereof, as well as a package insert describing the methods one can use to selectively cleave a particular DNA sequence in the genome of the cell in order to incorporate the polynucleotide encoding an antagonistic TNFR2 antibody into the genome at this site.

5 Optionally, the kit may provide a polynucleotide encoding a fusion protein that contains an antagonistic TNFR2 antibody or fragment thereof and an additional polypeptide, such as, e.g., those described herein.

### Examples

The following examples are put forth so as to provide those of ordinary skill in the art with a description of how the compositions and methods claimed herein are performed, made, and evaluated, and are intended to be purely exemplary of the invention and are not intended to limit the scope of what the inventor regards as her invention.

#### 15 **Example 1. Mapping the discrete epitopes within TNFR2 that interact with TNFRAB1 and TNFRAB2**

Libraries of linear, cyclic, and bicyclic peptides derived from human TNFR2 were screened for distinct sequences within the protein that exhibit high affinity for TNFR2 antibody TNFRAB2. In order to screen conformational epitopes within TNFR2, peptides from distinct regions of the primary protein sequence were conjugated to one another to form chimeric peptides. These peptides contained cysteine residues at strategic positions within their primary sequences (see, e.g., Figure 3, SEQ ID NOs: 34-117 and 134-252). This facilitated an intramolecular cross-linking strategy that was used to constrain individual peptides to a one of a wide array of three dimensional conformations. Unprotected thiols of cysteine residues were cross-linked via nucleophilic substitution reactions with divalent and trivalent electrophiles, such as 2,6-bis(bromomethyl)pyridine and 1,3,5-tris(bromomethyl)benzene, so as to form conformationally restricted cyclic and bicyclic peptides, respectively. In this way, peptides containing unique combinations of amino acids from disparate regions of the TNFR2 primary sequence were constrained so as to structurally pre-organize epitopes that may resemble those presented in the native TNFR2 tertiary structure. Libraries containing these peptides were screened by immobilizing peptides to distinct regions of a solid surface and treating the surface in turn with TNFRAB1 or TNFRAB2, secondary antibody conjugated to horseradish peroxidase (HRP), and HRP substrate (2,2'-azino-di-3-ethylbenzthiazoline sulfonate) in the presence of hydrogen peroxide. The solid surface was washed in between treatment with successive reagents so as to remove excess or non-specifically bound materials. The luminescence of each region of each surface was subsequently analyzed using a charge coupled device (CCD) - camera and an image processing system.

35 The "Constrained Libraries of Peptides on Surfaces" (CLIPS) platform starts with the conversion of the target protein, e.g., TNFR2, into a library of up to 10,000 overlapping peptide constructs, using a combinatorial matrix design (Timmerman et al., J. Mol. Recognit., 20: 283-29, 2007). On a solid carrier, a matrix of linear peptides is synthesized, which are subsequently shaped into spatially defined CLIPS constructs. Constructs representing multiple parts of the discontinuous epitope in the correct

conformation bind the antibody with high affinity, which is detected and quantified. Constructs presenting the incomplete epitope bind the antibody with lower affinity, whereas constructs not containing the epitope do not bind at all. Affinity information is used in iterative screens to define the sequence and conformation of epitopes in detail. The raw luminescence data obtained from these ELISA experiments are reported in Figures 3A and 3B for TNFRAB1 and TNFRAB2, respectively. These results informed the analysis of epitopes present on the surface of TNFR2 that bind antagonistic TNFR2 antibodies. Structural models of TNFR2 illustrating epitopes that bind such antibodies are shown in Figures 4 and 15A-15C.

#### 10 *Peptide synthesis*

To reconstruct epitopes of the target molecule a library of peptides was synthesized. An amino functionalized polypropylene support was obtained by grafting a proprietary hydrophilic polymer formulation via reaction with t-butyloxycarbonyl-hexamethylenediamine (BocHMDA) using dicyclohexylcarbodiimide (DCC) with N-hydroxybenzotriazole (HOBt) and subsequent cleavage of the Boc-groups using trifluoroacetic acid (TFA). Standard Fmoc-peptide synthesis was used to synthesize peptides on the amino-functionalized solid support by custom modified JANUS® liquid handling stations (Perkin Elmer). CLIPS technology allows one to structure peptides into single loops, double-loops, triple loops, sheet-like folds, helix-like folds and combinations thereof. CLIPS templates are coupled to cysteine residues. The side-chains of multiple cysteines in the peptides are coupled to one or two CLIPS templates. For example, a 0.5 mM solution of the CLIPS template (2,6-bis(bromomethyl)pyridine) is dissolved in ammonium bicarbonate (20 mM, pH 7.8)/acetonitrile (1:3(v/v)). This solution is added to a surface-bound peptide array. The CLIPS template will react with side-chains of two cysteines as present in the solid-phase bound peptides of the peptide-arrays (455 wells plate with 3 µl wells). The peptide arrays are gently shaken in the solution for 30 to 60 minutes while completely covered in solution. Finally, the peptide arrays are washed extensively with excess of H<sub>2</sub>O and sonicated in disrupt-buffer containing 1 % SDS/0.1 % beta-mercaptoethanol in PBS (pH 7.2) at 70°C for 30 minutes, followed by sonication in H<sub>2</sub>O for another 45 minutes.

#### *Analysis of binding affinities of antagonistic TNFR2 antibodies by surface plasmon resonance*

The affinities of antagonistic TNFR2 antibodies for recombinant human TNFR2 were measured using BIACORE™ Analysis Services (Precision Antibody). Briefly, the antibody was biotinylated at a 5:1 stoichiometric ratio using biotinyl-LC-LC-NOSE (Thermo-Fisher) in PBS. Excess biotinylation reagent was removed by centrifugation chromatography and the biotinylated antibody was captured on 3000 RU of streptavidin surface to a level of 100 RU. Theoretical maximum of signal with TNFR2 with that level of antibody capture was 26 RU and that signal was reached with a preliminary experiment using 500 nM TNFR2 in the running buffer. Analysis of the kinetics of antigen binding was performed at a flow of 60 µL/min with 2 min injections. Antibodies were injected at a concentration of 1 mg/ml to the final capture of 100 RU. The instrument used was BIACORE™ 3000 with the BioCap chip (GE Healthcare). Double reference method was used for analysis. Reference channel contained the identical level of streptavidin.

The thermodynamic and kinetic parameters of the binding of antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 to TNFR2 as measured using this assay are shown in Figure 13A.

#### *ELISA screening*

5           The binding of antibody to each of the synthesized peptides was tested in an ELISA format. Surface-immobilized peptide arrays were incubated with primary antibody solution (overnight at 4°C). After washing, the peptide arrays were incubated with a 1/1000 dilution of an appropriate antibody peroxidase conjugate (SBA) for one hour at 25°C. After washing, the peroxidase substrate 2,2'-azino-di-3-ethylbenzthiazoline sulfonate (ABTS) and 2 µl/ml of 3 percent H<sub>2</sub>O<sub>2</sub> were added. After one hour, the  
10           color development was measured. The color development was quantified with a charge coupled device (CCD) - camera and an image processing system. The values obtained from the CCD camera range from 0 to 3000 mAU, similar to a standard 96-well plate ELISA-reader. The results are quantified and stored into the Peplab database. Occasionally a well contains an air-bubble resulting in a false-positive value, the cards are manually inspected and any values caused by an air-bubble are scored as  
15           0.

To verify the quality of the synthesized peptides, a separate set of positive and negative control peptides was synthesized in parallel. These were screened with a negative control, antibody 57.9, an antibody that does not specifically bind TNFR2 (Posthumus et al. (J. Virology. 64:3304-3309, 1990)).

20           Peptides that bound TNFRAB1 and TNFRAB2 with high affinity are highlighted in Figures 3A and 3B, respectively. These peptides therefore contain residues within TNFR2 that are structurally configured into epitopes that are preferentially bound by TNFRAB1 and TNFRAB2.

#### *Epitope mapping*

ELISA was also used to determine linear epitopes present on the extracellular surface of TNFR2.  
25           Linear peptides corresponding to various regions within the TNFR2 primary sequence were purchased from GenScript (Piscataway, NJ), diluted in coating buffer and placed on Immulon 4HBX Flat Bottom Microtiter Plates (Thermo Scientific) at a concentration of 1 µg/well. Primary TNFR2 antagonistic antibodies (0.1 µg/well) were incubated with substrates. Secondary antibodies against rodent IgG were used to detect the primary antibodies. Absorbance was measured using the SPECTRAMAX® 190  
30           Absorbance Plate Reader and analyzed with SoftMax Pro 6.3 (Molecular Devices). Results of these ELISA-based assays are shown in Figure 13B and 13C.

## **Example 2. Antagonistic TNFR2 antibodies inhibit T-reg cell proliferation**

### *Materials and methods*

- Human T-reg Flow™ Kit (BioLegend, Cat. No. 320401)
    - Cocktail Anti-human CD4 PE-Cy5/CD25 PE (BioLegend, Part No. 78930)
    - Alexa Fluor® 488 Anti-human FOXP3, Clone 259D (BioLegend, Part No. 79467)
    - Alexa Fluor® 488 Mouse IgG1, k Isotype Ctrl (ICFC), Clone MOPC-21 (BioLegend, Part No. 79486)
- 40

- FOXP3 Fix/Perm Buffer (4X) (BioLegend, Cat. No. 421401)
- FOXP3 Perm Buffer (10X) (BioLegend, Cat. No. 421402)
- PE anti-human CD25, Clone: BC96 (BioLegend, Cat. No. 302606)
- Alexa Fluor® 488 Anti-human FOXP3, Clone 259D (BioLegend, Cat. No. 320212)
- 5 • PBS pH 7.4 (1X) (Gibco Cat. No. 10010-023)
- HBSS (1X) (Gibco Cat. No. 14175-095)
- FBS (heat inactivated)
- 15 ml tubes
- Bench top centrifuge with swing bucket rotor for 15 ml tubes (set speed 1100 rpm or 200 g)

10

Antagonistic TNFR2 antibodies (TNFRAB1 and TNFRAB2) were tested for the ability to suppress the proliferation of T-reg cells. Cultured T-reg cells were treated with varying concentrations of the antagonistic TNFR2 antibodies in the presence and absence of stimulatory growth factors (e.g., TNF $\alpha$ ) for set periods of time. T-reg cells were also cultured in the presence of TNFRAB1 at various concentrations ranging from 0.0008-25  $\mu$ g/ml in the presence and absence of TNF $\alpha$ . As controls, T-reg cells were also 15 incubated with TNF $\alpha$  alone at concentrations ranging from 0-40 ng/ml in order to select levels of TNF $\alpha$  that induce a high fractional increase in T-reg cell count. Additionally, T-reg cells were cultured in the presence of IL-2 alone and in the presence of TNFRAB2 alone.

Following the incubation of T-reg cells under the conditions described above, the cell counts were 20 determined using flow cytometry analysis. T-reg cells at a density of 0.2-1 x 10<sup>6</sup> cells/100  $\mu$ l were distributed into a 15-ml conical tube and centrifuged for 5 minutes in order to pellet the cells. The supernatant was discarded and cells were resuspended in 100  $\mu$ l of wash buffer (1x HBSS containing 2% FBS). 5  $\mu$ l of PE anti-human CD25 fluorophore-antibody conjugate were added to this mixture, and the cells were subsequently vortexed and incubated in the dark for 25 minutes. The cells were then washed 25 by adding 1 ml of wash buffer and subsequently centrifuging for 5 minutes. The supernatant was then discarded and 1 ml of FoxP3 fixation/permeabilization buffer (1:4 dilution of 4x FOXP3 Fix/Perm buffer in PBS) was added to the cells. The cells were then vortexed and incubated in the dark for 20 minutes. Cells were subsequently centrifuged for 5 minutes and supernatant was discarded. Cells were then resuspended in 1 ml of fresh wash buffer, vortexed, and centrifuged for 5 minutes. Cells were 30 subsequently resuspended in 1 ml of 1x FOXP3 Perm Buffer (1:10 dilution of 10x FOXP3 Perm Buffer in PBS), vortexed, and incubated in the dark for 15 minutes. Following incubation, cells were centrifuged for 5 minutes and supernatant was subsequently discarded. The cell pellet was then resuspended in 100  $\mu$ l of 1x FOXP3 Perm Buffer. At this point, 5  $\mu$ l of either Alexa Fluor® 488 anti-human FOXP3 or Alexa Fluor® 488 mouse IgG1, k isotype control were added to the cells. Cells were then vortexed and 35 incubated in the dark for 35 minutes. Following incubation, cells were washed by adding 1 ml of fresh wash buffer to the cells, vortexing the cells and centrifuging for 5 minutes. The supernatant was then discarded and the cell pellet was resuspended in 0.2-0.5 ml of 1x HBSS free of FBS. Cell counts were then determined by flow cytometry analysis.

As seen in Figure 5, incubation of antagonistic TNFR2 antibody TNFRAB1 suppressed T-reg cell 40 proliferation in a dose dependent manner even when cells were co-incubated with 20 ng/ml TNF $\alpha$ . Strikingly, this concentration of TNF $\alpha$  was capable of inducing the largest fractional increase in T-reg cell

count among the TNF $\alpha$  dosages analyzed in T-reg samples treated with TNF $\alpha$  alone. That TNFRAB1 is capable of diminishing T-reg cell proliferation even in the presence of activating levels of TNF $\alpha$  indicates that antagonistic TNFR2 antibodies are capable of not only competing with TNF $\alpha$  for receptor binding, but also exhibit the capacity to inhibit downstream signaling cascades that lead to T-reg cell growth and proliferation. For instance, when T-reg cells were incubated with TNF $\alpha$  alone at 20 ng/ml, the resulting T-reg population increased to 130% of untreated control cells. However, upon co-incubation of T-reg cells at 20 ng/ml with TNFRAB1, a steady dose-dependent suppression of cell proliferation is observed with concentrations ranging from 0.004-1.25  $\mu$ g/ml of TNFRAB1.

### 10 **Example 3. Generating antagonistic TNFR2 antibodies by phage display**

An exemplary method for *in vitro* protein evolution of antagonistic TNFR2 antibodies of the invention is phage display, a technique which is well known in the art. Phage display libraries can be created by making a designed series of mutations or variations within a coding sequence for the CDRs of an antibody or the analogous regions of an antibody-like scaffold (e.g., the BC, CD, and DE loops of <sup>10</sup>Fn3 domains). The template antibody-encoding sequence into which these mutations are introduced may be, e.g., a naive human germline sequence as described herein. These mutations can be performed using standard mutagenesis techniques described herein or known in the art. Each mutant sequence thus encodes an antibody corresponding in overall structure to the template except having one or more amino acid variations in the sequence of the template. Retroviral and phage display vectors can be engineered using standard vector construction techniques as described herein or known in the art. P3 phage display vectors along with compatible protein expression vectors, as is well known in the art, can be used to generate phage display vectors for antibody diversification as described herein.

The mutated DNA provides sequence diversity, and each transformant phage displays one variant of the initial template amino acid sequence encoded by the DNA, leading to a phage population (library) displaying a vast number of different but structurally related amino acid sequences. Due to the well-defined structure of antibody hypervariable regions, the amino acid variations introduced in a phage display screen are expected to alter the binding properties of the binding peptide or domain without significantly altering its structure.

In a typical screen, a phage library is contacted with and allowed to bind a TNFR2-derived peptide (e.g., a peptide having the sequence SEQ ID NO: 285 or 286), or a particular subcomponent thereof. To facilitate separation of binders and non-binders, it is convenient to immobilize the target on a solid support. Phage bearing a TNFR2-binding moiety can form a complex with the target on the solid support whereas non-binding phage remain in solution and can be washed away with excess buffer. Bound phage can then be liberated from the target by changing the buffer to an extreme pH (pH 2 or pH 10), changing the ionic strength of the buffer, adding denaturants, or other known means. To isolate the binding phage exhibiting the polypeptides of the present invention, a protein elution is performed.

The recovered phage can then be amplified through infection of bacterial cells and the screening process can be repeated with the new pool that is now depleted in non-binding antibodies and enriched for antibodies that bind the target peptide. The recovery of even a few binding phage is sufficient to

amplify the phage for a subsequent iteration of screening. After a few rounds of selection, the gene sequences encoding the antibodies or antigen-binding fragments thereof derived from selected phage clones in the binding pool are determined by conventional methods, thus revealing the peptide sequence that imparts binding affinity of the phage to the target. During the panning process, the sequence diversity of the population diminishes with each round of selection until desirable peptide-binding antibodies remain. The sequences may converge on a small number of related antibodies or antigen-binding fragments thereof, typically 10-50 out of about  $10^9$  to  $10^{10}$  original candidates from each library. An increase in the number of phage recovered at each round of selection is a good indication that convergence of the library has occurred in a screen. After a set of binding polypeptides is identified, the sequence information can be used to design other secondary phage libraries, biased for members having additional desired properties (See WO 2014/152660; incorporated herein by reference).

#### **Example 4. Treatment of cancer in a human patient by administration of antagonistic anti-TNFR2 antibodies**

The antagonistic TNFR2 antibodies of the invention can be administered to a human patient in order to treat a cell proliferation disorder, such as cancer. Administration of these antibodies suppresses the growth and proliferation of T-reg cells. Antibodies of the invention can also be administered to a patient in order to suppress a T-reg-mediated immune response. For instance, a human patient suffering from cancer, e.g., a cancer described herein, can be treated by administering an antagonistic TNFR2 antibody of the invention by an appropriate route (e.g., intravenously) at a particular dosage (e.g., between 0.001 and 100 mg/kg/day) over a course of days, weeks, months, or years. If desired, the anti-TNFR2 antibody can be modified, e.g., by hyperglycosylation or by conjugation with PEG, so as to evade immune recognition and/or to improve the pharmacokinetic profile of the antibody.

The progression of the cancer that is treated with an antagonistic TNFR2 antibody of the invention can be monitored by any one or more of several established methods. A physician can monitor the patient by direct observation in order to evaluate how the symptoms exhibited by the patient have changed in response to treatment. A patient may also be subjected to MRI, CT scan, or PET analysis in order to determine if a tumor has metastasized or if the size of a tumor has changed, e.g., decreased in response to treatment with an anti-TNFR2 antibody of the invention. Optionally, cells can be extracted from the patient and a quantitative biochemical analysis can be conducted in order to determine the relative cell-surface concentrations of various growth factor receptors, such as the epidermal growth factor receptor. Based on the results of these analyses, a physician may prescribe higher/lower dosages or more/less frequent dosing of the antagonistic TNFR2 antibody in subsequent rounds of treatment.

#### **Example 5. Producing an scFv TNFR2 antagonist**

Antibody fragments of the invention include scFv fragments, which consist of the antibody variable regions of the light and heavy chains combined in a single peptide chain. A phenotype-neutral TNFR2 antibody can be used as a framework for the development of a scFv antibody fragment by recombinantly expressing a polynucleotide encoding the variable region of a light chain of the TNFR2

antibody operatively linked to the variable region of a heavy chain of that antibody. The polynucleotide encoding the variable region of the heavy chain may contain a CDR-H3 sequence derived, e.g., from TNFRAB1, TNFRAB2, or TNFR2A3. Recombinant polynucleotides encoding such variable regions can be produced, for example, using established mutagenesis protocols as described herein or known in the art. This polynucleotide can then be expressed in a cell (e.g., a CHO cell) and the scFv fragment can subsequently be isolated from the cell culture media.

Alternatively, scFv fragments derived from a TNFR2 antagonist can be produced by chemical synthetic methods (e.g., by Fmoc-based solid-phase peptide synthesis, as described herein). One of skill in the art can chemically synthesize a peptide chain consisting of the variable region of a light chain of a phenotype-neutral TNFR2 antibody operatively linked to the variable region of a heavy chain of the antibody such that the variable region of the heavy chain contains the CDR-H3 sequence of an antagonistic TNFR2 antibody, such as TNFRAB1, TNFRAB2, or TNFR2A3. Native chemical ligation can be used as a strategy for the synthesis of long peptides (e.g., greater than 50 amino acids). Native chemical ligation protocols are known in the art and have been described, e.g., by Dawson et al. (Science, 266:776-779, 1994); incorporated herein by reference.

**Example 6. Producing a humanized TNFR2 antibody**

One method for producing humanized TNFR2 antibodies of the invention is to import the CDRs of a TNFR2 antibody into a human antibody consensus sequence. Consensus human antibody heavy chain and light chain sequences are known in the art (see e.g., the “VBASE” human germline sequence database; Kabat et al. (Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91 -3242, 1991); Tomlinson et al. (J. Mol. Biol. 227:776-798, 1992); and Cox et al. (Eur. J. Immunol. 24:827- 836, 1994); incorporated herein by reference). Using established procedures, one can identify the variable domain framework residues and CDRs of a consensus antibody sequence (e.g., by sequence alignment (see Kabat, supra)). One can substitute, e.g., the CDR-H1, CDR-H2, CDR-L1, CDR-L2, and CDR-L3 sequences of the antibody with the corresponding sequences of a phenotype-neutral anti-TNFR2 antibody, as well as substitute the CDR-H3 of the consensus human antibody with the CDR-H3 an antagonistic TNFR2 antibody, such as TNFRAB1, TNFRAB2, or TNFR2A3 in order to produce a humanized, antagonistic TNFR2. Polynucleotides encoding the above-described CDR sequences can be produced synthetically or recombinantly, e.g., using gene editing techniques described herein or known in the art. One example of a variable domain of a consensus human antibody includes the heavy chain variable domain EVQLVESGGGLVQPGGSLRLS**CAASGFTFSDYAM**SWVRQAPGKGLEWVAVISENGSDTY**YADSVKGR**FTISRDDSKNTLYLQMN**SLRAEDTAVYYCARD****DRGGAVSYFDVW**GQGT**LVTVSS** (SEQ ID NO: 32) and the light chain variable domain DIQMTQSPSSLSASV**GD**RVTIT**CRASQDVSSYLAWY**QQKPGKAP**KLLIYAASSLES**GVPSRFSGSGSGT**DFTLTIS**SLQPEDFATYYC**QQYNSLPYTF**GQGTKVEIKRT (SEQ ID NO: 33), identified in US Patent No. 6,054,297; incorporated herein by reference (CDRs are shown in bold).

In order to produce humanized, antagonistic TNFR2 antibodies, one can recombinantly express a polynucleotide encoding the above consensus sequence in which the CDR-H1, CDR-H2, CDR-L1, CDR-L2, and CDR-L3 sequences are replaced with the corresponding CDR sequences of a phenotype-neutral, TNFR2-specific antibody. The CDR-H3 sequence of the consensus human antibody can be substituted  
5 with the CDR-H3 of an antagonistic TNFR2 antibody, such as TNFRAB1, TNFRAB2, or TNFR2A3 (i.e., SEQ ID NO: 25, 259, or 284, respectively).

A polynucleotide encoding the above heavy chain and light chain variable domains operatively linked to one another can be incorporated into an expression vector (e.g., an expression vector optimized for protein expression in prokaryotic or eukaryotic cells as described herein or known in the art). The  
10 single-chain antibody fragment (scFv) can thus be expressed in a host cell and subsequently purified from the host cell medium using established techniques, such as size-exclusion chromatography and/or affinity chromatography as described herein.

### **Example 7. Treatment of HIV in a human patient by administration of antagonistic anti-TNFR2 15 antibodies**

The antagonistic TNFR2 antibodies of the invention can be administered to a human patient in order to treat a viral infection, such as HIV. Administration of these antibodies suppresses the growth and proliferation of T-reg cells, which enhances the immune response of a patient by allowing the growth and proliferation of cytotoxic T-lymphocytes capable of mounting an attack on infected cells. For instance, a  
20 human patient suffering from HIV can be treated by administering an antagonistic TNFR2 antibody of the invention (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7) and has a non-native constant region, such as a TNFR2 antibody that contains the CDR-H3 sequence of  
25 TNFRAB1, TNFRAB2, or TNFR2A3) by an appropriate route (e.g., intravenously) at a particular dosage (e.g., between 0.001 and 100 mg/kg/day) over a course of days, weeks, months, or years. If desired, the anti-TNFR2 antibody can be modified, e.g., by hyperglycosylation or by conjugation with PEG, so as to evade immune recognition and/or to improve the pharmacokinetic profile of the antibody.

The progression of HIV that is treated with an antagonistic TNFR2 antibody of the invention can  
30 be monitored by any one or more of several established methods. A physician can monitor the patient by direct observation in order to evaluate how the symptoms exhibited by the patient have changed in response to treatment. A blood sample can also be withdrawn from the patient in order to analyze the cell count of one or more white blood cells in order to determine if the quantity of infected cells has changed (e.g., decreased) in response to treatment with an anti-TNFR2 antibody of the invention. Based on the  
35 results of these analyses, a physician may prescribe higher/lower dosages or more/less frequent dosing of the antagonistic TNFR2 antibody in subsequent rounds of treatment.



**Example 8. Treatment of *Mycobacterium tuberculosis* in a non-human mammal by administration of antagonistic anti-TNFR2 antibodies**

5 The antagonistic TNFR2 antibodies of the invention can be administered to a non-human mammal (e.g., a bovine mammal, pig, bison, horse, sheep, goat, cow, cat, dog, rabbit, hamster, guinea pig, or other non-human mammal) in order to treat a bacterial infection, such as *Mycobacterium tuberculosis*. Administration of these antibodies suppresses the growth and proliferation of T-reg cells, which enhances the immune response of a patient by allowing the growth and proliferation of cytotoxic T-lymphocytes capable of mounting an attack on the pathogenic organism. For instance, a non-human mammal suffering from *Mycobacterium tuberculosis* can be treated by administering an antagonistic TNFR2 antibody of the invention (e.g., a TNFR2 antibody that specifically binds an epitope containing one or more residues of the KCRPG sequence of TNFR2 (residues 142-146 of SEQ ID NO: 7) and that does not exhibit specific binding to an epitope containing the KCSPG sequence of TNFR2 (residues 56-60 of SEQ ID NO: 7) and has a non-native constant region, such as a TNFR2 antibody that contains the CDR-H3 sequence of TNFRAB1, TNFRAB2, or TNFR2A3) by an appropriate route (e.g., intravenously) at a particular dosage (e.g., between 0.001 and 100 mg/kg/day) over a course of days, weeks, months, or years. If desired, the anti-TNFR2 antibody can be modified, e.g., by hyperglycosylation or by conjugation with PEG, so as to evade immune recognition and/or to improve the pharmacokinetic profile of the antibody.

20 The progression of the *Mycobacterium tuberculosis* infection that is treated with an antagonistic TNFR2 antibody of the invention can be monitored by any one or more of several established methods. A physician can monitor the patient by direct observation in order to evaluate how the symptoms exhibited by the patient have changed in response to treatment. A blood sample can also be withdrawn from the patient in order to analyze the cell count of one or more white blood cells in order to determine if the immune response has changed (e.g., increased) in response to treatment with an anti-TNFR2 antibody of the invention. Based on the results of these analyses, a physician may prescribe higher/lower dosages or more/less frequent dosing of the antagonistic TNFR2 antibody in subsequent rounds of treatment.

**Example 9. Antagonistic TNFR2 antibodies inhibit T-reg cell proliferation in the presence of IL-2 and TNF**

30 The presence of an elevated quantity of T-reg cells can hamper the ability of the immune system to combat cancer and infectious disease. TNFR2 represents an important checkpoint in T-reg proliferation and thus constitutes an ideal target for immunomodulation. To characterize the functional activity of two antagonistic TNFR2 monoclonal antibodies (mAbs), TNFRAB1 and TNFRAB2, a cell-based assay developed for homogeneous T-reg expansion was employed. It was first confirmed that normal human CD4+ cells incubated with increasing concentrations of TNF $\alpha$  resulted in a dose-dependent increase in T-reg cells (Figures 6A and 7A). We also confirmed that the presence of IL-2 is required for T-reg proliferation (Figure 6B). As shown in Figures 6B-6G, relative to treatment with IL-2 alone, the effect on T-reg proliferation with TNF at 20 ng/ml is dramatic (>20% expansion) and enhanced further by co-

incubation with the TNFR2 agonist (>60% expansion).

Antagonistic TNFR2 antibodies elicit an opposite effect on T-reg proliferation as measured using this assay. Both TNFR2 antagonistic antibodies induced suppressive effects on T-reg proliferation that resulted in a 4-15% decrease in the percentage of remaining T-reg cells in normal blood donors.

5 Remarkably, the TNFR2 antagonistic effect is dominant and can even overcome the presence of a generous amount of TNF $\alpha$  (20mg/ml) (Figures 6C-6G). The TNFR2 antagonistic effect on T-reg was dose dependent (Figures 6D-6G). More remarkable was the observation the when the two TNFR2 antagonistic antibodies were studied in the presence of TNF $\alpha$ , both TNFR2 antagonist antibodies were able to overcome TNF $\alpha$  agonism in a dose dependent fashion. Both antagonistic antibodies were  
10 capable of attenuating T-reg expansion and inverting the TNF $\alpha$  agonistic curve (Figures 6A and 6C-6G). This assay was also performed by incubating T-reg cells with a fixed amount of TNFR2 antagonistic antibody and escalating doses of TNF $\alpha$  (Figures 6D-6G). Again both TNFR2 antagonists in a dose-dependent fashion were capable of reversing TNF $\alpha$  agonism. It should be noted that this 48 hour T-reg expansion assay is performed with IL-2, an agonist, in the culture to prevent non-specific human CD4+ T  
15 cell death. When the data obtained from these experiments were processed to determine the relative changes in T-reg proliferation in the presence of antagonistic TNFR2 antibodies as compared to the presence of IL-2 alone, the antagonistic properties of both antibodies persisted (Figures 7A-7E). Together these results demonstrate the functional ability of two TNFR2 antagonist antibodies to suppress T-reg proliferation in human CD4+ cells, and the effect is remarkably dominant over agonism driven by  
20 moderate to high doses of TNF $\alpha$ .

To conduct the T-reg suppression assays described above, peripheral blood mononuclear cells (PBMCs) were used as responders. PBMCs were isolated on the day of venipuncture using a Ficoll-  
Plaque Plus (GE Healthcare, Piscataway, NJ) density gradient and were cryopreserved at -80°C. Cells  
were thawed one day prior to mixing with T-reg cells and were rested overnight in RPMI 1640 and IL-2  
25 (10 U/ml). The next day, responder cells were stained with 1  $\mu$ M carboxyfluorescein diacetate succinimidyl ester (CFSE). Responder cells ( $5 \times 10^4$  cells) were then mixed with expanded T-reg cells at various ratios (0:1, 4:1, 2:1, 1:1), and stimulated with anti-CD3 mAb (HIT3a, BD Biosciences) and IL-2 (50 U/ml). Cells were collected after 4 days and analyzed by flow cytometry.

### 30 *Human subjects*

Human blood samples from over 100 donors were collected according to a human studies protocol approved by the Massachusetts General Hospital Human Studies Committee (MGH-  
2001P001379). All of the donors provided written informed consent. Blood was collected into BD  
Vacutainer EDTA tubes (BD Diagnostics) and processed within 2 hours of phlebotomy. T-reg samples  
35 isolated from ovarian cancer patients were obtained from women with newly diagnosed ovarian cancer prior to irradiation and prior to chemotherapy. These human studies were approved by the Massachusetts General Hospital Human Studies Committee (MGH-2015P002489; see Example 14 below).

*Blood and cell culture*

Fresh human blood was processed within 2 hours of venipuncture. Blood was washed twice with 1x HBSS (Invitrogen) plus 2% FBS (Sigma-Aldrich) and CD4+ cells were isolated using Dynabeads® CD4 Positive Isolation Kit (Invitrogen). Isolated CD4+ cells were resuspended in RPMI GlutaMAX™ (Life Technologies) plus 10% FBS (Sigma-Aldrich) and 1% penicillin-streptomycin (Life Technologies). Cells were seeded in 96-round-bottom well plates at a concentration of 0.2 - 1 x 10<sup>6</sup> cells/well, treated with either TNFR2 antagonist antibodies or TNFR2 agonists (as indicated in each example), and then incubated for up to 48 hours at 37 °C with 5% CO<sub>2</sub>. Since isolated and cultured human T cells die in the absence of IL-2 in the cell culture medium, all cell-based experiments described herein used a low level of IL-2 (100U/ml) in the culture media to prevent IL-2 withdrawal from influencing the data. T-reg cells isolated from sterile ovarian cancer ascites were obtained by first concentrating the cells in 50-ml conical tubes and then suspending the cell pellets to obtain CD4+ cell isolations (see Example 14 below).

*Reagents and flow cytometry*

Recombinant human TNF was purchased from Sigma-Aldrich and recombinant human IL-2 was purchased from Life Technologies. F(ab')<sub>2</sub> fragments of TNFRAB1 and TNFRAB2 were prepared using Pierce F(ab')<sub>2</sub> Preparation Kit (Life Technologies). Crosslinking antibodies against rodent IgG (ab9165 and ab99670) were purchased from Abcam (Cambridge, MA). Cells were prepared for flow cytometry using Human T-reg Flow™ Kit (BioLegend) according to the manufacturer instructions. Antibodies used for flow cytometry included Alexa Fluor® 488 Anti-human FOXP3, Clone 259D for intracellular staining of FOXP3, and PE Anti-human CD25 Clone BC96 for cell surface staining of CD25 (BioLegend). Fluorescently stained cells were resuspended in 1x HBSS (Invitrogen) and analyzed using a BD FACS Calibur flow cytometer machine (Becton Dickinson). FACS data was processed using FlowJo software (Version 10.0.8).

*Statistical analysis*

Data analysis was performed by the paired Student *t* test using Excel (Microsoft) or GraphPad Prism-5 software (GraphPad Software, La Jolla, CA). Significance was determined by a two-sided *p*-value less than 0.05.

**Example 10. Short term culture effects on activated T-reg cells by TNFR2 antagonist antibodies**

To investigate the ability of antagonistic TNFR2 antibodies to modulate TNFR2 secretion, soluble human TNFR2 was measured from cell culture supernatants using Quantikine® ELISA (R&D Systems). Briefly, supernatants were collected after 24 – 42 hour incubation of CD4+ cells with IL-2 (200 U/ml) alone or with TNF (20 ng/ml) or antagonistic TNFR2 antibodies (12.5 µg/ml) and either used immediately or frozen at -20 °C. ELISA was performed according to the manufacturer's instructions. Absorbance was measured using the SpectraMax® 190 Absorbance Plate Reader and analyzed with SoftMax Pro 6.3 (Molecular Devices).

T-reg cells exist in two states, activated (aT-reg) and resting (rT-reg); the two states can be

distinguished on the basis of the expression of CD45RA. The phenotype of an aT-reg cell is CD25<sup>Hi</sup>CD45RA<sup>Low</sup> while the phenotype of a rT-reg cell is CD25<sup>Med</sup>CD45RA<sup>Hi</sup>. aT-reg cells are more potent suppressors of immune function and therefore ideal targets for immunotherapy. To investigate the efficacy of inhibiting aT-reg cells, it was first confirmed that the total number of T-reg cells, rather than simply the proportion of T-reg cells, was reduced when CD4<sup>+</sup> cells were treated with the TNFR2 antagonists (Figures 8A-8H). Next, to determine which class of T-reg is inhibited by the TNFR2 antagonists, cells were stained by CD45RA. We found that while both classes of T-reg cells are inhibited, the aT-reg cells were suppressed to a greater extent than the rT-reg cells. These data suggest that the TNFR2 antagonist antibodies selectively inhibit the proliferation of aT-reg cells. High TNFR2 expression is another characteristic of suppressive T-reg cells. The level of TNFR2 expression was measured and it was found that TNFR2 antagonist treatment reduced the number of TNFR2<sup>Hi</sup>-expressing cells. In contrast, mean fluorescent intensity (MFI) of TNFR2 expression remained similar among all treatments (Figure 9A). Taken together, these data suggest that antagonistic TNFR2 antibodies, such as TNFRAB1 and TNFRAB2, are capable of selectively attenuating the proliferation of CD25<sup>Hi</sup>+, CD45RA<sup>Low</sup>+ T-reg cells.

The immune response is often characterized by an increase in soluble TNFR2 due to high protein turnover cells. The level of soluble TNFR2 was therefore measured in culture supernatant after treatment with TNFR2-modulating agents in order to determine the effect of these molecules on immune activity. It was observed that TNF and the TNFR2 agonist increased the quantity of soluble TNFR2, whereas the TNFR2 antagonist reduced the level of soluble TNFR2 (Figure 9B). Additionally, T-reg suppressor assays confirmed potent suppression of CD8<sup>+</sup> cells by TNFR2 antagonism (Figures 9A and 9C). These data demonstrate that treatment of human CD4<sup>+</sup> cells with a TNFR2 antagonist effectively reduces the number of activated and highly suppressive T-reg cells and had the additional benefit of inhibiting soluble decoy TNFR2 secretion.

To conduct T-reg suppression assays as described above, peripheral blood mononuclear cells (PBMCs) were used as responders. PBMCs were isolated on the day of venipuncture using a Ficoll-Plaque Plus (GE Healthcare, Piscataway, NJ) density gradient and cryopreserved at -80°C. PBMCs were thawed the day before mixing with T-reg cells and were rested overnight in RPMI 1640 and IL-2 (10 U/ml). The next day, responder cells were stained with 1 µM carboxyfluorescein diacetate succinimidyl ester (CFSE). Responder cells (5 x 10<sup>4</sup> cells) were then mixed with expanded T-reg cells at various ratios (0:1, 4:1, 2:1, 1:1), and stimulated with anti-CD3 mAb (HIT3a, BD Biosciences) and IL-2 (50 U/ml). Cells were collected after 4 days and analyzed by flow cytometry.

To measure the concentration of secreted TNFR2 as described above, the QUANTIKINE® ELISA assay kit was used (R&D Systems). Briefly, supernatants were collected after 24 -42 hour incubation of CD4<sup>+</sup> cells with IL-2 (200 U/ml) alone or with TNFα (20 ng/ml) or TNFR2 antagonist antibodies (12.5 µg/ml) and either used immediately or frozen at -20°C. ELISA assays were performed according to the manufacturer's instructions. Absorbance was measured using the SPECTRAMAX® 190 Absorbance Plate Reader and analyzed with SoftMax Pro 6.3 (Molecular Devices).

**Example 11. TNFR2 antagonist activity is independent of non-specific Fc region binding or cross-linking**

Non-specific binding by antibody Fc regions can result in arbitrary functional activity. Treatment of CD4+ cells with TNFR2 mAb F(ab')<sub>2</sub> fragments, with or without TNF, resulted in similar dose responses in T-reg cell quantities as observed with full monoclonal antibodies (Figures 10A-10D). This confirms that specific binding by the F(ab')<sub>2</sub> region of the antagonistic TNFR2 antibody to TNFR2, rather than non-specific binding mediated by the Fc region, is likely responsible for the suppressive activity. Purity of F(ab')<sub>2</sub> fragments and full antibodies were assessed by SDS-PAGE analysis (Figures 11A-11D).

Crosslinking can also result in aberrant functional activity of antibodies. To rule out the possibility that non-specific crosslinking was a cause of the observed functional activity, a dose response assay was performed in which the TNFR2 antagonist antibodies were incubated with T-reg cells with and without anti-IgG antibodies. The dose-dependent suppression of T-reg cells by TNFR2 antagonist antibodies was unaffected by the presence of anti-IgG (Figures 10C and 10D). Taken together, these data confirm that the functional activity of TNFR2 antagonist antibodies is independent of non-specific Fc region activity or crosslinking.

To conduct the SDS-PAGE analysis described above, protein samples were run alongside PRECISION PLUS™ (BioRad) or PERFECT PROTEIN™ (EMD Millipore) markers on NuPAGE 4-12% Bis-Tris Gels with MOPS SDS Running Buffer (Life Technologies) at 100V for 1 hour. Gels were stained for 24 hours with SIMPLY BLUE™ Safe Stain (Invitrogen).

**Example 12. NFκB activation and gene expression is inhibited by antagonistic TNFR2 antibodies**

NFκB signaling is required for TNF-mediated cell response and has been proposed as a potential target for cancer therapy. Upon observing a decrease in T-reg cell proliferation following treatment with TNFR2 antagonist antibodies, it was hypothesized that the underlying signaling mechanism would involve a reduction in NFκB activation. To investigate the molecular response to TNFR2 antagonism, the expression of eight promoters of NFκB activation were measured by real-time PCR analysis. These proteins included: CHUK, NFKBIE, KNKBIA, MAP3K11, TRAF2, TRAF3, relB, cIAP2/BIRCH. The expression of TNF and lymphotoxin were additionally monitored, as well as two markers of T-reg cells, FoxP3 and CD25. In each case, treatment with TNFRAB2 resulted in down-regulation of gene expression compared to treatment with TNF (Figures 12A and 12B). Next, using phosphorylated RelA/NFκB p65 as a marker, it was demonstrated that treatment of CD4+ cells with either TNFR2 antagonist antibody reduced NFκB activation, whereas treatment with TNF increased NFκB activation (Figures 12C-12E). This suggests the effect of the two TNFR2 antagonist antibodies on TNFR2 signal transduction is highly similar. Additionally, analysis of the kinetic parameters of binding of antagonist TNFR2 antibodies to recombinant human TNFR2 revealed that there was no significant difference in association or dissociation rates between TNFRAB1 and TNFRAB2 (Figure 13A).

To conduct gene expression assays, isolated CD4+ cells were incubated for 3 hours in the presence of IL-2 (50 U/ml) and TNFα (20 ng/ml) or TNFR2 antagonist antibody (2.5 μg/ml). Cells were collected and total RNA was isolated using RNeasy-4PCR Kit (Ambion). The total RNA was reverse

transcribed using High Capacity cDNA Reverse Transcription Kit (Applied-Biosystems). Real-time PCR was performed using the TaqMan® Array Human NFkB Pathway 96-well Plate with TaqMan® Gene Expression Master Mix and the ABI Prism 7000 Sequence Detection System (Applied-Biosystems).

NFkB activation was measured using the cell-based Human Phospho-RelA/NFkB p65

5 Immunoassay (R&D Systems). Briefly, fresh CD4+ cells were cultured in 96-well flat-bottom plates (0.2 x 10<sup>6</sup> cells/well) in the presence of IL-2 (200 U/ml) alone or in the presence of TNF or TNFR2 antagonists at the indicated concentrations for 10 minutes at 37°C. Cells were adhered to the plate by centrifugation and fixation and then stained according to the manufacturer's instructions. Fluorescence was read using the EnVision® Multilabel Plate Reader (Perkin Elmer) and normalized relative fluorescence units (RFU) were  
10 calculated.

### Example 13. Binding of antagonistic TNFR2 antibodies to TNFR2 maps to overlapping regions

To further investigate the specific binding properties of the TNFR2 antagonist antibodies TNFRAB1 and TNFRAB2, epitope mapping analysis was performed and epitopes within human TNFR2  
15 that bind these antibodies were correlated with a distinct location on the receptor surface. Linear peptide mapping of the two TNFR2 antagonists revealed that while both antagonistic antibodies exhibit a high affinity for the full-length target protein, these antibodies exhibited differential affinity for linear peptides. Specifically, TNFRAB1 exhibited moderate affinity to the epitope containing amino acids 112-139 of SEQ ID NO: 7 within human TNFR2, and exhibited strong affinity to the epitope containing amino acids 128-  
20 155 of SEQ ID NO: 7. TNFRAB2 did not bind to any linear peptide region (Figure 13B). The affinity of TNFRAB1 for TNFR2 was not perturbed by the presence of TNF $\alpha$ , indicating that TNF $\alpha$  is not a competitor with this antibody for TNFR2 binding (Figure 13C). To examine the conformational epitopes that bind the two antagonist antibodies, a three-dimensional binding analysis was conducted. For TNFRAB1, the 3D data was in agreement with the linear peptide mapping analysis and indicated that the  
25 region of amino acids 142-149 of SEQ ID NO: 7 within human TNFR2 were bound by TNFRAB1 with high affinity. Additionally, the 3D analysis revealed a new binding region at amino acids 161-169 of SEQ ID NO: 7 within human TNFR2 (Figures 13A-13C and 15A-15C). For TNFRAB2, even though there was no successful linear peptide binding, four binding regions were mapped by 3D analysis (Figures 15A-15C). Interestingly, there was partial overlap in the precise discontinuous epitopes of the two TNFR2 antagonist  
30 antibodies at amino acids 142-144 of SEQ ID NO: 7 within human TNFR2.

This later data was of interest since previous attempts to raise antagonistic TNFR2 antibodies against the TNFR2 binding site of the TNFR2 trimer signaling complex and/or to the exterior region of the trimer binding site to prevent TNF $\alpha$  entry and prevent stabilization of the TNF trimer had been unsuccessful. The solution structure of the TNF $\alpha$  and TNFR2 complexes had defined a central TNF $\alpha$   
35 homotrimer surrounded by three TNFR2 receptors (Mukai et al. Science Signaling 3: ra83 (2010)). This arrangement had also been observed by many previous TNF superfamily members including TNFR1 with lymphotoxin, DR5 with TRAIL ligand, and Ox40 receptor with Ox40L (Banner et al. Cell 73: 431-445 (1993); Cha et al. J. Biol. Chem. 275: 31171-31177 (2000); Compaan et al. Structure 14:1321-1330 (2006); Hymowitz et al. Mol. Cell 4:563-571 (1999); Mongkolsapaya et al. Nat. Struct. Biol. 6:1048-1053

(1999)).

Previous attempts to produce antagonistic antibodies to these regions to prevent TNF $\alpha$  binding and TNFR2 trimers yielded recessive-antagonistic antibodies with mild TNFR2 inhibitory activity having a common trait in T-reg proliferation assays. As Figures 14A-14D show, in the 48 hour T-reg assay these recessive-antagonistic antibodies performed as antagonists in the absence of a TNFR2-stimulating agent. Indeed, both recessive-antagonist TNFR2 antibodies A and B by themselves had a demonstration of dose response T-reg antagonism with a dose response from 0-25  $\mu$ g/ml (Figures 14A and 14C). Importantly, when TNF $\alpha$  (20 mg/ml) was added to the cultures, these TNFR2-directed recessive-antagonistic antibodies A and B competed poorly with TNF $\alpha$ . In each case, TNF $\alpha$  driven agonism was dominant over this form of antagonism, at least the partial and weak antagonism with antibodies to prevent TNF $\alpha$  or TNFR2 trimer formations (Figure 15C). This behavior is in contrast with the capacity of dominant antagonistic TNFR2 antibodies, such as TNFRAB1 and TNFRAB2 that bind the specific epitopes within TNFR2 identified and described herein, such as epitopes containing the KCRPG motif of TNFR2 and other epitopes as identified in the descriptions of TNFRAB1 and TNFRAB2 provided herein. As opposed to recessive-antagonistic TNFR2 antibodies A and B, TNFR2 antagonistic antibodies TNFRAB1 and TNFRAB2 displayed the ability to attenuate TNFR2 signaling and T-reg proliferation even in the presence of a TNFR2 agonist, such as TNF $\alpha$  and IL-2. Importantly, the epitopes identified herein can be used to raise antagonistic TNFR2 antibodies that display an antagonistic effect that persists in the presence of TNFR2 stimulants.

Since linear peptide mapping only partially answered the question of why TNFRAB1 and TNFRAB2 were superior antagonists, we next explored identifying conformational epitopes of the two TNFR2 antagonists. We conducted three-dimensional (3D) binding analysis using the Pepscan technology (Pepscan, The Netherlands). For both TNFRAB1 and TNFRAB2, the 3D data showed overlapping regions from approximately aa138-aa150. What became apparent is that these binding regions did not appear to be able to bind to the classic TNFR2 trimer with trimeric TNF $\alpha$  since the site would have been on the interior of the trimer (Figure 15B). Since other research groups had reported alternative forms of TNF independent forms of TNF superfamily members that were parallel or anti-parallel models, we mapped the epitopes on those sites (Naismith et al. *J. Biol. Chem.* 270:13303-13307 (1995); Naismith et al. *Structure* 4:1251-1262 (1996)). Surprisingly, only one model of TNFR2 antagonistic binding was optimal: a model in which the anti-parallel dimer (Figure 15A) contains two TNFR2 antagonistic antibody binding regions that are spaced apart for the obligatory hinged TNFR2 antagonists and would appear to stabilize this TNF $\alpha$ -independent complex, another functional trait of these antibodies. With further modeling, it was apparent that the anti-parallel complex, but not the parallel dimer complex, would have intracellular regions that are distant from one another and would inhibit NF $\kappa$ B signaling as we had observed in our functional assays. Since all members of the TNF superfamily of receptors can display these less commonly studied anti-parallel conformations, antagonistic antibodies to any receptor of the TNFR superfamily can be made by designing or screening for antibodies or antigen-binding fragments thereof that bind surface-exposed epitopes within the anti-

parallel TNFRS member protein (see, e.g., Example 15, below). These antibodies or antigen-binding fragments thereof can stabilize the anti-parallel forms of these proteins and thus prevent signaling, as well as the formation of active trimeric forms of these receptors that frequently also bind soluble cognate ligands. Known members of the TNF superfamily of receptors known to exhibit anti-parallel dimer structures include: TNFR1, TNFR2, Fas, DCR3, DR3, TRAIL-R1(DR4), TRAIL-R2 (DR5), TRAIL-R3, TRAIL-R4, DR6, EDAR, CD271, OPG, RANK, LT $\beta$ R, TWEAK-R, HVEM, CD27, CD30, CD40, CD137, OX40, GITR, BCMA, TACI, BAFFR, EDAR2, TROY, and RELT, among others.

#### Example 14. TNFR2 Antagonist activity on cancer cells

T-reg cells present in patients suffering from cancer are potent immune suppressors. This is particularly true for T-reg cells from tumor sites as compared to the T-reg cells of peripheral blood of the cancer patients or control subjects. To begin to understand the potency of TNFR2 antagonist antibody on ovarian cancer T-reg cells, fresh ovarian cancer T-reg cells were isolated and their proliferation characterized as described in Example 2. First with TNF and then with TNFR2 agonist, it was indeed the case that ovarian cancer residing T-reg cells expanded far greater than the T-reg cells from normal donors, a sign of hyper activation (Figures 16A-16B and 17A-17H). TNFR2 antagonistic antibodies inhibited T-reg cell proliferation in a dose-dependent fashion and with higher variability as compared to the tight dose response data obtained from analysis of proliferation of T-reg cells isolated from healthy donors. Additionally, both antagonistic antibodies more potently inhibited the proliferation of T-reg cells isolated from ovarian cancer patients as compared to healthy donors.

The experiments described above demonstrate that antagonistic TNFR2 antibodies are capable of inhibiting both normal and cancer-associated T-reg cell proliferation. Such antibodies can eliminate or inactivate potent suppressive T-reg cells, both in terms of the quantity of T-reg cells in culture as well as in terms of T-reg proliferation. The traits of these antibodies include the ability to attenuate intracellular early phosphorylation events that precede NF $\kappa$ B activation and the capacity to change the phenotype of the remaining T-reg cells such that these cells expressed reduced quantities of activation markers, such as CD45RO. Additionally, antagonistic TNFR2 antibodies may diminish the secretion of soluble TNFR2, a proinflammatory protein. Remarkably even in the presence of generous amounts of agonistic TNF $\alpha$  or agonistic TNFR2 antibodies added to cell culture media, antagonistic TNFR2 antibodies still act as dominant antagonists.

It is worthwhile contrasting antibody or ligand agonism of the TNF $\alpha$  receptors with antibody antagonism. The requirement for TNF and other TNF superfamily agonism with the natural ligands is well studied and requires aggregation and clustering for efficient signal transduction (Das et al. *J. Mol. Endocrinol.* 53:81-91 (2014); Siegel et al. *J. Cell. Biol.* 167:735-744 (2004); Takeda et al. *Oncogene* 26:3745-3757 (2007)). The most common confirmation for the tumor necrosis factor receptor superfamily is a trimeric receptor paired with trimers of the ligand (Gommerman et al. *Nat. Rev. Immunol.* 3:642-655 (2003); Loetscher et al. *J. Biol. Chem.* 266:18324-18329 (1991); Smith et al. *Cell* 76:959-962 (1994); Tartaglia *J. Biol. Chem.* 267:4304-4307 (1992); Ware *Annu. Rev. Immunol.* 23:787-819 (2005)). Agonist antibodies seem to follow the same principles and also often require the Fc portions of their receptors for



the associated cells through antibody-dependent cell-mediated cytotoxicity (ADCC) mechanisms, something that would stabilize the extracellular lattices. This exterior receptor oligomerization and clustering observed with TNFR2 agonism permits internal oligomerization of the reciprocal TRAF lattice network for brisk NF $\kappa$ B signaling (Cabal-Hierro et al. *Cell Signal.* 26:2658-2666 (2014); Yin et al. *Nat. Struct. Mol. Biol.* 16:658-666 (2009); Zheng et al. *Mol. Cell.* 38:101-113 (2010)). The stabilization of agonist is also promoted by the cooperation of the added ligand to the receptor. This appears important for many TNF receptor superfamily members for therapeutic effectiveness (Graves et al. *Cancer Cell* 26:177-189 (2014)).

The shared receptor binding regions of two TNFR2 antagonist antibodies studied herein leads us to a very different possible model of antibody binding to the TNFR2 receptor to cause stable and dominant antagonism. The commonly studied trimeric form of TNFR2 would not allow the newly identified antibody antagonists to bind to their amino acid sequences and explain how these antagonistic antibodies are dominant over TNF $\alpha$  or IL-2 (Mukai et al. *Science Signal.* 3:ra83 (2010)). Indeed, years of work generating TNFR2 antibodies to the binding region of TNF $\alpha$  in the trimer TNFR2 structure or to the exterior surface of the TNF $\alpha$ -binding region of the trimer did not generate potent antagonists that maintained dominant inhibition of receptor signaling in the presence of TNFR2 agonists. TNFR2 trimer-directed antibodies designed to compete with TNF $\alpha$  were not dominant, but exhibited neutralizing effects at times when challenged with the inflammatory environment of TNF $\alpha$  or IL-2.

The trimeric form of TNFR2 is the most commonly studied form of the TNF $\alpha$  receptor, as it relates to cell growth signals involving NF $\kappa$ B. Previous studies have proposed that TNFR2 and similar TNF $\alpha$  superfamily members like the lymphotoxin receptor can also exist as parallel and anti-parallel forms. These forms lack the TNF binding site (Naismith et al. *J. Biol. Chem.* 270:13303-13307 (1995); Naismith et al. *Structure* 4:1251-1262 (1996)). The data described herein show no added benefit of adding a cross-linking reagent to either augment antagonism or to convert antagonism to agonism. It would be hard to imagine that high-affinity TNF $\alpha$  binding of TNF $\alpha$  to trimeric TNFR2 could be competitively inhibited by an antibody, even with extremely high affinity. The anti-parallel dimeric form of TNFR2 fits best with the assessable binding site for antagonistic antibodies and the functional assay but there is also another feature to support this observation – the exterior interface is considerably more extensive and thus this would also cause the intracellular tails of TNFR2 to be a further distance apart as supported by others data (Naismith et al. *Structure* 4:1251-1262 (1996)). With TNFR2 trimerization the intracellular signaling regions of the TNFR2 are pulled close together, thus facilitating TRAF direct or indirect recruitment of the intracellular domains of these TNF superfamily receptors (Napetschnig et al. *Annu. Rev. Biophys.* 42:443-468 (2013); Yin et al. *Nat. Struct. Mol. Biol.* 16:658-666 (2009)). This agonist signal would subsequently engage other signaling proteins to activate the inhibitor of  $\kappa$ B (I $\kappa$ B) kinase (IKK) and MAP kinases ultimately activating NF $\kappa$ B. The fact that the post-receptor signaling pathway is blocked to varying degrees with TNFR2 antagonistic antibodies suggests the recruitment of intracellular TRAFs are inhibited by the dominant stabilization of the exterior TNFR2 structure. It has been previously proposed by others that the anti-parallel dimers of TNFR1 could be an inhibitory complex and would not be able to bind TNF (Naismith et al. *Structure* 4:1251-1262 (1996)). The anti-parallel model more closely substantiates how

antagonistic formation of this complex would explain dominance over TNF co-culture since new activation trimers could not be formed.

It is worth mentioning that as reported by others, the T-reg cells in the cancer environment are extremely potent compared to the T-reg cells of non-cancerous donors or even the T-reg cells isolated from the peripheral blood of cancerous donors (Govindaraj et al. Clin. Cancer Res. 20: 724-735 (2013)). As described herein, antagonistic TNFR2 antibodies are capable of inhibiting the proliferation of potent T-reg cells isolated from ovarian cancer patients. It has also been observed that accentuated inhibition of T-reg cells isolated from ovarian cancer patients is achieved with TNFR2 antagonist antibodies TNFRAB1 and TNFRAB2. This activity is beneficial in view of recent reports identifying the features of the TNFR2 gene sequence that imparts enhanced potency to TNFR2 signaling in cancer patients. In the setting of cutaneous T cell lymphoma, for instance, the gene for TNFR2 is a gene duplication and/or may be mutated in the intracellular region to confer constitutive agonism. This genetic pressure to constantly maintain TNFR2 growth signals is in line with exaggerated growth.

The antagonist antibodies described herein bind to the restricted regions of the TNFR2 receptor that modulate T-reg inhibition and even dominant inhibition in the presence of TNF $\alpha$ . These antagonists are very different from the recessive antagonists also described herein that can mildly inhibit T-reg cell proliferation but, when used in an inflammatory environment of TNF and IL-2, agonism dominates (Figures 14A-14D). Taken together, the data described above provides a new platform for the creation of additional antagonist TNFR2 antibodies beyond those described herein that would be capable of modulating T-reg cell growth in patients suffering from a cancer in which cancer cells express elevated quantities of TNFR2 (e.g., ovarian cancer) and may display antagonistic effects even in the presence of TNFR2 agonists. Remarkably, such antagonistic TNFR2 antibodies are more potent on the T-reg cells of ovarian cancer patients than on the T-reg cells of non-cancerous donors.

#### **Example 15. Development of an antagonistic TNFR2 antibody by CDR-H3 sequence substitution**

In order to generate anti-TNFR2 antibodies, mice were immunized with full-length human TNFR2 using established immunization procedures. Serum was subsequently isolated from the immunized mice, and twelve distinct monoclonal antibodies were purified. The affinity of these twelve antibodies for human TNFR2 was verified by ELISA (Figure 18A) using microtiter plates coated with human TNFR2. The wells of microtiter plates used in these experiments were coated with antigen at 5  $\mu$ g/ml. The murine antibodies were subsequently added to each well at dilutions of 1:300, 1:900, 1:2700, 1:8100, 1:24300, 1:72900, and 1:218799 from rows A through G of the microtiter plate. Readings derived from row H correspond to background fluorescence. Notably, a positive titer will have an optical density reading of twice the background at a 1:2700 dilution. The added antibody was detected by adding a developing antibody, such as a labeled goat anti-mouse immunoglobulin conjugated to a fluorescent agent. The microtiter plate was subsequently analyzed using a fluorescence plate reader. The ELISA screening raw data was then analyzed numerically using Excel. Any microtiter well coated with antigen that has an optical density (OD) value greater than the positive threshold is be considered a "positive hit" provided the corresponding well on the counter screen-coated plate has an OD less than the negative threshold.

Based on its high affinity for TNFR2 (as evidenced, e.g., by the fluorescence reading shown in row B, column 3 in Figure 18A), murine clone 3 was selected for CDR-H3 mutagenesis. The CDR-H3 sequence of clone 3 was substituted with the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284) using recombinant gene expression techniques known in the art in order to produce the antagonistic TNFR2 antibody TNFR2A3. The precursor clone 3 was not capable of antagonizing the TNFR2 target, while the recombinantly produced TNFR2A3 exhibited antagonistic characteristics. As shown in column 3 of Figures 18B and 18C, as well as in columns two and three of Figure 20, TNFR2A3 was capable of specifically binding two human TNFR2-derived peptides having the amino acid sequence LRKCRPGFGVA (SEQ ID NO: 285) and VVCKPCAPGTFSN (SEQ ID NO: 286), respectively. This selective binding was evidenced by a dose-dependent increase in fluorescence within increasing concentrations of TNFR2A3 in each well of the microtiter plate. TNFR2A3 binds TNFR2 in a site-specific manner, as this antibody was found to exhibit negligible binding affinity for an unrelated TNFR2-derived peptide isolated from a distal region of the human TNFR2 primary structure (see, e.g., column 3 of Figure 19). Collectively, these findings demonstrate two important facets of the CDR-H3 sequence with respect to TNFR2 antagonism. First, the CDR-H3 sequence of an antagonistic TNFR2 antibody is the primary molecular determinant of the antigen-binding properties of the antibody. Secondly, the CDR-H3 motif is a modular domain that can be imported into an anti-TNFR2 antibody that does not exhibit antagonistic activity in order to impart such an antibody with the ability to bind regions of TNFR2 that promote receptor antagonism.

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**Example 16. Treatment of cancer or an infectious disease in a human patient by administration of antagonistic anti-TNFR2 antibodies in combination with an immunotherapy agent**

The antagonistic TNFR2 antibodies, antigen-binding fragments, single-chain polypeptides, and constructs of the invention can be administered to a human patient in combination with (for instance, admixed with, co-administered with, or administered separately from) an immunotherapy agent in order to treat a cell proliferation disorder, such as cancer, or an infectious disease, such as a viral, bacterial, fungal, or parasitic infection. Administration of the antibody, antigen-binding fragment, single-chain polypeptide, or construct can suppress the growth and proliferation of T-reg cells and/or cancer cells that express TNFR2. Immunotherapy agents, such as anti-CTLA-4 agents, anti-PD-1 agents, anti-PD-L1 agents, anti-PD-L2 agents, TNF- $\alpha$  cross-linking agents, TRAIL cross-linking agents, anti-CD27 agents, anti-CD30 agents, anti-CD40 agents, anti-4-1BB agent, anti-GITR agents, anti-OX40 agents, anti-TRAILR1 agents, anti-TRAILR2 agent, and anti-TWEAKR agents can function in tandem with antagonist TNFR2 antibodies, antigen-binding fragments thereof, single-chain polypeptides, or constructs, as immunotherapy agents are capable of downregulating the signal transduction of immune checkpoint receptors and/or ligands that would otherwise lead to tolerance toward tumor-associated antigens and downregulation of the cytotoxic T cell response. Additional examples of immunotherapy agents that may be used in conjunction with an antagonistic TNFR2 antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct include Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-

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chemokines, Vorinostat, gabapentin, antibodies to lymphoid cell surface receptors and/or lymphokines, antibodies to surface cancer proteins, and/or small molecular therapies like Vorinostat.

5 A physician of skill in the art may administer an antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct that specifically binds TNFR2 as an antagonist, for instance, as described herein, to a human patient suffering from a cancer or infectious disease in combination with an immunotherapy agent. The antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct and the immunotherapy agent may be administered to the patient by an appropriate route of administration (for example, intravenously, intramuscularly, or subcutaneously, among others) at a particular dosage (for example, between 0.001 and 100 mg/kg/day, among other ranges) over a course of 10 days, weeks, months, or years. If desired, the anti-TNFR2 antibody, antigen-binding fragment, single-chain polypeptide, or construct can be modified, for instance, by hyperglycosylation or by conjugation with PEG, so as to evade immune recognition and/or to improve the pharmacokinetic profile of the antibody, antigen-binding fragment, single-chain polypeptide, or construct.

The progression of the cancer or infectious disease that is treated in this fashion can be 15 monitored by any one or more of several established methods. A physician can monitor the patient by direct observation in order to evaluate how the symptoms exhibited by the patient have changed in response to treatment. A patient may also be subjected to MRI, CT scan, or PET analysis in order to determine if a tumor has metastasized or if the size of a tumor has changed, for example, decreased in response to treatment with an anti-TNFR2 antibody, antigen-binding fragment, single-chain polypeptide, 20 or construct and an immunotherapy agent. Optionally, cells can be extracted from the patient and a quantitative biochemical analysis can be conducted in order to determine the relative cell-surface concentrations of various growth factor receptors, such as the epidermal growth factor receptor. Based on the results of these analyses, a physician may prescribe higher/lower dosages or more/less frequent dosing of the antagonistic TNFR2 antibody, antigen-binding fragment, single-chain polypeptide, or 25 construct and immunotherapy agent in subsequent rounds of treatment.

**Example 17. Combinatorial analysis of the effect of CDR-H and CDR-L regions of antagonistic TNFR2 polypeptides on the killing of activated T-reg cells and the proliferation of T effector cells**

It has presently been discovered that antagonistic TNFR2 polypeptides, such as antibodies, 30 antigen-binding fragments, single-chain polypeptides, and constructs, that contain certain combinations of CDR-H and CDR-L regions are particularly capable of promoting T-reg cell death and augmenting T effector cell (e.g., CD8+ T cell) proliferation. To test the effects of various combinations of CDR-H1 and CDR-L3 regions on the antagonistic activity of anti-TNFR2 polypeptides, a series of monoclonal antibodies was developed containing all four possible combinations of the two CDR-H1 regions: 35 GYTFTDYL (SEQ ID NO: 274) and GYTFTDYI (SEQ ID NO: 275) and the two CDR-L3 regions: CLQYVNLLT (SEQ ID NO: 272) and CLQYVNLIT (SEQ ID NO: 273). The remaining CDR regions were the same as those described for TNFRAB2 (CDR-H2: VDPEYGST (SEQ ID NO: 258), CDR-H3: ARDDGSYSPFDYWG (SEQ ID NO: 259), CDR-L1: QNINKY (SEQ ID NO: 260), CDR-L2: TYS or YTS).

The monoclonal antibodies containing each of the four possible combinations of the foregoing

CDR-H1 and CDR-L3 regions were then tested for the ability to induce T-reg cell death and promote CD8+ cell proliferation using standard CD4+CD25+ and CD8+ cell counting procedures, such as those described in Example 2 above. The abilities of each monoclonal antibody to induce T-reg cell death and induce CD8+ T cell proliferation were ranked on a qualitative scale of from 1 to 5, in which 1 corresponds to measurable biological activity and 5 corresponds to robust biological activity. The results of these experiments are summarized in Table 3, below:

Table 3. Effects of CDR-H1 and CDR-L3 combinations on T-reg suppression and CD8+ T cell induction properties of antagonistic TNFR2 monoclonal antibodies

Combination of CDR-H1 and CDR-L3 Regions	Capacity to promote T-reg cell death	Capacity to promote CD8+ T cell proliferation
GYTFTDYL (SEQ ID NO: 274) and CLQYVNLIT (SEQ ID NO: 272)	2	5
GYTFTDYL (SEQ ID NO: 274) and CLQYVNLIT (SEQ ID NO: 273)	5	5
GYTFTDYI (SEQ ID NO: 275) and CLQYVNLIT (SEQ ID NO: 272)	1	3
GYTFTDYI (SEQ ID NO: 275) and CLQYVNLIT (SEQ ID NO: 273)	4	4

The results reported in Table 3 demonstrate that antagonistic TNFR2 polypeptides, such as antibodies, antigen-binding fragments, single-chain polypeptides, and constructs as described herein, that contain a CDR-H1 having the amino acid sequence GYTFTDYL (SEQ ID NO: 274) and a CDR-L3 having the amino acid sequence CLQYVNLIT (SEQ ID NO: 273) are particularly effective in promoting the selective killing of activated T-reg cells and potentiating augmented T effector cell proliferation. As described herein, these phenotypes are beneficial for the treatment of cancers and infectious diseases, as the ability to deplete activated T-reg cell populations in a patient suffering from such pathologies can lessen the attenuation of cytotoxic CD8+ T cells, thereby enabling effector cells to both function and or expand to mount an immune response against cancerous and infectious cells.

**Example 18. Antagonistic TNFR2 polypeptides exhibit effects on T-reg cells, T effector cells, and TNFR2+ cancer cells**

Antagonistic TNFR2 polypeptides, such as antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, may exert biological activities on T-reg cells and T effector cells. To investigate these effects, antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 were incubated with cultured T-reg cells at ascending concentrations of antibody, and the percentage change in the quantity of T-reg cells in culture was subsequently recorded. The results of these experiments are shown in Figures 21A and 21B, and demonstrate that antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 reduce or inhibit the proliferation of T-reg cells in culture in a dose-dependent

fashion.

Additionally, antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 promote the proliferation of T effector cells. To investigate this activity, antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 were incubated with cultured CD8+ T cells at ascending concentrations of antibody, and the percentage change in the quantity of CD8+ T cells in culture was subsequently recorded. The results of these experiments are shown in Figure 21C, and demonstrate that antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 increase the proliferation of T effector cells in a dose-dependent fashion.

The antagonistic TNFR2 antibodies TNFRAB1 and TNFRAB2 also directly kill TNFR2-expressing cancer cells. The antagonistic TNFR2 antibody TNFRAB1, was incubated with cultured OVCAR3 cells, a line of TNFR2+ ovarian cancer cells, at ascending concentrations of antibody, and the percentage change in the quantity of CD8+ T cells in culture was subsequently recorded. The results of this experiments are shown in Figure 21D, and demonstrate that the antagonistic TNFR2 antibody TNFRAB1 suppresses the proliferation of TNFR2+ cancer cells in a dose-dependent fashion.

Taken together, the data shown in Figures 21A-21D demonstrate that antagonistic TNFR2 polypeptides, such as anti-TNFR2 antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, are capable of exerting therapeutic effects through several distinct mechanisms. Antagonistic TNFR2 polypeptides can suppress T-reg cell proliferation and increase the proliferation of T effector cells, which can then mount an immune response against, for example, a cancer cell or a cell of an infectious pathogen. Additionally, antagonistic TNFR2 polypeptides can directly kill cancer cells that express TNFR2. Through these mechanisms, for example, antagonistic TNFR2 polypeptides, such as those described herein, can be used to treat patients suffering from a variety of cancers and infectious diseases, such as those conditions described herein.

**Example 19. Antagonistic TNFR2 polypeptides kill T-reg cells and expand T effector cells in the tumor microenvironment**

Antagonistic TNFR2 polypeptides, such as antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, may preferentially reduce the proliferation of T-reg cells and increase the proliferation of T effector in the tumor microenvironment of a cancer patient. To investigate this property, the antagonistic TNFR2 antibody, TNFRAB1, was incubated with either fresh human ovarian cancer ascites or a blood sample obtained from a human subject without cancer. TNFRAB1 was present in these samples in ascending doses, and the quantities of T-reg cells and T effector cells present in each sample were recorded following an incubation period. The results of these experiments are reported in Figures 22A and 22B. As shown therein, TNFRAB1 killed or reduced the proliferation of T-reg cells in the ovarian cancer ascites sample in a dose-dependent fashion. TNFRAB1 also killed or reduced proliferation of T-reg cells in the sample obtained from a human without cancer, but to a lesser extent. Conversely, TNFRAB1 increased T effector cell proliferation in the ovarian cancer ascites sample to a greater extent than in the sample obtained from a human without cancer. Collectively, these data demonstrate that antagonistic TNFR2 polypeptides, such as anti-TNFR2 antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, can preferentially deplete T-reg cells in the tumor microenvironment, such as in a patient suffering

from a cancer described herein, relative to T-reg cells in an environment free of cancer cells, such as in a healthy human subject.

**Example 20. Antagonistic TNFR2 polypeptides kill T-reg cells, expand T effector cells, and deplete TNFR2+ CD26- cells**

Antagonistic TNFR2 polypeptides, such as antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, exhibit the ability to kill T-reg cells, increase T effector cell proliferation, and kill TNFR2-expressing cancer cells in the tumor microenvironment. To further investigate these activities, the antagonistic TNFR2 antibody TNFRAB1 was incubated with blood samples obtained from healthy human subjects and human patients suffering from advanced cutaneous T cell lymphoma. These patients were receiving background treatment with one or more immunotherapy agents, such as Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, and gabapentin, among others, and were failing to respond to the immunotherapy at the time the present experiments were conducted.

After an incubation period, the quantities of effector T cells, T-reg cells, and TNFR2+ CD26- cells were measured in each sample. The absence of CD26 expression by a T cell is an indicator of T cell lymphoma. Thus, effects exerted on these cells are indicative of effects on cancer cells in a T cell lymphoma patient. The results of these experiments are reported in Figures 23A-23C. These data demonstrate that antagonistic TNFR2 polypeptides, such as TNFRAB1, can simultaneously modulate a cancer patient's T-reg, T effector, and TNFR2+ CD26- cell populations. Antagonistic TNFR2 polypeptides described herein, such as antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs, may demonstrate all three of these beneficial characteristics so as to impart a therapeutic effect on patients suffering from cancer, such as T cell lymphoma or another cancer described herein.

Additionally, the results shown in Figures 23A-23C demonstrate that antagonistic TNFR2 polypeptides, such as antibodies, antigen-binding fragments thereof, single-chain polypeptides, and constructs described herein, can be used in combination with immunotherapy agents for the treatment of cancer in a patient. The T cell lymphoma patients studied in the foregoing experiments were not responsive to immunotherapy alone. Upon treatment of isolated blood samples from these patients with TNFRAB1, a favorable in vitro response was observed, as the proliferation of T-reg cells and TNFR2+ CD26- cells decreased and the proliferation of T effector cells increased. These results show that antagonistic TNFR2 polypeptides can be used in combination with immunotherapy agents, such as an immunotherapy agent described herein (for example, Targretin, Interferon-alpha, clobetasol, Peg Interferon (e.g., PEGASYS®), prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, and gabapentin), to improve treatment efficacy in cancer patients.

Moreover, the results of the above experiments demonstrate that antagonistic TNFR2 polypeptides of the invention exhibit therapeutic effects in patients having a variety of cancers. Antagonistic TNFR2 antibodies can be used to suppress ovarian cancer cell proliferation (see, e.g., Example 14, above) and T cell lymphoma cell proliferation, as presently described. Cells of both of these

cancers exhibit the common property expressing TNFR2. Thus, antagonistic TNFR2 polypeptides can be used to treat a wide array of cancer types, such as those in which TNFR2 is expressed on the cancer cell surface.

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### Other Embodiments

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

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While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the invention that come within known or customary practice within the art to which the invention pertains and may be applied to the essential features hereinbefore set forth, and follows in the scope of the claims.

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Other embodiments are within the claims.



**CLAIMS**

1. An antibody or antigen-binding fragment thereof capable of specifically binding human tumor necrosis factor receptor 2 (TNFR2), wherein the antibody or antigen-binding fragment thereof comprises a complementarity determining region-heavy chain 3 (CDR-H3) having the amino acid sequence of:

(a) JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279);

(b) AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266); or

(c) ARDDGSYSPFDYWG (SEQ ID NO: 259) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain.

2. The antibody or antigen-binding fragment thereof of claim 1, wherein in the presence of said CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding a peptide comprising the amino acid sequence of LRKCRPGFGVA (SEQ ID NO: 285) or VVCKPCAPGTFNS (SEQ ID NO: 286).

3. The antibody or antigen-binding fragment thereof of claim 1 or 2, wherein in the presence of said CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding an epitope within amino acids 142-149 (KCRPGFGV) or amino acids 161-169 (CKPCAPGTF) of SEQ ID NO: 7.

4. The antibody or antigen-binding fragment thereof of any one of claims 1-3, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259).

5. The antibody or antigen-binding fragment thereof of any one of claims 1-3, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

6. The antibody or antigen-binding fragment thereof of any one of claims 1-5, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):

(a) a CDR-H1 having the amino acid sequence GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277);

(b) a CDR-H2 having the amino acid sequence (J)<sub>5</sub>GSJ;

(c) a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y;

- (d) a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and
  - (e) a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T;
- wherein each J is independently a naturally occurring amino acid.

7. The antibody or antigen-binding fragment thereof of any one of claims 1-5, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X;
- (b) a CDR-H2 having the amino acid sequence VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264);
- (c) a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268);
- (d) a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and
- (e) a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271);

wherein each Z<sup>1</sup> is independently an amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently an amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently an amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine;

each Z<sup>5</sup> is independently an amino acid comprising a hydrophobic side-chain; and

each X is independently leucine or isoleucine.

8. The antibody or antigen-binding fragment thereof of any one of claims 1-5, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
  - (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
  - (c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
  - (d) a CDR-L2 having the amino acid sequence TYS or YTS; and
  - (e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
- wherein each X is independently leucine or isoleucine.

9. The antibody or antigen-binding fragment thereof of any one of claims 6-8, wherein said antibody or antigen-binding fragment comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257);
- (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258);
- (c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260);

- (d) a CDR-L2 having the amino acid sequence TYS or YTS; and
  - (e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261);
- wherein each X is independently leucine or isoleucine.

10. The antibody or antigen-binding fragment thereof of claim 9, wherein said CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274).

11. The antibody or antigen-binding fragment thereof of claim 9, wherein said CDR-H1 has the amino acid sequence GYTFTDYI (SEQ ID NO: 275).

12. The antibody or antigen-binding fragment thereof of any one of claims 9-11, wherein said CDR-L2 has the amino acid sequence TYS.

13. The antibody or antigen-binding fragment thereof of any one of claims 9-11, wherein said CDR-L2 has the amino acid sequence YTS.

14. The antibody or antigen-binding fragment thereof of any one of claims 9-13, wherein said CDR-L3 has the amino acid sequence CLQYVNLLT (SEQ ID NO: 272).

15. The antibody or antigen-binding fragment thereof of any one of claims 9-13, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

16. The antibody or antigen-binding fragment thereof of any one of claims 9-15, wherein said antibody or antigen-binding fragment thereof comprises a framework region comprising the amino acid sequence LLIR (SEQ ID NO: 262) bound to the N-terminus of said CDR-L2.

17. The antibody or antigen-binding fragment thereof of any one of claims 9-16, wherein said antibody or antigen-binding fragment thereof comprises a framework region comprising the amino acid sequence TLE bound to the C-terminus of said CDR-L2.

18. The antibody or antigen-binding fragment thereof of any one of claims 1-17, wherein said antibody or antigen-binding fragment does not comprise one or more of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GFTFSSY (SEQ ID NO: 23);
- (b) a CDR-H2 having the amino acid sequence SSGGSY (SEQ ID NO: 24);
- (c) a CDR-L1 having the amino acid sequence SASSSVYYMY (SEQ ID NO: 26);
- (d) a CDR-L2 having the amino acid sequence STSNLAS (SEQ ID NO: 27);
- (e) a CDR-L3 having the amino acid sequence QRRNYPYT (SEQ ID NO: 28);
- (f) a CDR-L1 comprising the amino acid sequence RASKSVSTSGYSYMH (SEQ ID NO: 29);
- (g) a CDR-L2 comprising the amino acid sequence LASNLES (SEQ ID NO: 30); and
- (h) a CDR-L3 comprising the amino acid sequence QHSRELPRT (SEQ ID NO: 31).

19. The antibody or antigen-binding fragment thereof of any one of claims 1-18, wherein said antibody or antigen-binding fragment thereof comprises a non-native constant region.

20. The antibody or antigen-binding fragment thereof of claim 19, wherein said non-native constant region is a human constant region.

21. The antibody or antigen-binding fragment thereof of any one of claims 1-18, wherein said antibody or antigen-binding fragment thereof lacks all or a portion of an Fc domain, lacks all or a portion of a native Fc domain, or lacks an Fc domain altogether.

22. The antibody or antigen-binding fragment thereof of any one of claims 1-21, wherein said antibody or antigen-binding fragment thereof specifically binds to a peptide comprising the amino acid sequence of any one of SEQ ID NOs: 11, 19, 20, and 34-117 with a  $K_D$  of less than about 100 nM and does not bind a peptide comprising amino acids 56-60 (KCSPG) of SEQ ID NO: 7.

23. The antibody or antigen-binding fragment thereof of any one of claims 1-22, wherein said antibody or antigen-binding fragment thereof specifically binds a peptide comprising one or more of amino acids 142-146 of SEQ ID NO: 7 (KCRPG) and does not bind a peptide comprising amino acids 56-60 of SEQ ID NO: 7 (KCSPG).

24. The antibody or antigen-binding fragment thereof of any one of claims 1-23, wherein said antibody or antigen-binding fragment thereof inhibits TNFR2 signaling.

25. The antibody or antigen-binding fragment thereof of any one of claims 1-24, wherein said antibody or antigen-binding fragment thereof inhibits the expression of one or more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3.

26. The antibody or antigen-binding fragment thereof of any one of claims 1-25, wherein said antibody or antigen-binding fragment thereof inhibits NF $\kappa$ B activation.

27. The antibody or antigen-binding fragment thereof of any one of claims 1-26, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of T-reg cells.

28. The antibody or antigen-binding fragment thereof of any one of claims 1-27, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of cancer cells that express TNFR2.

29. The antibody or antigen-binding fragment thereof of claim 28, wherein said cancer cells are selected from the group consisting of T cell lymphoma cells, such as Hodgkin's or cutaneous non-Hodgkin's lymphoma cells, ovarian cancer cells, colon cancer cells, multiple myeloma cells, and renal cell carcinoma cells.

30. The antibody or antigen-binding fragment thereof of any one of claims 1-29, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of myeloid-derived suppressor cells.

31. The antibody or antigen-binding fragment thereof of any one of claims 1-30, wherein said antibody or antigen-binding fragment thereof does not require TNF $\alpha$  to reduce or inhibit the proliferation of T-reg cells.

32. The antibody or antigen-binding fragment thereof of any one of claims 1-31, wherein said antibody or antigen-binding fragment thereof promotes proliferation of T effector cells.

33. A method of identifying a TNFR2 antagonist antibody or antigen-binding fragment thereof comprising:

(a) exposing a heterogeneous mixture of antibodies or fragments thereof to a peptide having the amino acid sequence of ID NO: 285 or 286, or an amino acid sequence having up to two amino acid substitutions relative to said sequences; and

(b) retaining antibodies or fragments thereof that specifically bind said peptide and removing antibodies or fragments thereof that do not specifically bind said peptide, thereby producing an enriched antibody mixture comprising at least one said TNFR2 antagonist antibody or antigen-binding fragment thereof.

34. The method of claim 33, wherein said method comprises determining the amino acid sequence of one or more of the antibodies or antigen-binding fragments thereof in said enriched antibody mixture.

35. The method of claim 33 or 34, wherein said peptide is bound to a surface.

36. The method of any one of claims 33-35, wherein said antibody or antigen-binding fragment thereof is expressed on the surface of a phage, bacterial cell, or yeast cell.

37. The method of any one of claims 33-35, wherein said antibody or antigen-binding fragment thereof is expressed as one or more polypeptide chains non-covalently bound to ribosomes or covalently bound to mRNA or cDNA.

38. The method of any one of claims 33-37, wherein said peptide is conjugated to a detectable label.

39. The method of claim 38, wherein said detectable label is selected from the group consisting of a fluorescent molecule, an epitope tag, and a radiolabel.

40. The method of claim 39, wherein said fluorescent molecule is selected from the group consisting of green fluorescent protein, cyan fluorescent protein, yellow fluorescent protein, red fluorescent protein, phycoerythrin, allophycocyanin, hoescht, 4',6-diamidino-2-phenylindole (DAPI), propidium iodide, fluorescein, coumarin, rhodamine, tetramethylrhoadmine, and cyanine.

41. The method of claim 39, wherein said epitope tag is selected from the group consisting of a maltose-binding protein, glutathione-S-transferase, a poly-histidine tag, a FLAG-tag, a myc-tag, human influenza hemagglutinin (HA) tag, biotin, and streptavidin.

42. The method of any one of claims 33-41, wherein steps (a) and (b) are sequentially repeated one or more times.

43. A method of producing a TNFR2 antagonist antibody or antigen-binding fragment thereof comprising immunizing a non-human mammal with a peptide comprising the sequence of SEQ ID NO: 285 or 286, or an amino acid sequence having up to two amino acid substitutions relative to said sequences, and collecting serum comprising said TNFR2 antagonist antibody or antigen-binding fragment thereof.

44. The method of claim 43, wherein said non-human mammal is selected from the group consisting of a rabbit, mouse, rat, goat, guinea pig, hamster, horse, and sheep.

45. An antibody or antigen-binding fragment thereof that is produced by the method of any one of claims 33-44.

46. The antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45, wherein said antibody or antigen-binding fragment thereof is selected from the group consisting of a monoclonal antibody or antigen-binding fragment thereof, a polyclonal antibody or antigen-binding fragment thereof, a humanized antibody or antigen-binding fragment thereof, a primatized antibody or antigen-binding fragment thereof, a bispecific antibody or antigen-binding fragment thereof, a multi-specific antibody or antigen-binding fragment thereof, a dual-variable immunoglobulin domain, a monovalent antibody or antigen-binding fragment thereof, a chimeric antibody or antigen-binding fragment thereof, a single-chain Fv molecule (scFv), a diabody, a triabody, a nanobody, an antibody-like protein scaffold, a domain antibody, a Fv fragment, a Fab fragment, a F(ab')<sub>2</sub> molecule, and a tandem scFv (taFv).

47. The antibody or antigen-binding fragment thereof of claim 46, wherein said antibody or antigen-binding fragment thereof is a F(ab')<sub>2</sub> molecule.

48. The antibody or antigen-binding fragment thereof of any one of claims 1-32, 45, and 46, wherein said antibody or antigen-binding fragment thereof has an isotype selected from the group consisting of IgG, IgA, IgM, IgD, and IgE.

49. The antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-48, wherein said antibody is conjugated to a therapeutic agent.

50. The antibody or antigen-binding fragment thereof of claim 49, wherein said therapeutic agent is a cytotoxic agent.

51. A single-chain polypeptide capable of specifically binding human TNFR2, wherein the single-chain polypeptide comprises a CDR-H1, a CDR-H2, and a CDR-H3, wherein the CDR-H3 comprises an amino acid sequence of:

(a) JRJDGSY(J)<sub>2</sub>FD(J)<sub>3</sub> (SEQ ID NO: 279);

(b) AZ<sup>1</sup>DZ<sup>2</sup>Z<sup>4</sup>Z<sup>3</sup>Z<sup>5</sup>SPZ<sup>5</sup>Z<sup>2</sup>Z<sup>5</sup>WG (SEQ ID NO: 266); or

(c) ARDDGSYSPFDYWG (SEQ ID NO: 259) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain.

52. The single-chain polypeptide of claim 51, wherein said CDR-H1 and CDR-H2 are from an anti-TNFR2 antibody capable of specifically binding an epitope within amino acids 70-180 of SEQ ID NO: 7.

53. The single-chain polypeptide of claim 52, wherein said CDR-H1 and CDR-H2 are from an anti-TNFR2 antibody capable of specifically binding an epitope within amino acids 142-149 of SEQ ID NO: 7 (KCRPGFGV).

54. The single-chain polypeptide of claim 52, wherein said CDR-H1 and CDR-H2 are from an anti-TNFR2 antibody capable of specifically binding an epitope within amino acids 137-144 of SEQ ID NO: 7 (CAPLRKCR).

55. The single-chain polypeptide of claim 52, wherein said CDR-H1 and CDR-H2 are from an anti-TNFR2 antibody capable of specifically binding an epitope within amino acids 161-169 of SEQ ID NO: 7 (CKPCAPGTF).

56. The single-chain polypeptide of claim 52, wherein said CDR-H1 and CDR-H2 are from an anti-TNFR2 antibody capable of specifically binding an epitope within amino acids 80-86 (DSTYTQL), 91-98 (PECLSCGS), and 116-123 (RICTCRPG) of SEQ ID NO: 7.

57. The single-chain polypeptide of any one of claims 51-56, wherein in the presence of said CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding a peptide comprising the amino acid sequence of LRKCRPGFGVA (SEQ ID NO: 285) or VVCKPCAPGTFNS (SEQ ID NO: 286).

58. The single-chain polypeptide of any one of claims 51-57, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259).

59. The single-chain polypeptide of any one of claims 51-57, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

60. The single-chain polypeptide of any one of claims 51-59, wherein said CDR-H1 has the amino acid sequence:

(a) GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277);

(b) Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X; or

(c) GYTFTDYX (SEQ ID NO: 257) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain;

and

each X is independently leucine or isoleucine.

61. The single-chain polypeptide of claim 60, wherein said CDR-H1 has the amino acid sequence GYTFTDYX (SEQ ID NO: 257).

62. The single-chain polypeptide of claim 61, wherein said CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274).

63. The single-chain polypeptide of claim 61, wherein said CDR-H1 has the amino acid sequence GYTFTDYI (SEQ ID NO: 275).

64. The single-chain polypeptide of any one of claims 51-63, wherein said CDR-H2 has the amino acid sequence:

(a) (J)<sub>5</sub>GSJ;

(b) VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264); or

(c) VDPEYGST (SEQ ID NO: 258) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;



each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain.

65. The single-chain polypeptide of claim 64, wherein said CDR-H2 has the amino acid sequence VDPEYGST (SEQ ID NO: 258).

66. The single-chain polypeptide of any one of claims 51-65, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y;

(b) a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and

(c) a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T.

wherein each J is independently a naturally occurring amino acid.

67. The single-chain polypeptide of any one of claims 51-65, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268);

(b) a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and

(c) a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271);

wherein each Z<sup>1</sup> is independently an amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently an amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently an amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine;

each Z<sup>5</sup> is independently an amino acid comprising a hydrophobic side-chain; and

each X is independently leucine or isoleucine.

68. The single-chain polypeptide of any one of claims 51-65, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

(b) a CDR-L2 having the amino acid sequence TYS or YTS; and

(c) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each X is independently leucine or isoleucine.

69. The single-chain polypeptide of any one of claims 66-68, wherein said CDR-L2 has the amino acid sequence TYS.

70. The single-chain polypeptide of any one of claims 66-68, wherein said CDR-L2 has the amino acid sequence YTS.

71. The single-chain polypeptide of any one of claims 66-70, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 272).

72. The single-chain polypeptide of any one of claims 66-70, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

73. The single-chain polypeptide of any one of claims 66-72, wherein said single-chain polypeptide comprises a framework region comprising the amino acid sequence LLIR (SEQ ID NO: 262) bound to the N-terminus of said CDR-L2.

74. The single-chain polypeptide of any one of claims 66-72, wherein said single-chain polypeptide comprises a framework region comprising the amino acid sequence TLE bound to the C-terminus of said CDR-L2.

75. The single-chain polypeptide of any one of claims 51-74, wherein said single-chain polypeptide does not comprise one or more of the following CDRs:

- (a) a CDR-H1 having the amino acid sequence GFTFSSY (SEQ ID NO: 23);
- (b) a CDR-H2 having the amino acid sequence SSGGSY (SEQ ID NO: 24); and
- (c) a CDR-L1 having the amino acid sequence SASSSVYYMY (SEQ ID NO: 26);
- (d) a CDR-L2 having the amino acid sequence STSNLAS (SEQ ID NO: 27);
- (e) a CDR-L3 having the amino acid sequence QQRRNYPYT (SEQ ID NO: 28);
- (f) a CDR-L1 having the amino acid sequence RASKSVSTSGYSYMH (SEQ ID NO: 29);
- (g) a CDR-L2 having the amino acid sequence LASNLES (SEQ ID NO: 30); and
- (h) a CDR-L3 having the amino acid sequence QHSRELPRT (SEQ ID NO: 31).

76. A construct comprising a first polypeptide domain and a second polypeptide domain, wherein said first polypeptide domain and said second polypeptide domain each independently comprise a single-chain polypeptide of any one of claims 51-75.

77. The construct of claim 76, wherein said first polypeptide domain and said second polypeptide domain are bound by a covalent linker.

78. The construct of claim 77, wherein said covalent linker comprises an amide bond.

79. The construct of claim 77, wherein said covalent linker comprises a disulfide bond.

80. A polynucleotide encoding the antibody or antigen-binding fragment thereof of any one of claims 1-32.
81. A polynucleotide encoding the single-chain polypeptide of any one of claims 51-75.
82. A polynucleotide encoding the construct of any one of claims 76-79.
83. A vector comprising the polynucleotide of any one of claims 80-82.
84. The vector of claim 83, wherein said vector is an expression vector.
85. The vector of claim 84, wherein said expression vector is a eukaryotic expression vector.
86. The vector of claim 83, wherein said vector is a viral vector.
87. The vector of claim 86, wherein said viral vector is selected from the group consisting of adenovirus (Ad), retrovirus, poxvirus, adeno-associated virus, baculovirus, herpes simplex virus, and a vaccinia virus.
88. The vector of claim 87, wherein said adenovirus is a serotype 5, 26, 35, or 48 adenovirus.
89. The vector of claim 87, wherein said retrovirus is a  $\gamma$ -retrovirus or a lentivirus.
90. The vector of claim 87, wherein said vaccinia virus is a modified vaccinia Ankara (MVA).
91. An isolated host cell comprising the vector of any one of claims 83-90.
92. The host cell of claim 91, wherein said host cell is a prokaryotic cell.
93. The host cell of claim 91, wherein said host cell is a eukaryotic cell.
94. The host cell of claim 93, wherein said eukaryotic cell is a mammalian cell.
95. The host cell of claim 94, wherein said mammalian cell is a CHO cell.
96. A pharmaceutical composition comprising the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any one of claims 51-75, or the construct of any one of claims 76-79 and a pharmaceutically acceptable carrier or excipient.
97. The pharmaceutical composition of claim 96, wherein said pharmaceutical composition further comprises an additional therapeutic agent.
98. The pharmaceutical composition of claim 97, wherein said additional therapeutic agent is an immunotherapy agent.
99. The pharmaceutical composition of claim 98, wherein said immunotherapy agent is selected from the group consisting of an anti-CTLA-4 agent, an anti-PD-1 agent, an anti-PD-L1 agent, an anti-PD-

L2 agent, a TNF- $\alpha$  cross-linking agent, a TRAIL cross-linking agent, an anti-CD27 agent, an anti-CD30 agent, an anti-CD40 agent, an anti-4-1BB agent, an anti-GITR agent, an anti-OX40 agent, an anti-TRAILR1 agent, an anti-TRAILR2 agent, an anti-TWEAKR agent, Targretin, Interferon-alpha, clobetasol, Peg Interferon, prednisone, Romidepsin, Bexarotene, methotrexate, Triamcinolone cream, anti-chemokines, Vorinostat, and/or gabapentin.

100. A method of producing the antibody or antigen-binding fragment thereof of any one of claims 1-32, said method comprising expressing a polynucleotide encoding said antibody or antigen-binding fragment thereof in a host cell and recovering the antibody or antigen-binding fragment thereof from host cell medium.

101. A method of producing the single-chain polypeptide of any one of claims 51-75, said method comprising expressing a polynucleotide encoding said single-chain polypeptide in a host cell and recovering the single-chain polypeptide from host cell medium.

102. A method of producing the construct of any one of claims 76-79, said method comprising expressing a polynucleotide encoding said construct in a host cell and recovering the construct from host cell medium.

103. A method of inhibiting an immune response mediated by a regulatory T cell in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99.

104. A method of treating a cell proliferation disorder in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99.

105. The method of claim 104, wherein said cell proliferation disorder is a cancer selected from the group consisting of leukemia, lymphoma, liver cancer, bone cancer, lung cancer, brain cancer, bladder cancer, gastrointestinal cancer, breast cancer, cardiac cancer, cervical cancer, uterine cancer, head and neck cancer, gallbladder cancer, laryngeal cancer, lip and oral cavity cancer, ocular cancer, melanoma, pancreatic cancer, prostate cancer, colorectal cancer, testicular cancer, and throat cancer.

106. The method of claim 104, wherein said cell proliferation disorder is a cancer selected from the group consisting of acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), adrenocortical carcinoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytoma, atypical

teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, extrahepatic cancer, ewing sarcoma family, osteosarcoma and malignant fibrous histiocytoma, central nervous system embryonal tumors, central nervous system germ cell tumors, craniopharyngioma, ependymoma, bronchial tumors, burkitt lymphoma, carcinoid tumor, primary lymphoma, chordoma, chronic myeloproliferative neoplasms, colon cancer, extrahepatic bile duct cancer, ductal carcinoma in situ (DCIS), endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, extracranial germ cell tumor, extragonadal germ cell tumor, fallopian tube cancer, fibrous histiocytoma of bone, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular germ cell tumor, gestational trophoblastic disease, glioma, childhood brain stem glioma, hairy cell leukemia, hepatocellular cancer, langerhans cell histiocytosis, hodgkin lymphoma, hypopharyngeal cancer, islet cell tumors, pancreatic neuroendocrine tumors, wilms tumor and other childhood kidney tumors, langerhans cell histiocytosis, small cell lung cancer, cutaneous T cell lymphoma, intraocular melanoma, merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasm, myelodysplastic syndromes, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-hodgkin lymphoma (NHL), non-small cell lung cancer (NSCLC), epithelial ovarian cancer, germ cell ovarian cancer, low malignant potential ovarian cancer, pancreatic neuroendocrine tumors, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, pleuropulmonary blastoma, primary peritoneal cancer, rectal cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, kaposi sarcoma, rhabdomyosarcoma, sézary syndrome, small intestine cancer, soft tissue sarcoma, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, urethral cancer, endometrial uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, and Waldenström macroglobulinemia.

107. A method of treating an infectious disease in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99.

108. The method of claim 107, wherein said infectious disease is caused by one or more agents selected from the group consisting of a virus, a bacterium, a fungus, or a parasite.

109. The method of claim 108, wherein said infectious disease is caused by a virus selected from the group consisting of hepatitis C virus, Yellow fever virus, Kadam virus, Kyasanur Forest disease virus, Langat virus, Omsk hemorrhagic fever virus, Powassan virus, Royal Farm virus, Karshi virus, tick-borne encephalitis virus, Neudoerfl virus, Sofjin virus, Louping ill virus, Negishi virus, Meaban virus, Saumarez Reef virus, Tyuleniy virus, Aroa virus, dengue virus, Kedougou virus, Cacipacore virus, Koutango virus, Japanese encephalitis virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus, Bagaza virus, Ilheus virus, Israel

turkey meningoencephalo-myelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, Tamana bat virus, cell fusing agent virus, Ippy virus, Lassa virus, lymphocytic choriomeningitis virus (LCMV), Mobala virus, Mopeia virus, Amapari virus, Flexal virus, Guanarito virus, Junin virus, Latino virus, Machupo virus, Oliveros virus, Paraná virus, Pichinde virus, Pirital virus, Sabiá virus, Tacaribe virus, Tamiami virus, Whitewater Arroyo virus, Chapare virus, Lujo virus, Hantaan virus, Sin Nombre virus, Dugbe virus, Bunyamwera virus, Rift Valley fever virus, La Crosse virus, California encephalitis virus, Crimean-Congo hemorrhagic fever (CCHF) virus, Ebola virus, Marburg virus, Venezuelan equine encephalitis virus (VEE), Eastern equine encephalitis virus (EEE), Western equine encephalitis virus (WEE), Sindbis virus, rubella virus, Semliki Forest virus, Ross River virus, Barmah Forest virus, O'nyong'nyong virus, and the chikungunya virus, smallpox virus, monkeypox virus, vaccinia virus, herpes simplex virus, human herpes virus, cytomegalovirus (CMV), Epstein-Barr virus (EBV), Varicella-Zoster virus, Kaposi's sarcoma associated-herpesvirus (KSHV), influenza virus, severe acute respiratory syndrome (SARS) virus, rabies virus, vesicular stomatitis virus (VSV), human respiratory syncytial virus (RSV), Newcastle disease virus, hendravirus, nipahvirus, measles virus, rinderpest virus, canine distemper virus, Sendai virus, human parainfluenza virus (e.g., 1, 2, 3, and 4), rhinovirus, mumps virus, poliovirus, human enterovirus (A, B, C, and D), hepatitis A virus, coxsackievirus, hepatitis B virus, human papilloma virus, adeno-associated virus, astrovirus, JC virus, BK virus, SV40 virus, Norwalk virus, rotavirus, human immunodeficiency virus (HIV), and human T-lymphotropic virus Types I and II.

110. The method of claim 108, wherein said infectious disease is caused by a bacterium belonging to a genus selected from the group consisting of *Salmonella*, *Streptococcus*, *Bacillus*, *Listeria*, *Corynebacterium*, *Nocardia*, *Neisseria*, *Actinobacter*, *Moraxella*, *Enterobacteriaceae*, *Pseudomonas*, *Escherichia*, *Klebsiella*, *Serratia*, *Enterobacter*, *Proteus*, *Salmonella*, *Shigella*, *Yersinia*, *Haemophilus*, *Bordetella*, *Legionella*, *Pasturella*, *Francisella*, *Brucella*, *Bartonella*, *Clostridium*, *Vibrio*, *Campylobacter*, and *Staphylococcus*.

111. The method of claim 108, wherein said infectious disease is caused by a fungus selected from the group consisting of *Aspergillus*, *Candida*, *Malassezia*, *Trichosporon*, *Fusarium*, *Acremonium*, *Rhizopus*, *Mucor*, *Pneumocystis*, and *Absidia*.

112. The method of claim 108, wherein said infectious disease is caused by a parasite selected from the group consisting of *Entamoeba histolytica*, *Giardia lamblia*, *Cryptosporidium muris*, *Trypanosomatida gambiense*, *Trypanosomatida rhodesiense*, *Trypanosomatida cruzi*, *Leishmania mexicana*, *Leishmania braziliensis*, *Leishmania tropica*, *Leishmania donovani*, *Toxoplasma gondii*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium falciparum*, *Trichomonas vaginalis*, and *Histomonas meleagridis*. Exemplary helminthic parasites include *richuris trichiura*, *Ascaris*

*lumbricoides*, *Enterobius vermicularis*, *Ancylostoma duodenale*, *Necator americanus*, *Strongyloides stercoralis*, *Wuchereria bancrofti*, and *Dracunculus medinensis*, *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Fasciola hepatica*, *Fasciola gigantica*, *Heterophyes*, *Paragonimus westermani*, *Taenia solium*, *Taenia saginata*, *Hymenolepis nana*, and *Echinococcus granulosus*.

113. A composition comprising the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99 for inhibiting an immune response mediated by a regulatory T cell in a human.

114. A composition comprising the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99 for treating a cell proliferation disorder in a human.

115. The composition of claim 114, wherein said cell proliferation disorder is a cancer selected from the group consisting of leukemia, lymphoma, liver cancer, bone cancer, lung cancer, brain cancer, bladder cancer, gastrointestinal cancer, breast cancer, cardiac cancer, cervical cancer, uterine cancer, head and neck cancer, gallbladder cancer, laryngeal cancer, lip and oral cavity cancer, ocular cancer, melanoma, pancreatic cancer, prostate cancer, colorectal cancer, testicular cancer, and throat cancer.

116. The composition of claim 114, wherein said cell proliferation disorder is a cancer selected from the group consisting of acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), adrenocortical carcinoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytoma, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, extrahepatic cancer, ewing sarcoma family, osteosarcoma and malignant fibrous histiocytoma, central nervous system embryonal tumors, central nervous system germ cell tumors, craniopharyngioma, ependymoma, bronchial tumors, burkitt lymphoma, carcinoid tumor, primary lymphoma, chordoma, chronic myeloproliferative neoplasms, colon cancer, extrahepatic bile duct cancer, ductal carcinoma in situ (DCIS), endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, extracranial germ cell tumor, extragonadal germ cell tumor, fallopian tube cancer, fibrous histiocytoma of bone, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular germ cell tumor, gestational trophoblastic disease, glioma, childhood brain stem glioma, hairy cell leukemia, hepatocellular cancer, langerhans cell histiocytosis, hodgkin lymphoma, hypopharyngeal cancer, islet cell tumors, pancreatic neuroendocrine tumors, wilms tumor and other childhood kidney tumors, langerhans cell histiocytosis, small cell lung cancer, cutaneous T cell lymphoma, intraocular melanoma, merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell

neoplasm, myelodysplastic syndromes, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-hodgkin lymphoma (NHL), non-small cell lung cancer (NSCLC), epithelial ovarian cancer, germ cell ovarian cancer, low malignant potential ovarian cancer, pancreatic neuroendocrine tumors, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, pleuropulmonary blastoma, primary peritoneal cancer, rectal cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, kaposi sarcoma, rhabdomyosarcoma, sézary syndrome, small intestine cancer, soft tissue sarcoma, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, urethral cancer, endometrial uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, and Waldenström macroglobulinemia.

117. A composition the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, or the pharmaceutical composition of any one of claims 96-99 for treating an infectious disease in a human.

118. The composition of claim 117, wherein said infectious disease is caused by one or more agents selected from the group consisting of a virus, a bacterium, a fungus, or a parasite.

119. The composition of claim 118, wherein said infectious disease is caused by a virus selected from the group consisting of hepatitis C virus, Yellow fever virus, Kadam virus, Kyasanur Forest disease virus, Langat virus, Omsk hemorrhagic fever virus, Powassan virus, Royal Farm virus, Karshi virus, tick-borne encephalitis virus, Neudoerfl virus, Sofjin virus, Louping ill virus, Negishi virus, Meaban virus, Saumarez Reef virus, Tyuleniy virus, Aroa virus, dengue virus, Kedougou virus, Cacipacore virus, Koutango virus, Japanese encephalitis virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey meningoencephalo-myelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, Tamana bat virus, cell fusing agent virus, Ippy virus, Lassa virus, lymphocytic choriomeningitis virus (LCMV), Mobala virus, Mopeia virus, Amapari virus, Flexal virus, Guanarito virus, Junin virus, Latino virus, Machupo virus, Oliveros virus, Paraná virus, Pichinde virus, Pirital virus, Sabiá virus, Tacaribe virus, Tamiama virus, Whitewater Arroyo virus, Chapare virus, Lujo virus, Hantaan virus, Sin Nombre virus, Dugbe virus, Bunyamwera virus, Rift Valley fever virus, La Crosse virus, California encephalitis virus, Crimean-Congo hemorrhagic fever (CCHF) virus, Ebola virus, Marburg virus, Venezuelan equine encephalitis virus (VEE), Eastern equine encephalitis virus (EEE), Western equine encephalitis virus (WEE), Sindbis virus, rubella virus, Semliki Forest virus, Ross River virus, Barmah Forest virus, O'nyong'nyong virus, and the chikungunya virus, smallpox virus,



monkeypox virus, vaccinia virus, herpes simplex virus, human herpes virus, cytomegalovirus (CMV), Epstein-Barr virus (EBV), Varicella-Zoster virus, Kaposi's sarcoma associated-herpesvirus (KSHV), influenza virus, severe acute respiratory syndrome (SARS) virus, rabies virus, vesicular stomatitis virus (VSV), human respiratory syncytial virus (RSV), Newcastle disease virus, hendravirus, nipahvirus, measles virus, rinderpest virus, canine distemper virus, Sendai virus, human parainfluenza virus (e.g., 1, 2, 3, and 4), rhinovirus, mumps virus, poliovirus, human enterovirus (A, B, C, and D), hepatitis A virus, coxsackievirus, hepatitis B virus, human papilloma virus, adeno-associated virus, astrovirus, JC virus, BK virus, SV40 virus, Norwalk virus, rotavirus, human immunodeficiency virus (HIV), and human T-lymphotropic virus Types I and II.

120. The composition of claim 118, wherein said infectious disease is caused by a bacterium belonging to a genus selected from the group consisting of *Salmonella*, *Streptococcus*, *Bacillus*, *Listeria*, *Corynebacterium*, *Nocardia*, *Neisseria*, *Actinobacter*, *Moraxella*, *Enterobacteriaceae*, *Pseudomonas*, *Escherichia*, *Klebsiella*, *Serratia*, *Enterobacter*, *Proteus*, *Salmonella*, *Shigella*, *Yersinia*, *Haemophilus*, *Bordetella*, *Legionella*, *Pasturella*, *Francisella*, *Brucella*, *Bartonella*, *Clostridium*, *Vibrio*, *Campylobacter*, and *Staphylococcus*.

121. The composition of claim 118, wherein said infectious disease is caused by a fungus selected from the group consisting of *Aspergillus*, *Candida*, *Malassezia*, *Trichosporon*, *Fusarium*, *Acremonium*, *Rhizopus*, *Mucor*, *Pneumocystis*, and *Absidia*.

122. The composition of claim 118, wherein said infectious disease is caused by a parasite selected from the group consisting of *Entamoeba histolytica*, *Giardia lamblia*, *Cryptosporidium muris*, *Trypanosomatida gambiense*, *Trypanosomatida rhodesiense*, *Trypanosomatida cruzi*, *Leishmania mexicana*, *Leishmania braziliensis*, *Leishmania tropica*, *Leishmania donovani*, *Toxoplasma gondii*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium falciparum*, *Trichomonas vaginalis*, and *Histomonas meleagridis*. Exemplary helminthic parasites include *richuris trichiura*, *Ascaris lumbricoides*, *Enterobius vermicularis*, *Ancylostoma duodenale*, *Necator americanus*, *Strongyloides stercoralis*, *Wuchereria bancrofti*, and *Dracunculus medinensis*, *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Fasciola hepatica*, *Fasciola gigantica*, *Heterophyes*, *Paragonimus westermani*, *Taenia solium*, *Taenia saginata*, *Hymenolepis nana*, and *Echinococcus granulosus*.

123. A kit comprising an agent selected from the group consisting of the antibody or antigen-binding fragment thereof of any one of claims 1-32 and 45-50, the single-chain polypeptide of any of claims 51-75, the construct of any one of claims 76-79, the polynucleotide of any one of claims 80-82, the vector of any one of claims 83-90, the host cell of any one of claims 91 and 93-95, and the pharmaceutical composition of any one of claims 96-99.

124. The kit of claim 123, wherein said kit comprises the antibody or antigen-binding fragment thereof any one of claims 1-32 and 45-50.

125. The kit of claim 123, wherein said kit comprises the single-chain polypeptide of any of claims 51-75.
126. The kit of claim 123, wherein said kit comprises the construct of any of claims 76-79.
127. The kit of claim 123, wherein said kit comprises the polynucleotide of any one of claims 80-82.
128. The kit of claim 123, wherein said kit comprises the vector of any one of claims 83-90.
129. The kit of claim 128, wherein said kit further comprises instructions for transfecting said vector into a host cell.
130. The kit of claim 129, wherein said kit further comprises instructions for expressing said antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct in said host cell.
131. The kit of claim 123, wherein said kit comprises the host cell of any one of claims 91-95.
132. The kit of claim 123, wherein said kit comprises the pharmaceutical composition of any one of claims 96-99.
133. The kit of claim 123, wherein said kit further comprises a reagent that can be used to express the antibody, antigen-binding fragment thereof, single-chain polypeptide, or construct in said host cell.
134. The kit of claim 123, further comprising instructions for administering said agent to a human patient.
135. The kit of claim 123, further comprising instructions for making or using said agent.
136. The antibody or antigen-binding fragment thereof of claim 1, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259).
137. The antibody or antigen-binding fragment thereof of claim 1, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).
138. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):
- (a) a CDR-H1 having the amino acid sequence GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277);
  - (b) a CDR-H2 having the amino acid sequence (J)<sub>5</sub>GSJ;
  - (c) a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y;
  - (d) a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and
  - (e) a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T;
- wherein each J is independently a naturally occurring amino acid.

139. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X;
- (b) a CDR-H2 having the amino acid sequence VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264);
- (c) a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268);
- (d) a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and
- (e) a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271);

wherein each Z<sup>1</sup> is independently an amino acid comprising a cationic side-chain at physiological

pH;

each Z<sup>2</sup> is independently an amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently an amino acid comprising a polar, uncharged side-chain at physiological

pH;

each Z<sup>4</sup> is independently a glycine or alanine;

each Z<sup>5</sup> is independently an amino acid comprising a hydrophobic side-chain; and

each X is independently leucine or isoleucine.

140. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment further comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
- (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
- (c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;
- (d) a CDR-L2 having the amino acid sequence TYS or YTS; and
- (e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each X is independently leucine or isoleucine.

141. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment comprises one or more, or all, of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GYTFTDYX (SEQ ID NO: 257);
- (b) a CDR-H2 having the amino acid sequence VDPEYGST (SEQ ID NO: 258);
- (c) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260);
- (d) a CDR-L2 having the amino acid sequence TYS or YTS; and
- (e) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261);

wherein each X is independently leucine or isoleucine.

142. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274).

143. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-H1 has the amino acid sequence GYTFTDYI (SEQ ID NO: 275).

144. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-L2 has the amino acid sequence TYS.

145. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-L2 has the amino acid sequence YTS.

146. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-L3 has the amino acid sequence CLQYVLLT (SEQ ID NO: 272).

147. The antibody or antigen-binding fragment thereof of claim 141, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

148. The antibody or antigen-binding fragment thereof of claim 141, wherein said antibody or antigen-binding fragment thereof comprises a framework region comprising the amino acid sequence LLIR (SEQ ID NO: 262) bound to the N-terminus of said CDR-L2.

149. The antibody or antigen-binding fragment thereof of claim 141, wherein said antibody or antigen-binding fragment thereof comprises a framework region comprising the amino acid sequence TLE bound to the C-terminus of said CDR-L2.

150. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment does not comprise one or more of the following regions (CDRs):

- (a) a CDR-H1 having the amino acid sequence GFTFSSY (SEQ ID NO: 23);
- (b) a CDR-H2 having the amino acid sequence SSGGSY (SEQ ID NO: 24);
- (c) a CDR-L1 having the amino acid sequence SASSSVYYMY (SEQ ID NO: 26);
- (d) a CDR-L2 having the amino acid sequence STSNLAS (SEQ ID NO: 27);
- (e) a CDR-L3 having the amino acid sequence QQRRNYPYT (SEQ ID NO: 28);
- (f) a CDR-L1 comprising the amino acid sequence RASKSVSTSGYSYMH (SEQ ID NO: 29);
- (g) a CDR-L2 comprising the amino acid sequence LASNLES (SEQ ID NO: 30); and
- (h) a CDR-L3 comprising the amino acid sequence QHSRELPRT (SEQ ID NO: 31).

151. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof comprises a non-native constant region.

152. The antibody or antigen-binding fragment thereof of claim 151, wherein said non-native constant region is a human constant region.

153. The antibody or antigen-binding fragment thereof of claim 1 wherein said antibody or antigen-binding fragment thereof lacks all or a portion of an Fc domain, lacks all or a portion of a native Fc domain, or lacks an Fc domain altogether.

154. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof specifically binds to a peptide comprising the amino acid sequence of any one of SEQ ID NOs: 11, 19, 20, and 34-117 with a  $K_D$  of less than about 100 nM and does not bind a peptide comprising amino acids 56-60 (KCSPG) of SEQ ID NO: 7.

155. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof specifically binds a peptide comprising one or more of amino acids 142-146 of SEQ ID NO: 7 (KCRPG) and does not bind a peptide comprising amino acids 56-60 of SEQ ID NO: 7 (KCSPG).

156. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof inhibits TNFR2 signaling.

157. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof inhibits the expression of one or more genes selected from the group consisting of CHUK, NFKBIE, NFKBIA, MAP3K11, TRAF2, TRAF3, relB, and cIAP2/BIRC3.

158. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof inhibits NF $\kappa$ B activation.

159. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of T-reg cells.

160. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of cancer cells that express TNFR2.

161. The antibody or antigen-binding fragment thereof of claim 160, wherein said cancer cells are selected from the group consisting of T cell lymphoma cells, such as Hodgkin's or cutaneous non-Hodgkin's lymphoma cells, ovarian cancer cells, colon cancer cells, multiple myeloma cells, and renal cell carcinoma cells.

162. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof is capable of reducing or inhibiting the proliferation of myeloid-derived suppressor cells.

163. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof does not require TNF $\alpha$  to reduce or inhibit the proliferation of T-reg cells.

164. The antibody or antigen-binding fragment thereof of claim 1, wherein said antibody or antigen-binding fragment thereof is capable of directly expanding T effector cells.

165. The single-chain polypeptide of any one of claims 51-56, wherein in the presence of said CDR-H3, the antibody or antigen-binding fragment thereof is capable of specifically binding a peptide comprising the amino acid sequence of LRKCRPGFGVA (SEQ ID NO: 285) or VVCKPCAPGTFSN (SEQ ID NO: 286).

166. The single-chain polypeptide of claim 51, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYWG (SEQ ID NO: 259).

167. The single-chain polypeptide of claim 51, wherein said CDR-H3 has the amino acid sequence ARDDGSYSPFDYFG (SEQ ID NO: 284).

168. The single-chain polypeptide of claim 51, wherein said CDR-H1 has the amino acid sequence:

(a) GJTF(J)<sub>2</sub>YJ (SEQ ID NO: 277);

(b) Z<sup>4</sup>YZ<sup>3</sup>Z<sup>5</sup>TDZ<sup>5</sup>X; or

(c) GYTFTDYX (SEQ ID NO: 257) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain;

and

each X is independently leucine or isoleucine.

169. The single-chain polypeptide of claim 168, wherein said CDR-H1 has the amino acid sequence GYTFTDYX (SEQ ID NO: 257).

170. The single-chain polypeptide of claim 169, wherein said CDR-H1 has the amino acid sequence GYTFTDYL (SEQ ID NO: 274).

171. The single-chain polypeptide of claim 169, wherein said CDR-H1 has the amino acid sequence GYTFTDYI (SEQ ID NO: 275).

172. The single-chain polypeptide of claim 51, wherein said CDR-H2 has the amino acid sequence:

(a) (J)<sub>5</sub>GSJ;

(b) VDPEYZ<sup>4</sup>Z<sup>3</sup>T (SEQ ID NO: 264); or

(c) VDPEYGST (SEQ ID NO: 258) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

wherein each J is independently a naturally occurring amino acid;

each Z<sup>1</sup> is independently a naturally occurring amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently a naturally occurring amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently a naturally occurring amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine; and

each Z<sup>5</sup> is independently a naturally occurring amino acid comprising a hydrophobic side-chain.

173. The single-chain polypeptide of claim 172, wherein said CDR-H2 has the amino acid sequence VDPEYGST (SEQ ID NO: 258).

174. The single-chain polypeptide of claim 51, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence (J)<sub>5</sub>Y;

(b) a CDR-L2 having the amino acid sequence (J)<sub>2</sub>S; and

(c) a CDR-L3 having the amino acid sequence (J)<sub>3</sub>Y(J)<sub>4</sub>T.

wherein each J is independently a naturally occurring amino acid.

175. The single-chain polypeptide of claim 51, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence QNINKZ<sup>5</sup> (SEQ ID NO: 268);

(b) a CDR-L2 having the amino acid sequence TYZ<sup>3</sup> or YTZ<sup>3</sup>; and

(c) a CDR-L3 having the amino acid sequence CLQZ<sup>5</sup>VNLXZ<sup>3</sup> (SEQ ID NO: 271);

wherein each Z<sup>1</sup> is independently an amino acid comprising a cationic side-chain at physiological pH;

each Z<sup>2</sup> is independently an amino acid comprising an anionic side-chain at physiological pH;

each Z<sup>3</sup> is independently an amino acid comprising a polar, uncharged side-chain at physiological pH;

each Z<sup>4</sup> is independently a glycine or alanine;

each Z<sup>5</sup> is independently an amino acid comprising a hydrophobic side-chain; and

each X is independently leucine or isoleucine.

176. The single-chain polypeptide of claim 51, wherein said single-chain polypeptide further comprises one or more, or all, of the following CDRs:

(a) a CDR-L1 having the amino acid sequence QNINKY (SEQ ID NO: 260) or an amino acid sequence having up to two amino acid substitutions relative to said sequence;

- (b) a CDR-L2 having the amino acid sequence TYS or YTS; and
- (c) a CDR-L3 having the amino acid sequence CLQYVNLXT (SEQ ID NO: 261) or an amino acid sequence having up to two amino acid substitutions relative to said sequence; wherein each X is independently leucine or isoleucine.

177. The single-chain polypeptide of claim 174, wherein said CDR-L2 has the amino acid sequence TYS.

178. The single-chain polypeptide of claim 174, wherein said CDR-L2 has the amino acid sequence YTS.

179. The single-chain polypeptide of claim 174, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 272).

180. The single-chain polypeptide of claim 174, wherein said CDR-L3 has the amino acid sequence CLQYVNLIT (SEQ ID NO: 273).

181. The single-chain polypeptide of claim 174, wherein said single-chain polypeptide comprises a framework region comprising the amino acid sequence LLIR (SEQ ID NO: 262) bound to the N-terminus of said CDR-L2.

182. The single-chain polypeptide of claim 174, wherein said single-chain polypeptide comprises a framework region comprising the amino acid sequence TLE bound to the C-terminus of said CDR-L2.

183. The single-chain polypeptide of claim 51, wherein said single-chain polypeptide does not comprise one or more of the following CDRs:

- (a) a CDR-H1 having the amino acid sequence GFTFSSY (SEQ ID NO: 23);
- (b) a CDR-H2 having the amino acid sequence SSGGSY (SEQ ID NO: 24); and
- (c) a CDR-L1 having the amino acid sequence SASSSVYYMY (SEQ ID NO: 26);
- (d) a CDR-L2 having the amino acid sequence STSNLAS (SEQ ID NO: 27);
- (e) a CDR-L3 having the amino acid sequence QRRNYPYT (SEQ ID NO: 28);
- (f) a CDR-L1 having the amino acid sequence RASKSVSTSGYSYMH (SEQ ID NO: 29);
- (g) a CDR-L2 having the amino acid sequence LASNLES (SEQ ID NO: 30); and
- (h) a CDR-L3 having the amino acid sequence QHSRELPRT (SEQ ID NO: 31).

184. A method of inhibiting an immune response mediated by a regulatory T cell in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of claim 1.

185. A method of treating a cell proliferation disorder in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of claim 1.



186. The method of claim 185, wherein said cell proliferation disorder is a cancer selected from the group consisting of leukemia, lymphoma, liver cancer, bone cancer, lung cancer, brain cancer, bladder cancer, gastrointestinal cancer, breast cancer, cardiac cancer, cervical cancer, uterine cancer, head and neck cancer, gallbladder cancer, laryngeal cancer, lip and oral cavity cancer, ocular cancer, melanoma, pancreatic cancer, prostate cancer, colorectal cancer, testicular cancer, and throat cancer.

187. The method of claim 185, wherein said cell proliferation disorder is a cancer selected from the group consisting of acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), adrenocortical carcinoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytoma, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, extrahepatic cancer, ewing sarcoma family, osteosarcoma and malignant fibrous histiocytoma, central nervous system embryonal tumors, central nervous system germ cell tumors, craniopharyngioma, ependymoma, bronchial tumors, burkitt lymphoma, carcinoid tumor, primary lymphoma, chordoma, chronic myeloproliferative neoplasms, colon cancer, extrahepatic bile duct cancer, ductal carcinoma in situ (DCIS), endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, extracranial germ cell tumor, extragonadal germ cell tumor, fallopian tube cancer, fibrous histiocytoma of bone, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular germ cell tumor, gestational trophoblastic disease, glioma, childhood brain stem glioma, hairy cell leukemia, hepatocellular cancer, langerhans cell histiocytosis, hodgkin lymphoma, hypopharyngeal cancer, islet cell tumors, pancreatic neuroendocrine tumors, wilms tumor and other childhood kidney tumors, langerhans cell histiocytosis, small cell lung cancer, cutaneous T cell lymphoma, intraocular melanoma, merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasm, myelodysplastic syndromes, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-hodgkin lymphoma (NHL), non-small cell lung cancer (NSCLC), epithelial ovarian cancer, germ cell ovarian cancer, low malignant potential ovarian cancer, pancreatic neuroendocrine tumors, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, pleuropulmonary blastoma, primary peritoneal cancer, rectal cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, kaposi sarcoma, rhabdomyosarcoma, sézary syndrome, small intestine cancer, soft tissue sarcoma, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, urethral cancer, endometrial uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, and Waldenström macroglobulinemia.

188. A method of treating an infectious disease in a human, said method comprising administering to the human the antibody or antigen-binding fragment thereof of claim 1.

189. The method of claim 188, wherein said infectious disease is caused by one or more agents selected from the group consisting of a virus, a bacterium, a fungus, or a parasite.

190. The method of claim 189, wherein said infectious disease is caused by a virus selected from the group consisting of hepatitis C virus, Yellow fever virus, Kadam virus, Kyasanur Forest disease virus, Langat virus, Omsk hemorrhagic fever virus, Powassan virus, Royal Farm virus, Karshi virus, tick-borne encephalitis virus, Neudoerfl virus, Sofjin virus, Louping ill virus, Negishi virus, Meaban virus, Saumarez Reef virus, Tyuleniy virus, Aroa virus, dengue virus, Kedougou virus, Cacipacore virus, Koutango virus, Japanese encephalitis virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey meningoencephalo-myelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, Tamana bat virus, cell fusing agent virus, Ippy virus, Lassa virus, lymphocytic choriomeningitis virus (LCMV), Mobala virus, Mopeia virus, Amapari virus, Flexal virus, Guanarito virus, Junin virus, Latino virus, Machupo virus, Oliveros virus, Paraná virus, Pichinde virus, Pirital virus, Sabiá virus, Tacaribe virus, Tamiami virus, Whitewater Arroyo virus, Chapare virus, Lujo virus, Hantaan virus, Sin Nombre virus, Dugbe virus, Bunyamwera virus, Rift Valley fever virus, La Crosse virus, California encephalitis virus, Crimean-Congo hemorrhagic fever (CCHF) virus, Ebola virus, Marburg virus, Venezuelan equine encephalitis virus (VEE), Eastern equine encephalitis virus (EEE), Western equine encephalitis virus (WEE), Sindbis virus, rubella virus, Semliki Forest virus, Ross River virus, Barmah Forest virus, O'nyong'nyong virus, and the chikungunya virus, smallpox virus, monkeypox virus, vaccinia virus, herpes simplex virus, human herpes virus, cytomegalovirus (CMV), Epstein-Barr virus (EBV), Varicella-Zoster virus, Kaposi's sarcoma associated-herpesvirus (KSHV), influenza virus, severe acute respiratory syndrome (SARS) virus, rabies virus, vesicular stomatitis virus (VSV), human respiratory syncytial virus (RSV), Newcastle disease virus, hendravirus, nipahvirus, measles virus, rinderpest virus, canine distemper virus, Sendai virus, human parainfluenza virus (e.g., 1, 2, 3, and 4), rhinovirus, mumps virus, poliovirus, human enterovirus (A, B, C, and D), hepatitis A virus, coxsackievirus, hepatitis B virus, human papilloma virus, adeno-associated virus, astrovirus, JC virus, BK virus, SV40 virus, Norwalk virus, rotavirus, human immunodeficiency virus (HIV), and human T-lymphotropic virus Types I and II.

191. The method of claim 189, wherein said infectious disease is caused by a bacterium belonging to a genus selected from the group consisting of *Salmonella*, *Streptococcus*, *Bacillus*, *Listeria*, *Corynebacterium*, *Nocardia*, *Neisseria*, *Actinobacter*, *Moraxella*, *Enterobacteriaceae*, *Pseudomonas*, *Escherichia*, *Klebsiella*, *Serratia*, *Enterobacter*, *Proteus*, *Salmonella*, *Shigella*, *Yersinia*, *Haemophilus*, *Bordetella*, *Legionella*, *Pasturella*, *Francisella*, *Brucella*, *Bartonella*, *Clostridium*, *Vibrio*, *Campylobacter*, and *Staphylococcus*.

192. The method of claim 189, wherein said infectious disease is caused by a fungus selected from the group consisting of *Aspergillus*, *Candida*, *Malassezia*, *Trichosporon*, *Fusarium*, *Acremonium*, *Rhizopus*, *Mucor*, *Pneumocystis*, and *Absidia*.

193. The method of claim 189, wherein said infectious disease is caused by a parasite selected from the group consisting of *Entamoeba histolytica*, *Giardia lamblia*, *Cryptosporidium muris*, *Trypanosomatida gambiense*, *Trypanosomatida rhodesiense*, *Trypanosomatida cruzi*, *Leishmania mexicana*, *Leishmania braziliensis*, *Leishmania tropica*, *Leishmania donovani*, *Toxoplasma gondii*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, *Plasmodium falciparum*, *Trichomonas vaginalis*, and *Histomonas meleagridis*. Exemplary helminthic parasites include *richuris trichiura*, *Ascaris lumbricoides*, *Enterobius vermicularis*, *Ancylostoma duodenale*, *Necator americanus*, *Strongyloides stercoralis*, *Wuchereria bancrofti*, and *Dracunculus medinensis*, *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Fasciola hepatica*, *Fasciola gigantica*, *Heterophyes*, *Paragonimus westermani*, *Taenia solium*, *Taenia saginata*, *Hymenolepis nana*, and *Echinococcus granulosus*.

FIG. 1A. DNA and Amino Acid Sequences of TNFRAB1 Heavy Chain

## TNFRAB1 Heavy Chain

## DNA Sequence

```
GACCAGGCATCCCAGGGTCACCATGGAGTTAGTTTGGGCAGCAGATCCAGGGGCCAGTGGATAGA
CAGATGGGGGTGTCGTTTTGGCTGAGGAGACGGTGACCGCGGTCCCTGCGCCCCAGACATCGAAG
TACCAGTAGCTGGAGTAACCATCAACCOCTCTGTCGTGCACAGTAATACATGGCCGTGTCCTCAGACC
TCAGACTGCTCATTTCAGGTACAGGGTGTTCTTGCCATTGTCTCTGGAGATGGTGAATCGCCCTT
CACACTGTCTGGATAGTAGGTGTAACCTACCACCACTACTAATGGTTGCGACCCACTCCAGCCTCTC
TCCGGAGTCTGGCGAACCCAAGACATGACATAACTACTGAAAGTGAATCCAGAGGCTGCACAGSAG
AGTTTCAGGGACCOCTCCAGGCTTCACTAAGCCTCCCCCTGACTCCTGCAGCTGCACCTCCGGAAGC
CTGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCG-AGCATGCATCTAGAGGCCCAT
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## Amino acid sequence

```
EVQLQESGGGLVFKPGGSLKLSCAASGFTFSSYVMSWVROTPFKRLEWVATISSGGSYTYYPDSVKGRF
TISRDNKNTLYLQMSSLRSEDAMYYCARQRVDGYSSYWYFDVWGAGTAVTVSS
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FIG. 1B. DNA and Amino Acid Sequences of TNFRAB1 Light Chain

TNFRAB1 Light Chain

DNA sequence

CTCCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCAGGGGGACATTGTGCTGACCCAGTCT  
 CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATAACCTGCAGTGCCAGCTCAAGTGTAT  
 ATTACATGTACTGGTTCCAGCAGAAGCCAGGCACCTTCTCCCAAACCTCTGGATTTATAGCACATCCAAC  
 CTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGCTCTGGGACCTTTACTCTCTCACAATCA  
 GCCGAATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAAAGGAGGAATTACCCGTACACGTT  
 CGGAGGGGGGACCAAGTTGGAAATAAACGGGCTGATGCTCCACCAACTGTATCCATCTTCCCACC  
 ATCCAGTGAGCAGTTACCTGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA  
 CCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACT 7/16

Amino acid sequence

DIVLTQSPAIMSASPGEKVTITCSASSSVYYMYWFOQKPGTSPKLWIYSTSNLASGVFVRFSGSGGTSY  
 SLTISRMEAEDAATYYCQRRNYPYTFGGGTKLEIKRA

FIG. 2A. Epitopes within TNFR2 bound by TNFRAB1

10	20	30	40	50
MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYYDQTA
60	70	80	90	100
QMCCSKCSPG	QHAKVFCTKT	SDTVCDSCED	STYTQLWNWV	PECLSCGSRG
110	120	130	140	150
SSDQVETQAC	TREQNRICTC	RPGWYCALS	QEGCRLCAPL	RKCEPSTGVA
160	170	180	190	200
RPGTETSDVV	RKCEPSTGVA	NTTSSTDICR	PHQTCNVVAI	PGNASMDAVC
210	220	230	240	250
TSTSPTRSM	PGAVHLPQPV	STRSQHTQPT	PEPSTAPSTS	ELLPMGPSPF
260	270	280	290	300
AEGSTGDFAL	PVGLIVGVTA	LGLLIIGVVN	CVINTQVKKK	PLCLQREAKV
310	320	330	340	350
PHLPADKARG	TQGPEQQHLL	ITAPSSSSSS	LESSASALDR	RAPTRNQPQA
360	370	380	390	400
PGVEASGAGE	ARASTGSSDS	SPGGHGTQVN	VTCIVNVCSS	SDHSSQCSSQ
410	420	430	440	450
ASSTMGDTDS	SPSESEKDEQ	VPPSKEECA	RSQLETPETL	LGSTEEKPLF
460				
LGVPDAGMKP	S			

FIG. 2B. Epitopes within TNFR2 bound by TNFRAB2

10	20	30	40	50
MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYYDQTA
60	70	80	90	100
QMCCSKCSPG	QHAKVFCTKT	SDTVCDSCEN	STYTQIWNWV	PECLSCGSRG
110	120	130	140	150
SSDQVETQAC	TREQN	EPGWYCALS	KQEGCRL	APL
160	170	180	190	200
RPGETETSDVV	CKPCAPGTFS	NTTSSTDICR	PHQICNVVAI	PGNASMDAVC
210	220	230	240	250
TSTSPTRSMA	PGAVHLPQPV	STRSQHTQPT	PEPSTAPSTS	FLLPMGPPSP
260	270	280	290	300
AEGSTGDFAL	FVGLIVGVTA	LGLLIIGVNV	CVIMTQVKKK	PLCLQREAKV
310	320	330	340	350
PHLPADKARG	TQGPEQQHLL	ITAPSSSSSS	LESSASALDR	RAPTRNQPPA
360	370	380	390	400
PGVEASGAGE	ARASTGSSDS	SPGGHGTQVN	VTCIVNVCSS	SDHSSQCSSQ
410	420	430	440	450
ASSTMGDGDS	SPSESPKDEQ	VPFSKEECA	RSQLETPETL	LGSTEEKPLP
460				
LGVPDAGMKP	S			

FIG. 3A. Epitope mapping of TNFRAB1

SEQ ID NO.	Peptide Sequence	Structural Group	Raw luminescence data
134	SRCS5DQVETQGG5GGTREQNRICT2R	CYS.S	177
135	RCSSDQVETQAGG5GGTREQNRICT2R	CYS.S	125
136	CS5DQVETQA2GG5GGTREQNRICT2R	CYS.S	179
137	VPE2LS2GSRCGG5GGREQNRICT2RP	CYS.S	318
138	PE2LS2GSRC5GG5GGREQNRICT2RP	CYS.S	291
139	E2LS2GSRCSS5GG5GGREQNRICT2RP	CYS.S	323
140	2LS2GSRCSSDGG5GGREQNRICT2RP	CYS.S	262
141	LS2GSRCSSDQGG5GGREQNRICT2RP	CYS.S	261
142	S2GSRCSSDQVGG5GGREQNRICT2RP	CYS.S	247
143	2GSRCSSDQVEGG5GGREQNRICT2RP	CYS.S	228
144	GSRCSSDQVETGG5GGREQNRICT2RP	CYS.S	166
145	SRCS5DQVETQGG5GGREQNRICT2RP	CYS.S	157
146	RCSSDQVETQAGG5GGREQNRICT2RP	CYS.S	130
147	CSSDQVETQA2GG5GGREQNRICT2RP	CYS.S	250
148	VPE2LS2GSRCGG5GGEQNRICT2RPG	CYS.S	225
149	PE2LS2GSRC5GG5GGEQNRICT2RPG	CYS.S	229
150	E2LS2GSRCSS5GG5GGEQNRICT2RPG	CYS.S	152
151	2LS2GSRCSSDGG5GGEQNRICT2RPG	CYS.S	214
152	LS2GSRCSSDQGG5GGEQNRICT2RPG	CYS.S	244
153	S2GSRCSSDQVGG5GGEQNRICT2RPG	CYS.S	235
154	2GSRCSSDQVEGG5GGEQNRICT2RPG	CYS.S	221
155	GSRCSSDQVETGG5GGEQNRICT2RPG	CYS.S	202
156	SRCS5DQVETQGG5GGEQNRICT2RPG	CYS.S	222
157	RCSSDQVETQAGG5GGEQNRICT2RPG	CYS.S	183
158	CSSDQVETQA2GG5GGEQNRICT2RPG	CYS.S	248
159	VPE2LS2GSRCGG5GGQNRICT2RPGW	CYS.S	577
160	PE2LS2GSRC5GG5GGQNRICT2RPGW	CYS.S	543
161	E2LS2GSRCSS5GG5GGQNRICT2RPGW	CYS.S	482
162	2LS2GSRCSSDGG5GGQNRICT2RPGW	CYS.S	345
163	LS2GSRCSSDQGG5GGQNRICT2RPGW	CYS.S	291
164	S2GSRCSSDQVGG5GGQNRICT2RPGW	CYS.S	364
165	2GSRCSSDQVEGG5GGQNRICT2RPGW	CYS.S	483
166	GSRCSSDQVETGG5GGQNRICT2RPGW	CYS.S	466
167	SRCS5DQVETQGG5GGQNRICT2RPGW	CYS.S	402
168	RCSSDQVETQAGG5GGQNRICT2RPGW	CYS.S	507
169	CSSDQVETQA2GG5GGQNRICT2RPGW	CYS.S	493



FIG. 3A (Continued)

170	VPE2LS2GSRCGGSGGNRICT2RPGWY	CYS.S	853
171	PE2LS2GSRCSSGGSGGNRICT2RPGWY	CYS.S	928
172	E2LS2GSRCSSGGSGGNRICT2RPGWY	CYS.S	389
173	2LS2GSRCSSDGGSGGNRICT2RPGWY	CYS.S	878
174	LS2GSRCSSDQGGSGGNRICT2RPGWY	CYS.S	822
175	S2GSRCSSDQVGGSGGNRICT2RPGWY	CYS.S	656
176	2GSRCSSDQVEGGSGGNRICT2RPGWY	CYS.S	588
177	GSRCSSDQVETGGSGGNRICT2RPGWY	CYS.S	587
178	SRCSSDQVETQGGSGGNRICT2RPGWY	CYS.S	482
179	RCSSDQVETQAGGSGGNRICT2RPGWY	CYS.S	247
180	CSSDQVETQA2GGSGGNRICT2RPGWY	CYS.S	487
181	VPE2LS2GSRCGGSGGRICT2RPGWY2	CYS.S	478
182	PE2LS2GSRCSSGGSGGRICT2RPGWY2	CYS.S	585
183	E2LS2GSRCSSGGSGGRICT2RPGWY2	CYS.S	478
184	2LS2GSRCSSDGGSGGRICT2RPGWY2	CYS.S	436
185	LS2GSRCSSDQGGSGGRICT2RPGWY2	CYS.S	546
186	S2GSRCSSDQVGGSGGRICT2RPGWY2	CYS.S	465
187	2GSRCSSDQVEGGSGGRICT2RPGWY2	CYS.S	614
188	GSRCSSDQVETGGSGGRICT2RPGWY2	CYS.S	594
189	SRCSSDQVETQGGSGGRICT2RPGWY2	CYS.S	568
190	RCSSDQVETQAGGSGGRICT2RPGWY2	CYS.S	543
191	CSSDQVETQA2GGSGGRICT2RPGWY2	CYS.S	597
192	VPE2LS2GSRCGGSGGICT2RPGWY2A	CYS.S	540
193	PE2LS2GSRCSSGGSGGICT2RPGWY2A	CYS.S	542
194	E2LS2GSRCSSGGSGGICT2RPGWY2A	CYS.S	454
195	2GSRCSSDQVEGGSGGICT2RPGWY2A	CYS.S	402
196	GSRCSSDQVETGGSGGICT2RPGWY2A	CYS.S	403
197	SRCSSDQVETQGGSGGICT2RPGWY2A	CYS.S	388
198	RCSSDQVETQAGGSGGICT2RPGWY2A	CYS.S	372
199	CSSDQVETQA2GGSGGICT2RPGWY2A	CYS.S	454
200	VPE2LS2GSRCGGSGGCT2RPGWY2AL	CYS.S	483
201	PE2LS2GSRCSSGGSGGCT2RPGWY2AL	CYS.S	697
202	E2LS2GSRCSSGGSGGCT2RPGWY2AL	CYS.S	605
203	2LS2GSRCSSDGGSGGCT2RPGWY2AL	CYS.S	603
204	LS2GSRCSSDQGGSGGCT2RPGWY2AL	CYS.S	510
205	S2GSRCSSDQVGGSGGCT2RPGWY2AL	CYS.S	538
206	2GSRCSSDQVEGGSGGCT2RPGWY2AL	CYS.S	480
207	GSRCSSDQVETGGSGGCT2RPGWY2AL	CYS.S	464
208	SRCSSDQVETQGGSGGCT2RPGWY2AL	CYS.S	391
209	RCSSDQVETQAGGSGGCT2RPGWY2AL	CYS.S	319
210	CSSDQVETQA2GGSGGCT2RPGWY2AL	CYS.S	265

FIG. 3A (Continued)

211	2TREQNRI2TCGGSGGRRPGWYCALSKQ	CYS.S	101
212	TREQNRI2TCRGGSGGRRPGWYCALSKQ	CYS.S	188
213	REQNRI2TCRPGGSGGRRPGWYCALSKQ	CYS.S	228
214	EQNRI2TCRPGGSGGRRPGWYCALSKQ	CYS.S	263
215	QNRI2TCRPGWGGSGGRRPGWYCALSKQ	CYS.S	240
216	NRI2TCRPGWYGGSGGRRPGWYCALSKQ	CYS.S	426
217	WY2ALSKQEGCGGSGG2APLRKCRPGF	CYS.S	327
218	Y2ALSKQEGCRGGSGG2APLRKCRPGF	CYS.S	308
219	2ALSKQEGCRLGGSGG2APLRKCRPGF	CYS.S	439
220	ALSKQEGCRL2GGSGG2APLRKCRPGF	CYS.S	560
221	LSKQEGCRL2AGGSGG2APLRKCRPGF	CYS.S	529
222	SKQEGCRL2APGGSGG2APLRKCRPGF	CYS.S	507
223	KQEGCRL2APLGGSGG2APLRKCRPGF	CYS.S	528
224	QEGCRL2APLRGGSGG2APLRKCRPGF	CYS.S	570
225	EGCRL2APLRKGGSGG2APLRKCRPGF	CYS.S	604
226	WY2ALSKQEGCGGSGGAPLRKCRPGFG	CYS.S	534
227	Y2ALSKQEGCRGGSGGAPLRKCRPGFG	CYS.S	553
228	2ALSKQEGCRLGGSGGAPLRKCRPGFG	CYS.S	418
229	ALSKQEGCRL2GGSGGAPLRKCRPGFG	CYS.S	321
230	LSKQEGCRL2AGGSGGAPLRKCRPGFG	CYS.S	253
231	SKQEGCRL2APGGSGGAPLRKCRPGFG	CYS.S	220
232	KQEGCRL2APLGGSGGAPLRKCRPGFG	CYS.S	242
233	QEGCRL2APLRGGSGGAPLRKCRPGFG	CYS.S	340
234	EGCRL2APLRKGGSGGAPLRKCRPGFG	CYS.S	312
235	WY2ALSKQEGCGGSGGPLRKCRPGFGV	CYS.S	341
236	Y2ALSKQEGCRGGSGGPLRKCRPGFGV	CYS.S	381
237	2ALSKQEGCRLGGSGGPLRKCRPGFGV	CYS.S	414
238	ALSKQEGCRL2GGSGGPLRKCRPGFGV	CYS.S	446
239	LSKQEGCRL2AGGSGGPLRKCRPGFGV	CYS.S	434
240	SKQEGCRL2APGGSGGPLRKCRPGFGV	CYS.S	389
241	KQEGCRL2APLGGSGGPLRKCRPGFGV	CYS.S	457
242	QEGCRL2APLRGGSGGPLRKCRPGFGV	CYS.S	558
243	EGCRL2APLRKGGSGGPLRKCRPGFGV	CYS.S	450
244	WY2ALSKQEGCGGSGGLRKCRPGFGVA	CYS.S	336
245	Y2ALSKQEGCRGGSGGRKCRPGFGVAR	CYS.S	463
246	2ALSKQEGCRLGGSGGRKCRPGFGVAR	CYS.S	443
247	ALSKQEGCRL2GGSGGRKCRPGFGVAR	CYS.S	455
248	LSKQEGCRL2AGGSGGRKCRPGFGVAR	CYS.S	474
249	SKQEGCRL2APGGSGGRKCRPGFGVAR	CYS.S	430
250	KQEGCRL2APLGGSGGRKCRPGFGVAR	CYS.S	430
251	QEGCRL2APLRGGSGGRKCRPGFGVAR	CYS.S	426

FIG. 3A (Continued)

252	EGCRL2APLRKGGSGGRKCRPGFGVAR	CYS.5	358
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FIG. 3B. Epitope mapping of TNFRAB2

SEQ ID NO.	Peptide Sequence	Structural Group	Raw luminescence data
34	PE2LS2GSRCSSGGSGGNRICT2RPGWY	CYS.S	928
35	2LS2GSRCSSDGGSGGNRICT2RPGWY	CYS.S	878
36	VPE2LS2GSRCSSGGSGGNRICT2RPGWY	CYS.S	853
37	LS2GSRCSSDQGGSGGNRICT2RPGWY	CYS.S	822
38	PE2LS2GSRCSSGGSGGCT2RPGWY2AL	CYS.S	697
39	S2GSRCSSDQVGGSGGNRICT2RPGWY	CYS.S	666
40	2GSRCSSDQVEGGSGGRICT2RPGWY2	CYS.S	614
41	E2LS2GSRCSSGGSGGCT2RPGWY2AL	CYS.S	605
42	EGCRL2APLRKGGSGG2APLRKCRPGF	CYS.S	604
43	2LS2GSRCSSDGGSGGCT2RPGWY2AL	CYS.S	603
44	CSSDQVETQA2GGSGGRICT2RPGWY2	CYS.S	597
45	GSRCSSDQVETGGSGGRICT2RPGWY2	CYS.S	594
46	2GSRCSSDQVEGGSGGNRICT2RPGWY	CYS.S	588
47	GSRCSSDQVETGGSGGNRICT2RPGWY	CYS.S	587
48	PE2LS2GSRCSSGGSGGRICT2RPGWY2	CYS.S	585
49	VPE2LS2GSRCSSGGSGGNRICT2RPGW	CYS.S	577
50	QEGCRL2APLRGGSGG2APLRKCRPGF	CYS.S	570
51	SRCSSDQVETQGGSGGRICT2RPGWY2	CYS.S	568
52	ALSKQEGCRL2GGSGG2APLRKCRPGF	CYS.S	560
53	QEGCRL2APLRGGSGGPLRKCRPGFGV	CYS.S	558
54	Y2ALSKQEGCRGGSGGAPLRKCRPGFG	CYS.S	553
55	LS2GSRCSSDQGGSGGRICT2RPGWY2	CYS.S	546
56	PE2LS2GSRCSSGGSGGQNRRICT2RPGW	CYS.S	543
57	RCSSDQVETQAGGSGGRICT2RPGWY2	CYS.S	543
58	PE2LS2GSRCSSGGSGGICT2RPGWY2A	CYS.S	542
59	VPE2LS2GSRCSSGGSGGICT2RPGWY2A	CYS.S	540
60	S2GSRCSSDQVGGSGGCT2RPGWY2AL	CYS.S	538
61	WY2ALSKQEGCGGSGGAPLRKCRPGFG	CYS.S	534
62	LSKQEGCRL2AGGSGG2APLRKCRPGF	CYS.S	529
63	KOEGCRL2APLGGSGG2APLRKCRPGF	CYS.S	528
64	LS2GSRCSSDQGGSGGCT2RPGWY2AL	CYS.S	510
65	RCSSDQVETQAGGSGGQNRRICT2RPGW	CYS.S	507
66	SKQEGCRL2APGGSGG2APLRKCRPGF	CYS.S	507
67	2GSRCSSDQVEGGSGGQNRRICT2RPGW	CYS.S	493
68	CSSDQVETQA2GGSGGQNRRICT2RPGW	CYS.S	493

FIG. 3B (Continued)

69	CSSDQVETQA2GG5GGNRICT2RPGWY	CYS.S	487
70	VPE2L52G5RCGG5GGCT2RPGWY2AL	CYS.S	488
71	E2L52G5RCSSGG5GGQNRICT2RPGW	CYS.S	482
72	SRCSSDQVETQGG5GGNRICT2RPGWY	CYS.S	482
73	2G5RCSSDQVEGG5GGCT2RPGWY2AL	CYS.S	480
74	VPE2L52G5RCGG5GGRICT2RPGWY2	CYS.S	478
75	E2L52G5RCSSGG5GGRICT2RPGWY2	CYS.S	478
76	L5KQEGCRL2AGG5GGGRKCRPGFGVAR	CYS.S	474
77	G5RCSSDQVETGG5GGQNRICT2RPGW	CYS.S	466
78	S2G5RCSSDQVGG5GGRICT2RPGWY2	CYS.S	465
79	G5RCSSDQVETGG5GGCT2RPGWY2AL	CYS.S	464
80	Y2AL5KQEGCRGG5GGGRKCRPGFGVAR	CYS.S	463
81	KQEGCRL2APLGG5GGPLRKCRPGFGV	CYS.S	457
82	AL5KQEGCRL2GG5GGGRKCRPGFGVAR	CYS.S	455
83	E2L52G5RCSSGG5GGICT2RPGWY2A	CYS.S	454
84	CSSDQVETQA2GG5GGICT2RPGWY2A	CYS.S	454
85	EGCRL2APLRKGG5GGPLRKCRPGFGV	CYS.S	450
86	AL5KQEGCRL2GG5GGPLRKCRPGFGV	CYS.S	446
87	2AL5KQEGCRLGG5GGGRKCRPGFGVAR	CYS.S	443
88	2AL5KQEGCRLGG5GG2APLRKCRPGF	CYS.S	439
89	2L52G5RCSSDGG5GGRICT2RPGWY2	CYS.S	436
90	L5KQEGCRL2AGG5GGPLRKCRPGFGV	CYS.S	434
91	SKQEGCRL2APGG5GGGRKCRPGFGVAR	CYS.S	430
92	KQEGCRL2APLGG5GGGRKCRPGFGVAR	CYS.S	430
93	QEGCRL2APLRGG5GGGRKCRPGFGVAR	CYS.S	426
94	2AL5KQEGCRLGG5GGAPLRKCRPGFG	CYS.S	418
95	2AL5KQEGCRLGG5GGPLRKCRPGFGV	CYS.S	414
96	G5RCSSDQVETGG5GGICT2RPGWY2A	CYS.S	403
97	SRCSSDQVETQGG5GGQNRICT2RPGW	CYS.S	402
98	2G5RCSSDQVEGG5GGICT2RPGWY2A	CYS.S	402
99	E2L52G5RCSSGG5GGNRICT2RPGWY	CYS.S	389
100	SRCSSDQVETQGG5GGICT2RPGWY2A	CYS.S	388
101	Y2AL5KQEGCRGG5GGPLRKCRPGFGV	CYS.S	381
102	RCSSDQVETQAGG5GGICT2RPGWY2A	CYS.S	372
103	SKQEGCRL2APGG5GGPLRKCRPGFGV	CYS.S	369
104	S2G5RCSSDQVGG5GGQNRICT2RPGW	CYS.S	364
105	EGCRL2APLRKGG5GGGRKCRPGFGVAR	CYS.S	358
106	2L52G5RCSSDGG5GGQNRICT2RPGW	CYS.S	345
107	WY2AL5KQEGCGG5GGPLRKCRPGFGV	CYS.S	341
108	QEGCRL2APLRGG5GGAPLRKCRPGFG	CYS.S	340
109	WY2AL5KQEGCGG5GG2APLRKCRPGF	CYS.S	327

FIG. 3B (Continued)

110	ALSKQEGCRLZGGSGGAPLRKCRPGFG	CYS.S	321
111	EGCRLZAPLRKGGSGGAPLRKCRPGFG	CYS.S	312
112	Y2ALSKQEGCRGGSGG2APLRKCRPGF	CYS.S	308
113	LS2GSRCS5SDQGGSGGQNR ICT2RPGW	CYS.S	291
114	LSKQEGCRLZAGGSGGAPLRKCRPGFG	CYS.S	253
115	RCS5DQVETOAGGSGGNR ICT2RPGWY	CYS.S	247
116	KQEGCRLZAPLGGSGGAPLRKCRPGFG	CYS.S	242
117	SKQEGCRLZAPGGSGGAPLRKCRPGFG	CYS.S	220

FIG. 4. Visualization of epitopes bound by TNFR2 antibodies

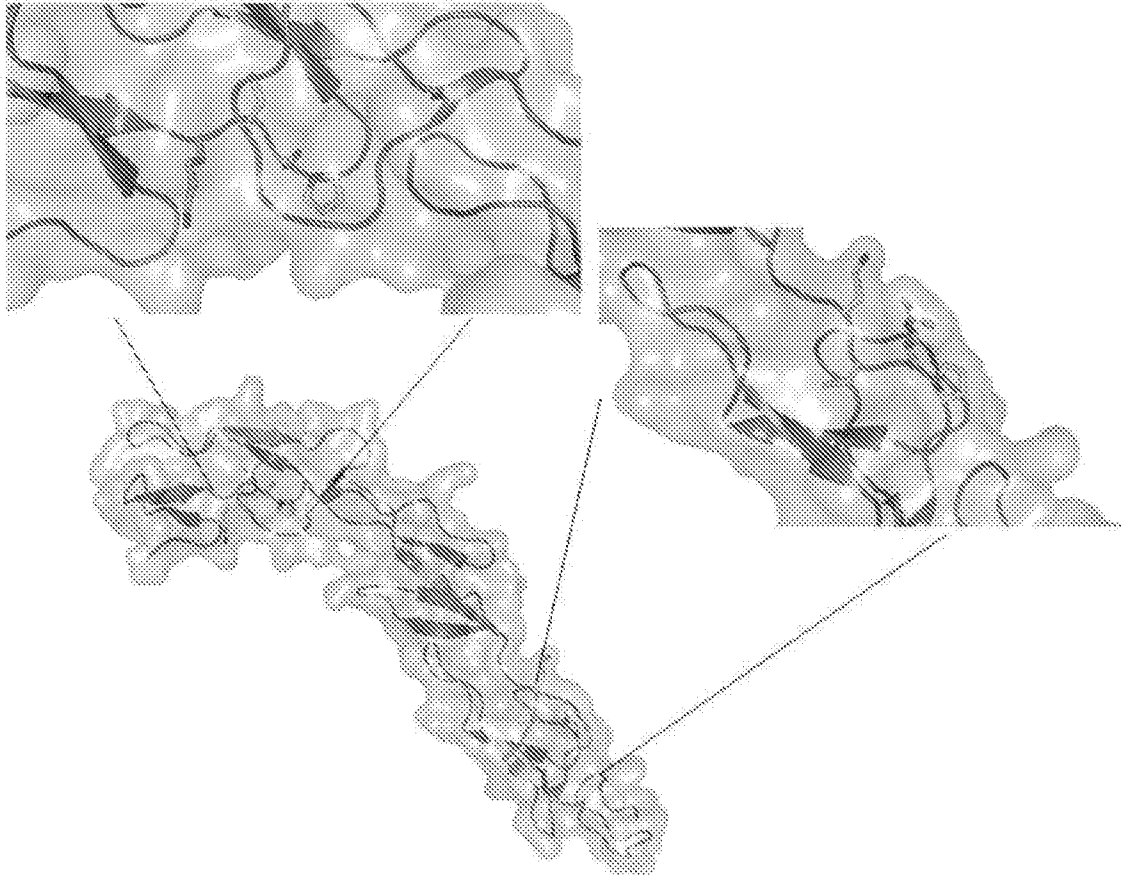
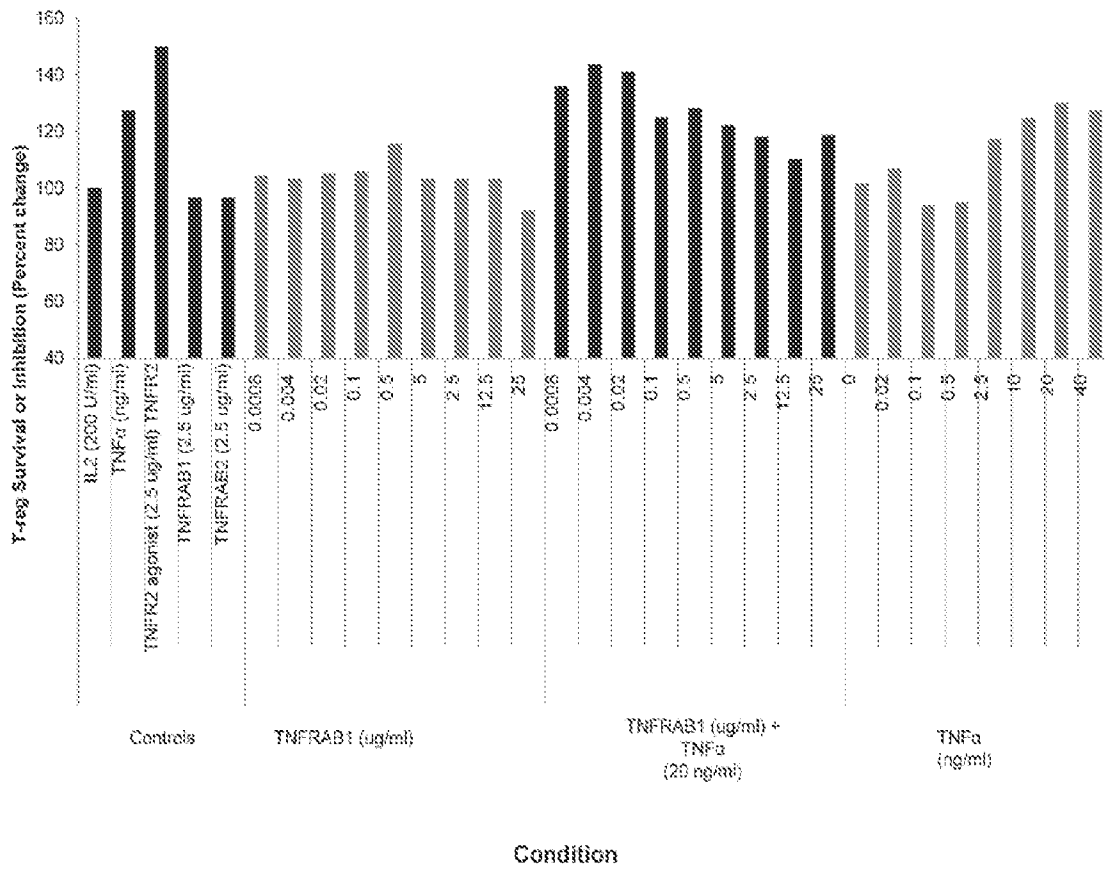
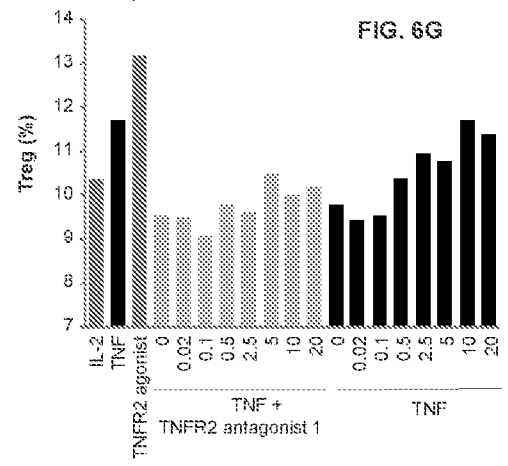
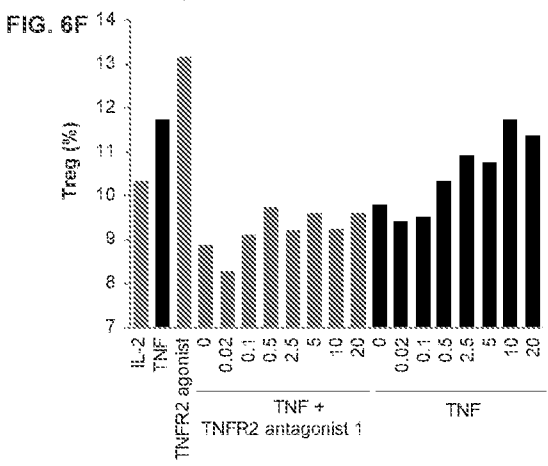
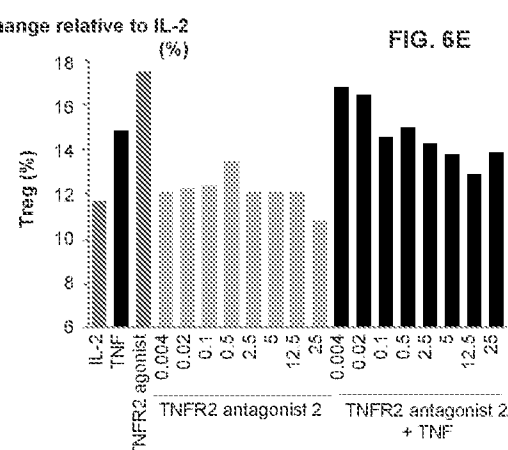
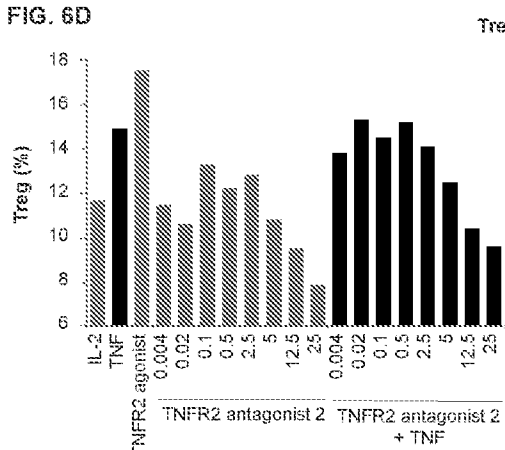
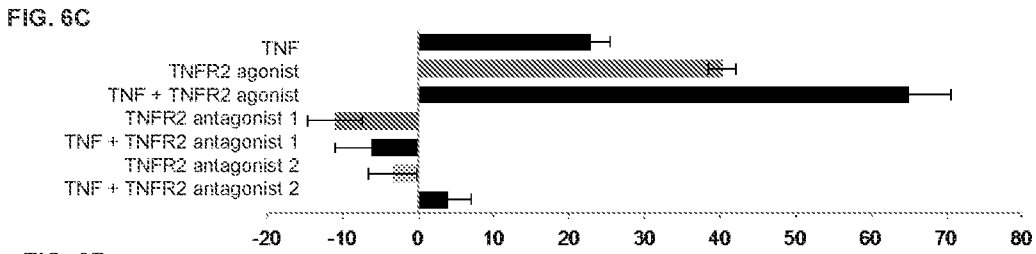
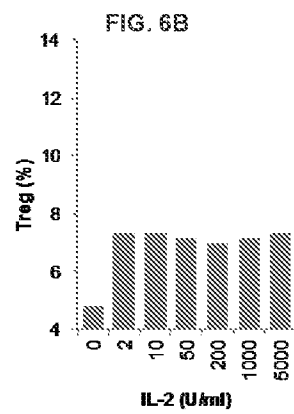
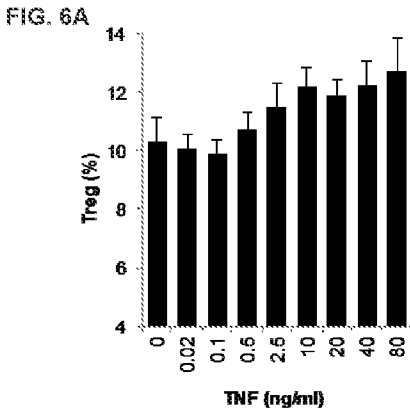
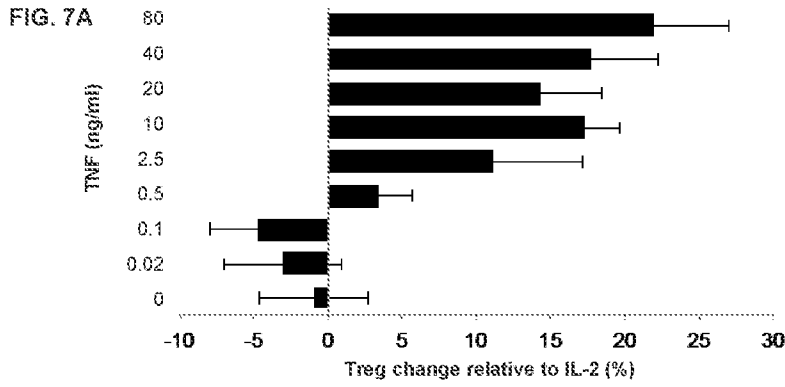


FIG. 5. T-reg Suppression Assay

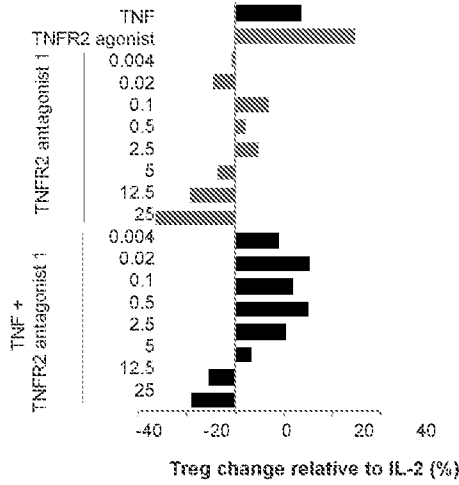




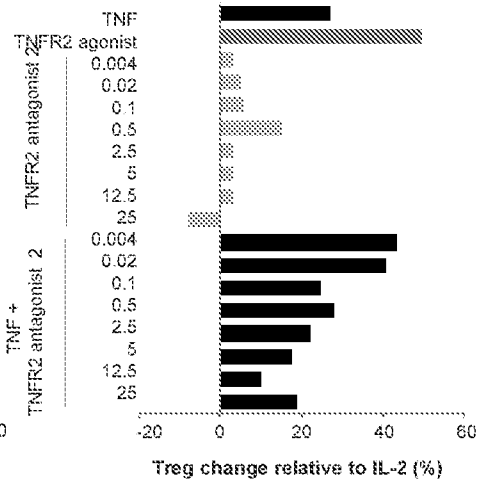




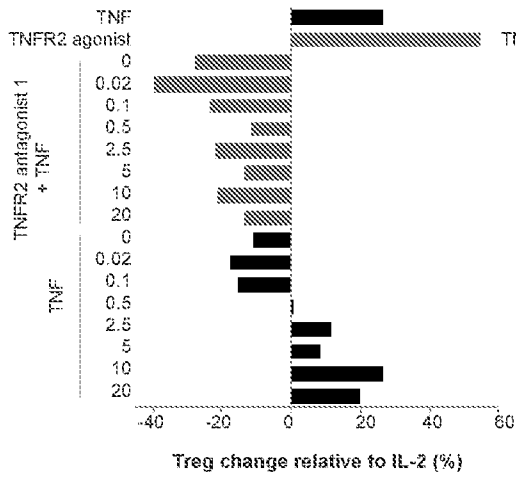
**FIG. 7B**



**FIG. 7C**



**FIG. 7D**



**FIG. 7E**

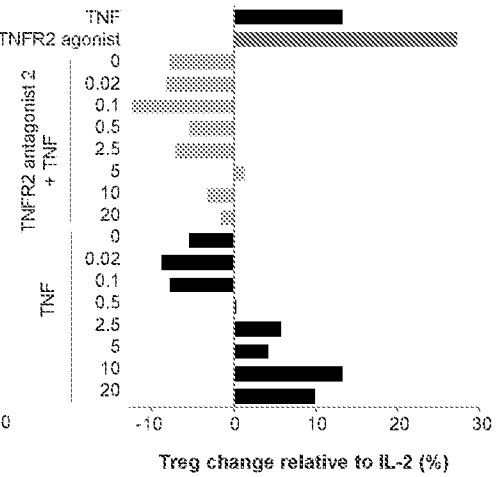


FIG. 8A

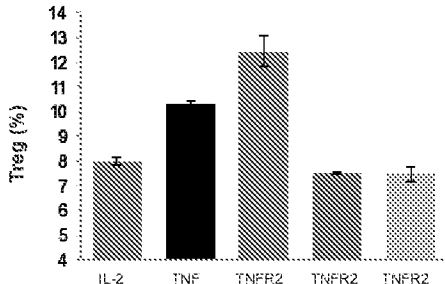


FIG. 8B

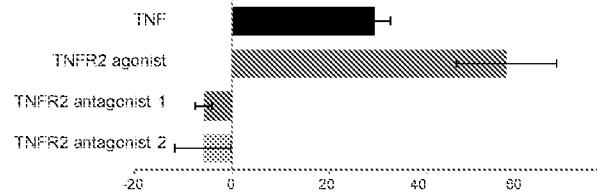


FIG. 8C

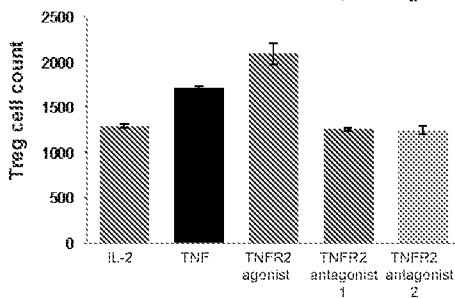


FIG. 8D

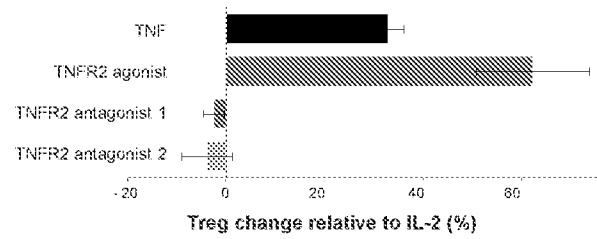


FIG. 8E

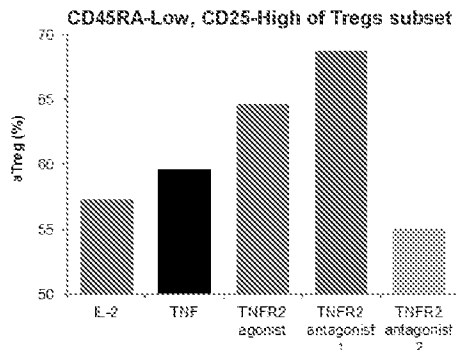


FIG. 8F

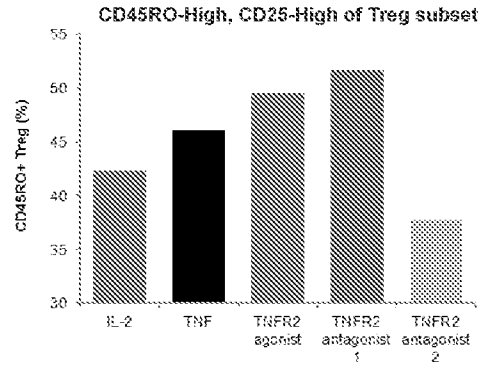


FIG. 8G

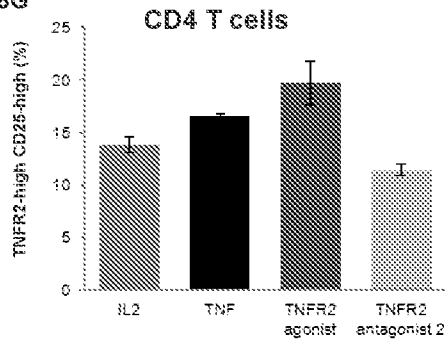


FIG. 8H

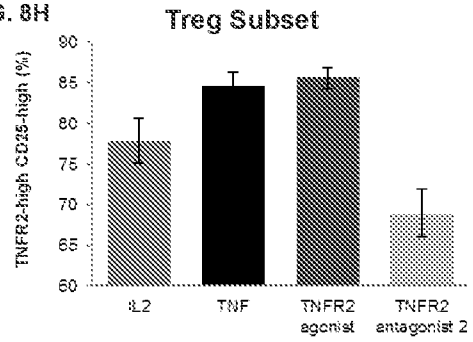


FIG. 9A

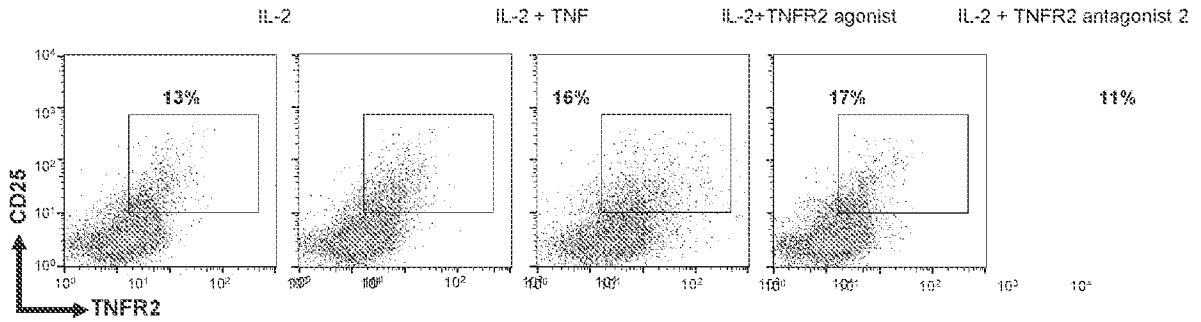


FIG. 9B

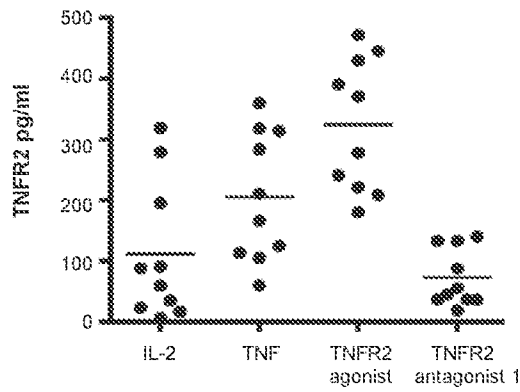


FIG. 9C

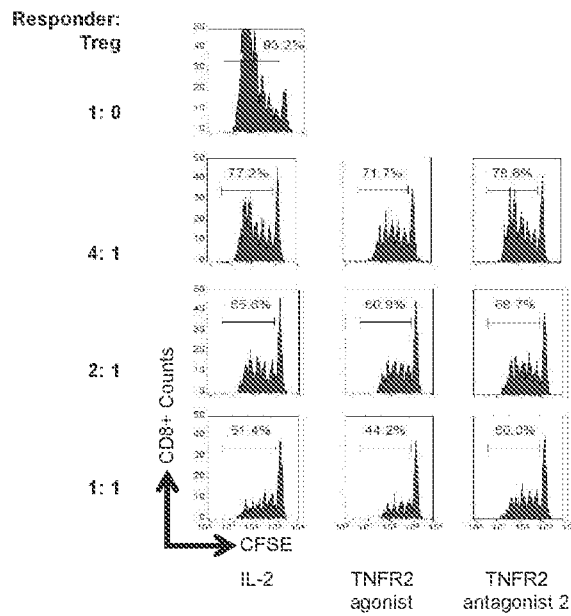


FIG. 10A

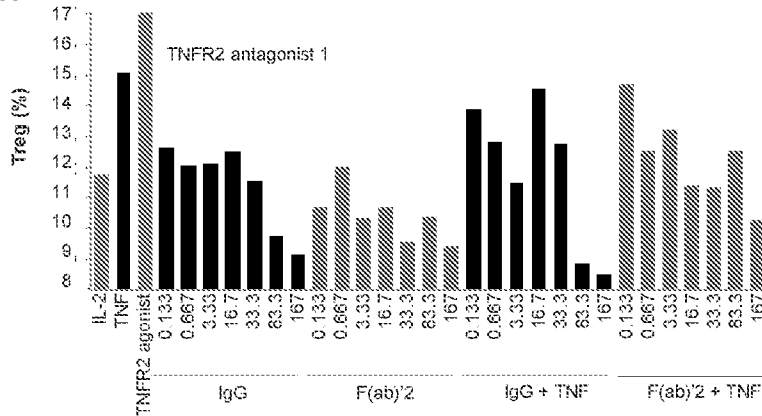


FIG. 10B

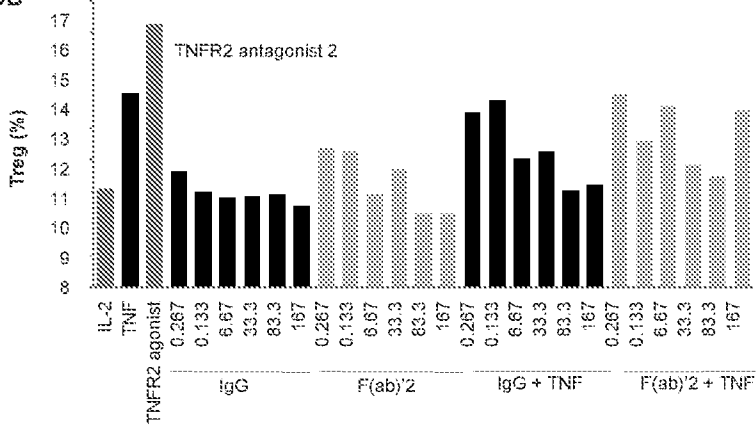


FIG. 10C

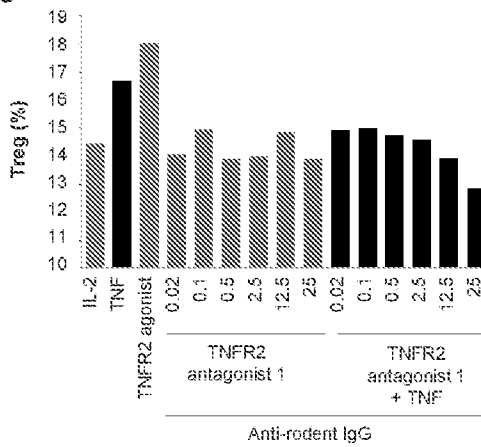


FIG. 10D

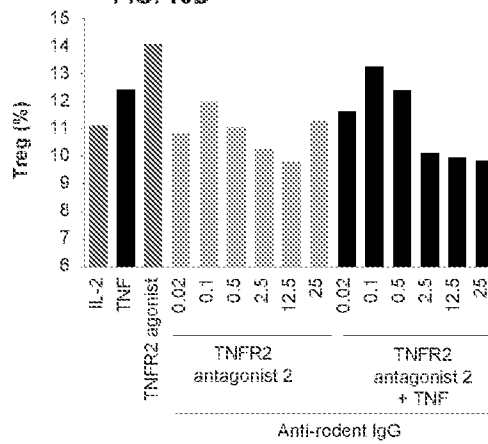


FIG. 11A

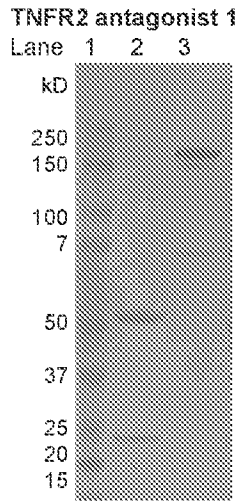
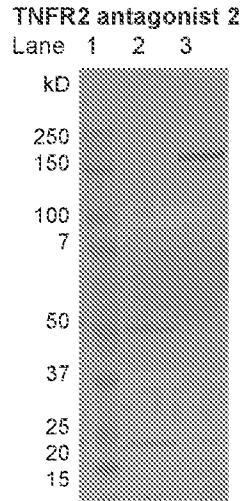
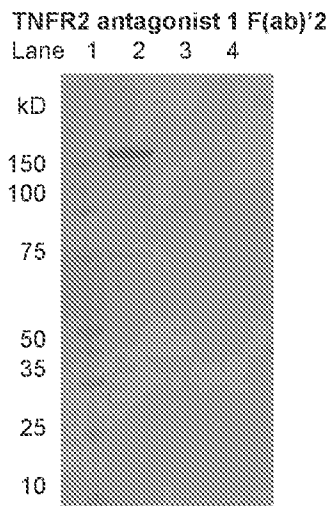


FIG. 11B



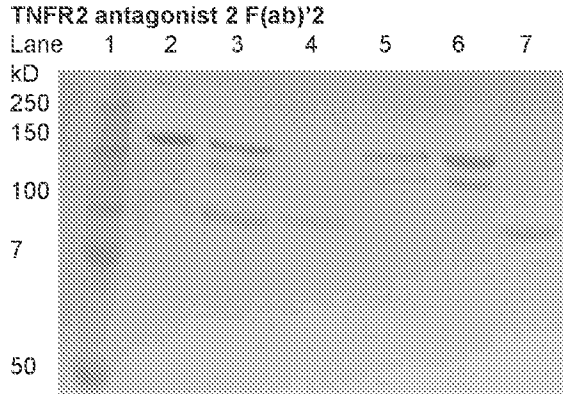
- Lane
1. Precision Plus Protein Marker (10 ul)
  2. Reduced (2.5 ug)
  3. Non-reduced (2.5 ug)

FIG. 11C



1. Perfect Protein™ marker (5 ul)
2. TNFR2 antagonist 1 (2.5 ug)
3. Purified F(ab)'2 (15 ul of 1.5 ml)
4. Protein A column elution (15 ul of 1 ml)

FIG. 11D



1. Precision Plus Protein marker (10 ul)
2. TNFR2 antagonist 2 (2.5 ug)
3. Digested IgG1 (15 ul of 2 ml)
4. Purified F(ab)'2 (15 ul of 3 ml)
5. Final flow through + elution (15 ul of 1.5 ml)
6. Protein A column elution (15 ul of 500 ul)
7. Concentrated F(ab)'2 (5 ul)

FIG. 12A

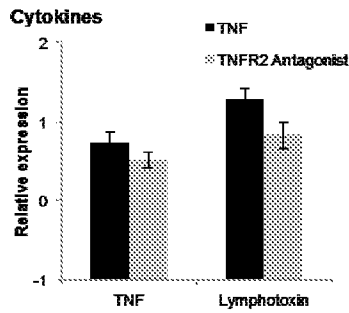


FIG. 12B

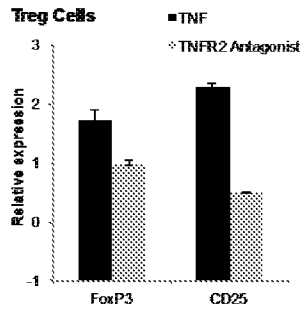


FIG. 12C

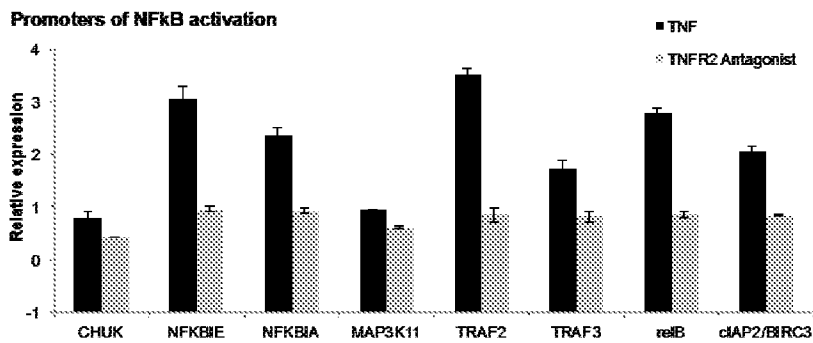


FIG. 12D

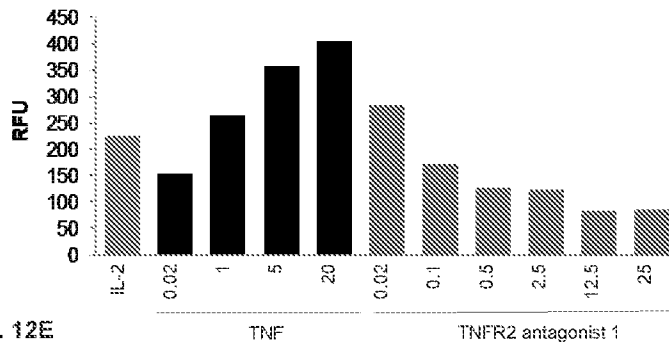


FIG. 12E

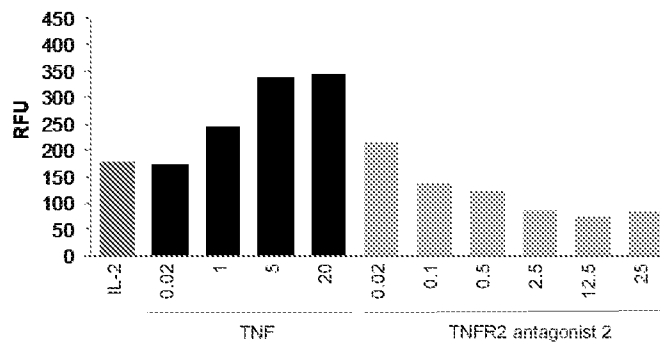


FIG. 13A

Binding affinity of antagonists to TNFR2

TNFR2 antagonist	$k_{on}$ (1/Ms)	$k_{off}$ (1/s)	$K_D$ (M)
1	4.98E+06	2.21E-04	4.44E-11
2	3.609(9)E+05	2.24E-04	6.21(2)E-10

$k_{on}$  =  $k_a$  – association rate constant

$k_{off}$  =  $k_d$  – dissociation rate constant

$K_D$  – equilibrium dissociation constant

FIG. 13B

Linear peptide mapping of TNFR2 antagonists

Peptide	Position	Sequence	TNFR2 antagonist 1		TNFR2 antagonist 2	
			Affinity	Reading	Affinity	Reading
TNFR2	hTNFR2 (23-207)	20kD	+++	1.2	+++	1.2
S04062	hTNFR2 (1-20)	LPAQVAFTPYAPEPGSTCRL	-	0	-	0
S03931	hTNFR2 (9-28)	PYAPEPGSTCRLREYYDQTA	-	0	-	0
S04063	hTNFR2 (17-36)	TCRLREYYDQTAQMCCSKCS	-	0	-	0
S03933	hTNFR2(26-45)	QTAQMCCSKCSPGQHAKVFC	+	0.1	-	0
S04064	hTNFR2(34-53)	KCSPGQHAKVFKTKSDTV	-	0	-	0
S04065	hTNFR2 (42-61)	KVFCTKTSDTVCDSCEDSTY	-	0	-	0
S04066	hTNFR2 (50-69)	DTVCDSCEDSTYQLWNWVP	-	0	-	0
S04067	hTNFR2 (58-77)	DSTYQLWNWVPECLSCGSR	-	0	-	0
S04068	hTNFR2 (66-85)	NWVPECLSCGSRSSDQVET	-	0	-	0
S04069	hTNFR2 (74-93)	CGSRCSSDQVETQACTREQN	-	0	-	0
S04070	hTNFR2 (82-101)	QVETQACTREQNRICTRPG	-	0	-	0
S04071	hTNFR2 (90-109)	REQNRICTRPGWYCALSKQ	++	0.5*	-	0
S04072	hTNFR2(98-117)	CRPGWYCALSKQEGCRLCAP	++	0.2*	-	0
S04073	hTNFR2(106-125)	LSKQEGCRLCAPLRKCRPGF	++++	1.2*	-	0
S03935	hTNFR2 (108-127)	KQEGCRLCAPLRKCRPGFV	++++	1.2	-	0
S04074	hTNFR2(114-133)	LCAPLRKCRPGFVARPGTE	++++	1.2*	-	0
S04075	hTNFR2 (122-141)	RPGFVARPGTETSDDVCKP	-	0	-	0
S04076	hTNFR2 (130-149)	PGTETSDDVCKPCAPGTFNS	-	0	-	0
S04077	hTNFR2 (138-157)	VCKPCAPGTFNSSTSDIC	-	0	-	0
S04078	hTNFR2 (146-165)	TFSNTSSTDICRPHQICNV	-	0	-	0
S04079	hTNFR2 (154-174)	TDICRPHQICNVVAIPGNAS	-	0	-	0
S04080	hTNFR2 (162-181)	ICNVVAIPGNASMDAVCTST	-	0	-	0
S04081	hTNFR2 (170-189)	GNASMDAVCTSTSPTRSMAP	-	0	-	0

\*Ratio (2x)

FIG. 13C

Linear peptide mapping of TNFR2 antagonists with TNF competition

Peptide	Position	Sequence	TNFR2 antagonist 1		TNFR2 antagonist 2	
			Affinity	Plus TNF	Affinity	Plus TNF
S03933	hTNFR2(26-45)	QTAQMCCSKCSPGQHAKVFC	+	No effect	-	n/a
S04071	hTNFR2 (90-109)	REQNRICTRPGWYCALSKQ	++	No effect	-	n/a
S04072	hTNFR2(98-117)	CRPGWYCALSKQEGCRLCAP	++	No effect	-	n/a
S04073	hTNFR2(106-125)	LSKQEGCRLCAPLRKCRPGF	++++	No effect	-	n/a
S03935	hTNFR2 (108-127)	KQEGCRLCAPLRKCRPGFV	++++	No effect	-	n/a
S04074	hTNFR2(114-133)	LCAPLRKCRPGFVARPGTE	++++	No effect	-	n/a



FIG. 14A

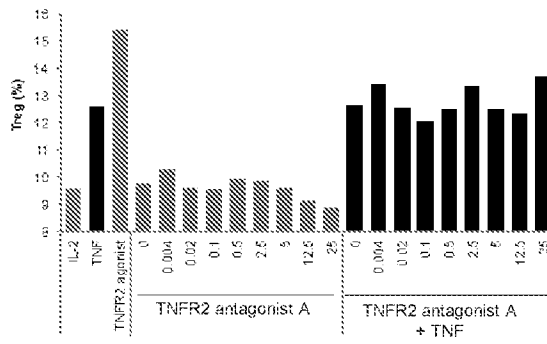


FIG. 14B

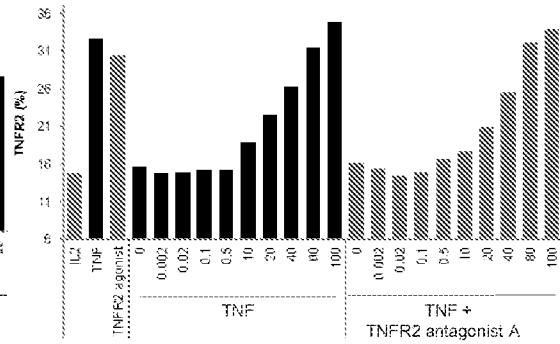


FIG. 14C

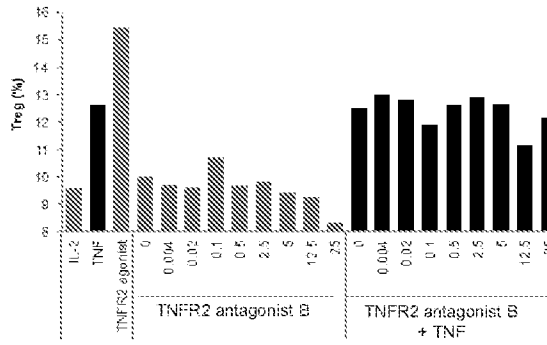


FIG. 14D

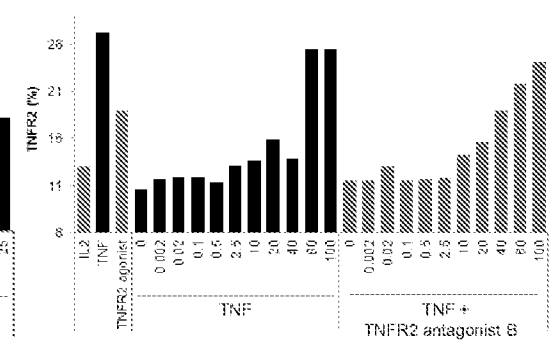


FIG. 15A TNFR2 antagonist

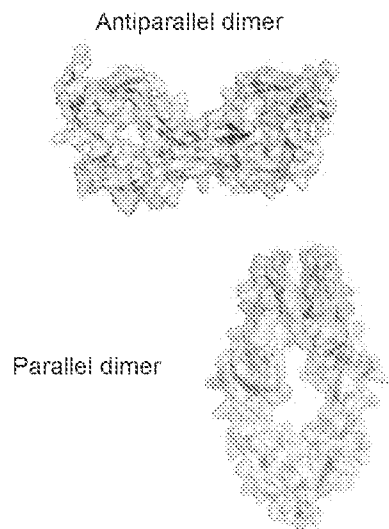


FIG. 15B

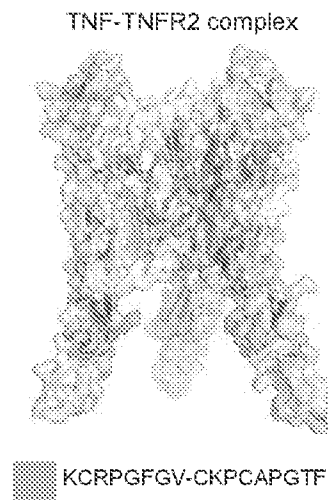


FIG. 15C

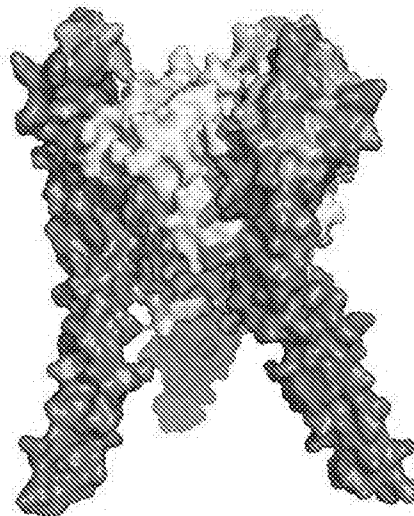


FIG. 16A

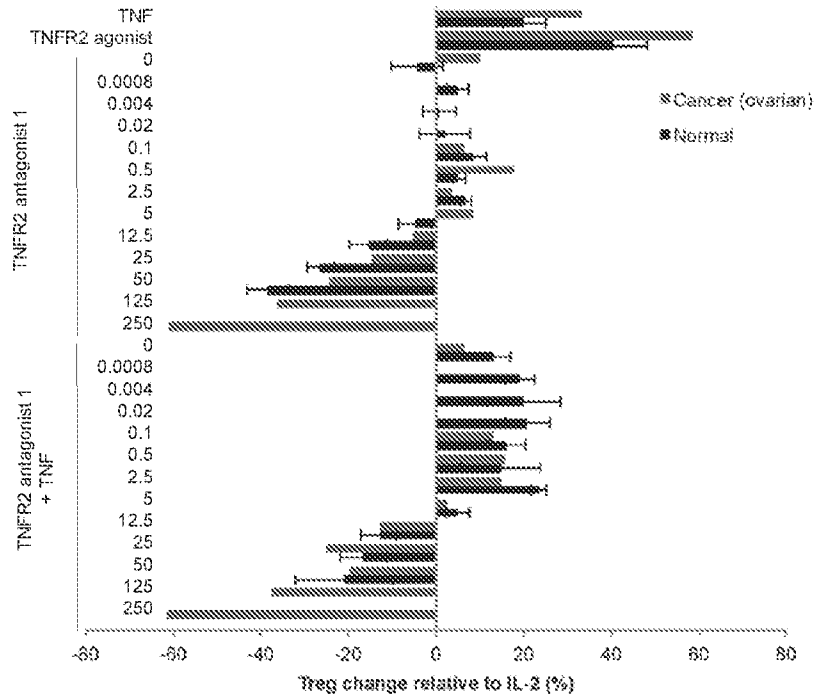


FIG. 16B

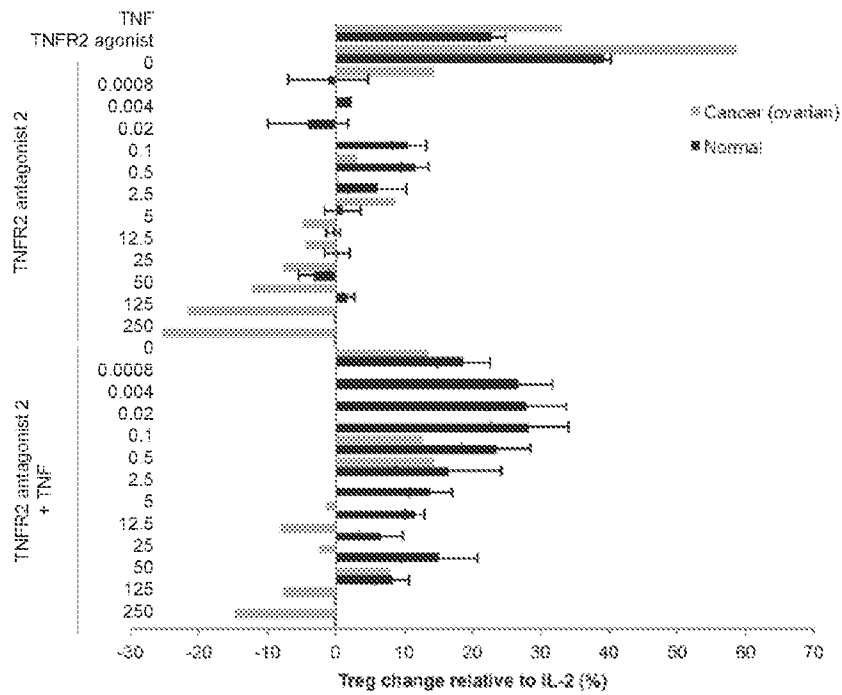


FIG. 17A

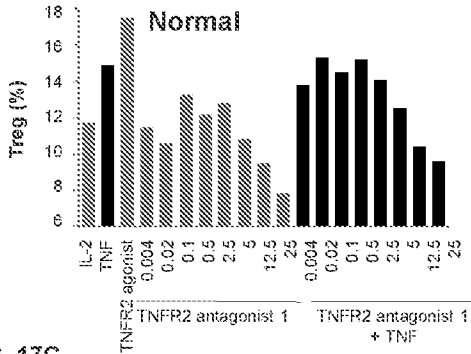


FIG. 17B

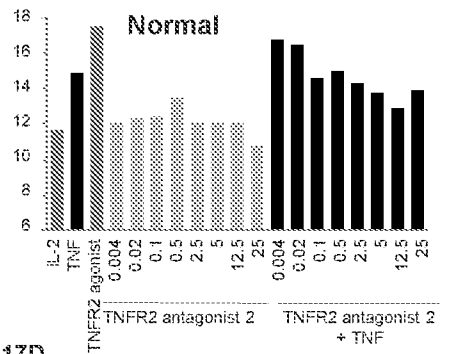


FIG. 17C

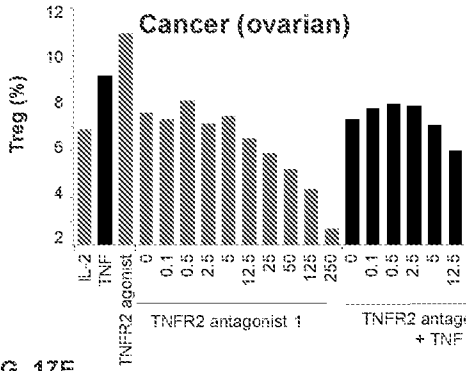


FIG. 17D

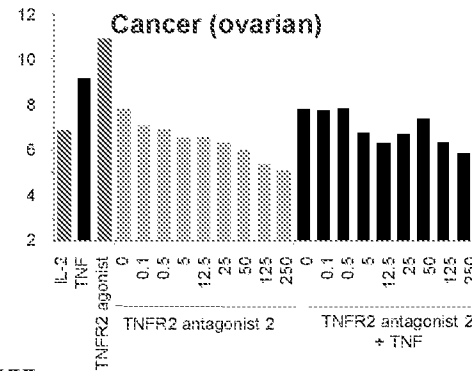


FIG. 17E

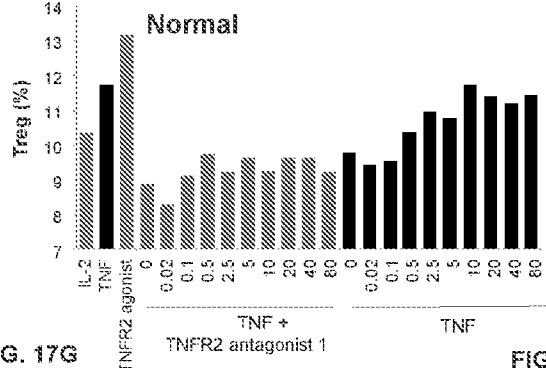


FIG. 17F

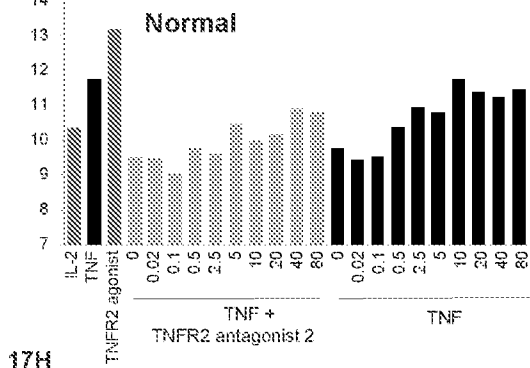


FIG. 17G

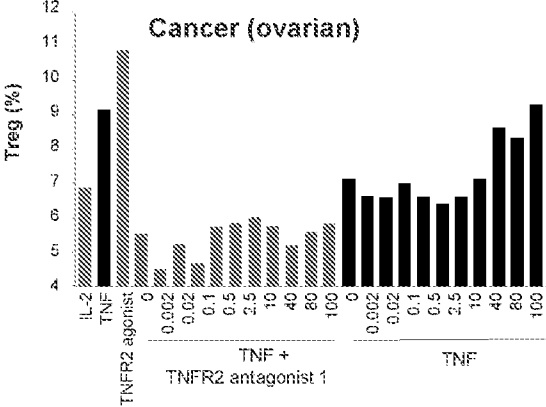


FIG. 17H

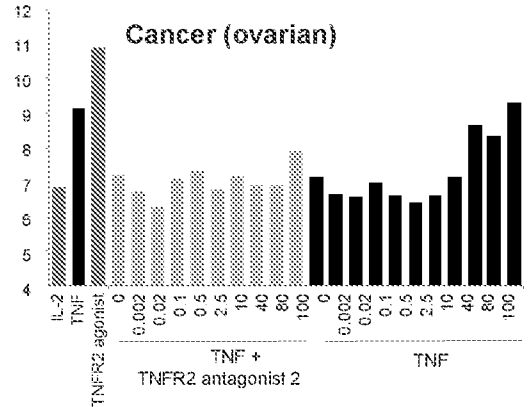


FIG. 18A

	TNFR2 (His tag)	2	3	4	5	6	7	8	9	10	11	12
A	0.7343	0.9569	2.06	1.7819	1.5397	2.0612	0.8179	1.0199	1.7822	1.1389	0.6703	2.0906
B	1.7086	0.5765	2.2819	0.9123	1.1618	1.0948	1.8849	0.95	1.6573	0.8771	0.4532	0.2122
C	0.3583	0.816	1.2101	0.5374	0.9112	2.1387	0.2366	1.5151	0.3053	0.341	0.2533	0.3898
D	0.5325	0.2733	0.4702	0.2977	0.3181	0.2634	0.3614	0.3185	0.3196	0.5459	0.2931	0.2907
E	0.5181	0.3717	0.5661	0.4143	0.1369	0.8391	0.4685	0.745	0.3131	0.1708	0.5585	0.404
F	0.6847	0.4672	0.3838	0.2758								
G												
H												1.8716

FIG. 18B

	1	2	3	4	5	6	7	8	9	10	11	12
A	0.226	0.3604	0.2365	0.2709	0.2178	0.1988	0.2378	0.2385	0.2251	0.1974	0.2979	0.2025
B	0.3087	0.2057	0.4868	0.1475	0.1285	0.1425	0.1656	0.1961	0.1391	0.1808	0.2196	0.2558
C	0.2171	0.2349	0.1375	0.1472	0.2326	0.1352	0.1311	0.1655	0.1519	0.1563	0.1646	0.2771
D	0.2075	0.2673	0.1732	0.1819	0.1323	0.1358	0.2061	0.1869	0.1564	0.1991	0.2613	0.2619
E	0.1988	0.1822	0.2136	0.2245	0.1617	0.1933	0.1256	0.2025	0.1831	0.1962	0.2078	0.2741
F	0.1763	0.22	0.2014	0.17								
G												
H												1.7986

FIG. 18C

	1	2	3	4	5	6	7	8	9	10	11	12
A	0.324	0.2473	0.2073	0.2273	0.2734	0.2517	0.3236	0.2442	0.2119	0.1593	0.2304	0.2337
B	0.3416	0.236	2.0012	0.1759	0.5953	0.1824	0.2086	0.2252	0.1523	0.1589	0.1566	0.2768
C	0.355	0.8769	0.1785	0.2729	0.2231	0.154	0.1569	0.1786	0.229	0.1432	0.1797	0.2439
D	0.2702	0.3636	0.4796	0.2145	0.1934	0.1425	0.223	0.153	0.1538	0.1642	0.1906	0.2612
E	0.3127	0.2553	0.2996	0.246	0.1577	0.1999	0.1385	0.2201	0.1778	0.2028	0.2801	0.2842
F	0.341	0.3486	0.2674	0.244								
G												
H												2.0342

FIG. 19

	1	2	3	4	5	6	7	8	9	10	11	12
A	0.2215	0.2506	0.2203	0.2627	0.2607	0.2515	0.268	0.2216	0.3177	0.2226	0.2251	0.2633
B	0.3336	0.322	0.3683	0.1895	0.1703	0.1842	0.1879	0.195	0.1412	0.1844	0.222	0.3184
C	0.2382	0.2777	0.1823	0.2073	0.2456	0.1422	0.1259	0.2215	0.162	0.1692	0.1689	0.2687
D	0.2953	0.441	0.1721	0.2691	0.1693	0.1505	0.2141	0.1975	0.1914	0.1539	0.2672	0.2721
E	0.249	0.2158	0.2437	0.2626	0.1467	0.2305	0.0986	0.2077	0.1422	0.2387	0.3012	0.4523
F	0.2368	0.2029	0.2802	0.1819								
G												
H												0.8038

FIG. 20

TNFR2A3 dilution factor	Raw luminescence: Target peptide 1	Raw luminescence: Target peptide 2	NMS
1:300	0.829	1.681	0.071
1:900	0.524	1.382	0.089
1:2700	0.306	0.998	0.066
1:8100	0.176	0.524	0.095
1:24300	0.099	0.320	0.093
1:72900	0.142	0.146	0.067
1:218799	0.069	0.116	0.087
BLK	0.059	0.064	0.085

FIG. 21A

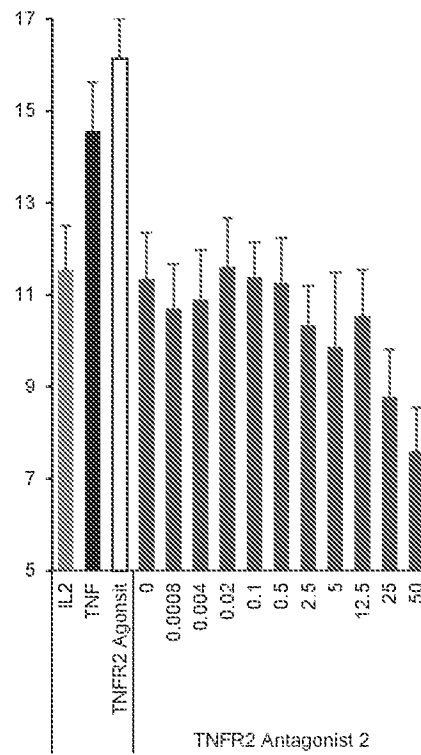


FIG. 21B

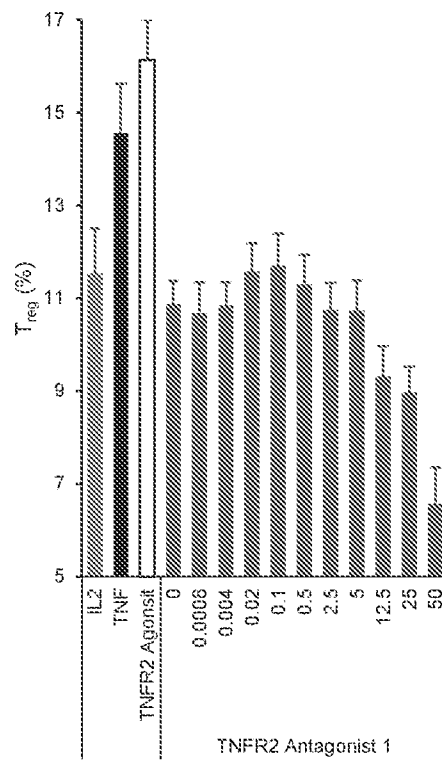




FIG. 21C

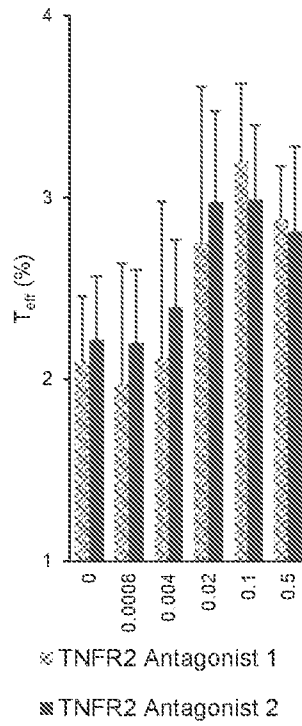


FIG. 21D

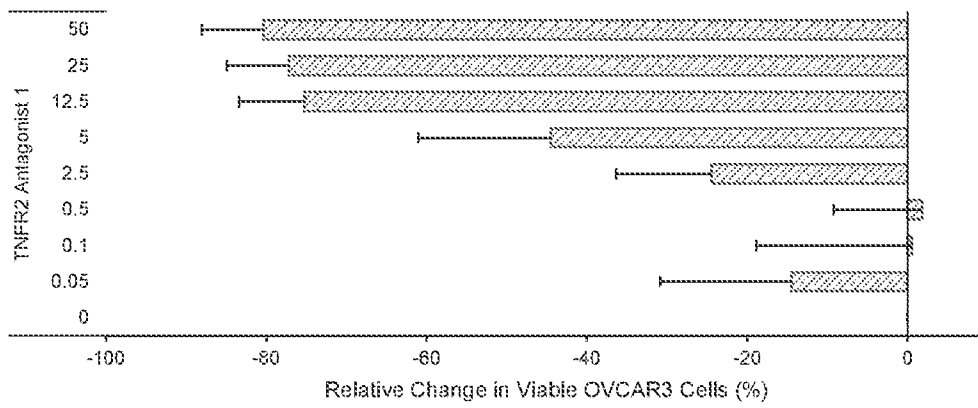


FIG. 22A

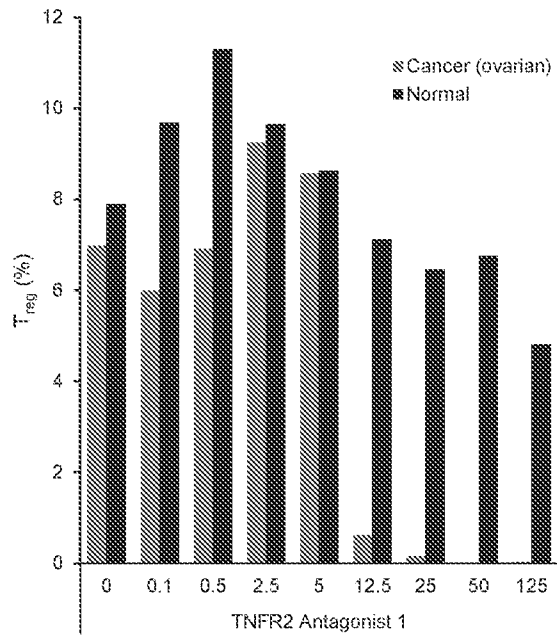


FIG. 22B

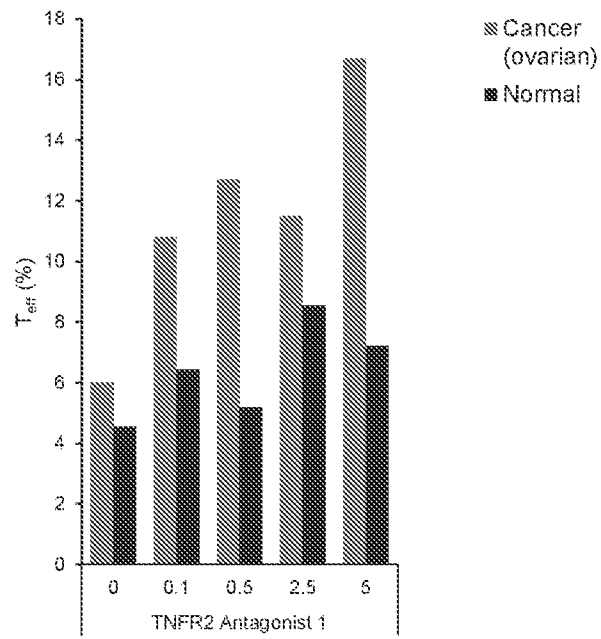


FIG. 23A

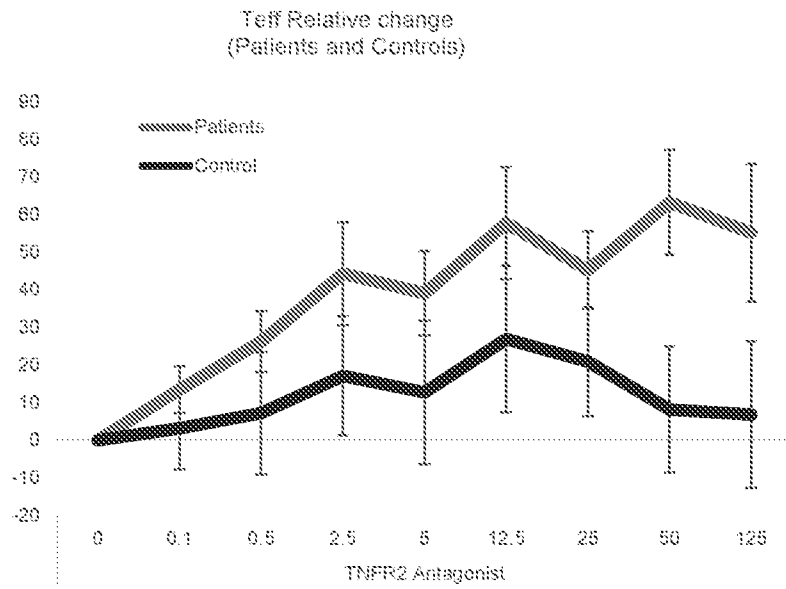


FIG. 23B

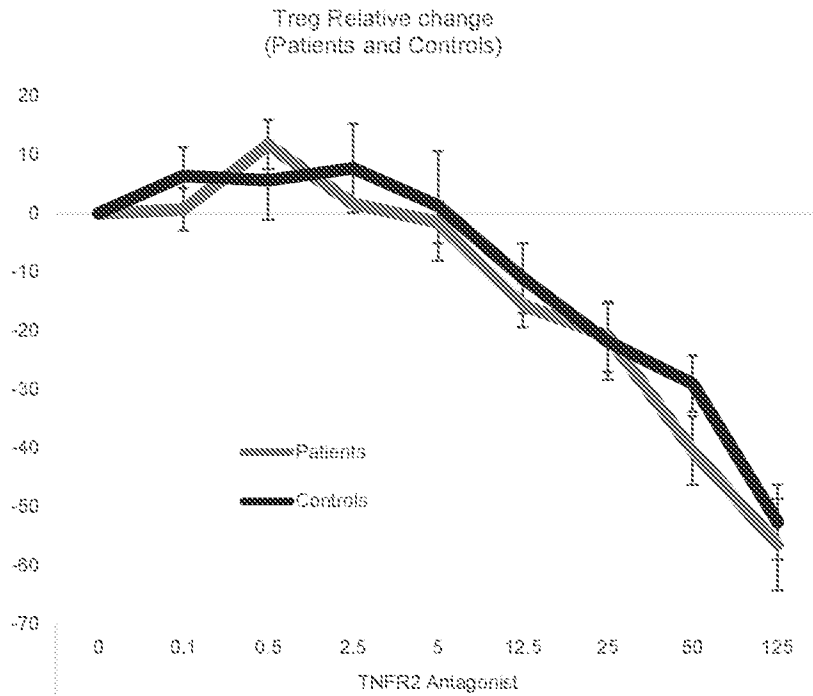


FIG. 23C

